

# Presence of PD-1 similarity genes in monocytes may promote the development of type 1 diabetes mellitus and poor prognosis of pancreatic cancer

Yuquan Huang,<sup>1</sup> Wenchuan Zhang,<sup>1</sup> Can Xu,<sup>1</sup> Qingxia Li,<sup>2</sup> Wu Zhang,<sup>3</sup> Wanfeng Xu,<sup>4</sup> Mingming Zhang 

**To cite:** Huang Y, Zhang W, Xu C, et al. Presence of PD-1 similarity genes in monocytes may promote the development of type 1 diabetes mellitus and poor prognosis of pancreatic cancer. *BMJ Open Diab Res Care* 2023;11:e003196. doi:10.1136/bmjdrc-2022-003196

► Additional supplemental material is published online only. To view, please visit the journal online (<http://dx.doi.org/10.1136/bmjdrc-2022-003196>).

Received 25 October 2022  
Accepted 15 April 2023



© Author(s) (or their employer(s)) 2023. Re-use permitted under CC BY-NC. No commercial re-use. See rights and permissions. Published by BMJ.

<sup>1</sup>Department of Pathology, Shengjing Hospital of China Medical University, Shenyang, Liaoning, China

<sup>2</sup>Department of Oncology, Hebei General Hospital, Shijiazhuang, Hebei, China

<sup>3</sup>Clinical School of Medicine, North China University of Science and Technology, Tangshan, Hebei, China

<sup>4</sup>Department of Endocrinology, Shengjing Hospital of China Medical University, Shenyang, Liaoning, China

**Correspondence to**  
Professor Mingming Zhang;  
mingefg@163.com

## ABSTRACT

**Introduction** To identify proteins and corresponding genes that share sequential and structural similarity with programmed cell death protein-1 (PD-1) in patients with type 1 diabetes mellitus (T1DM) via bioinformatics analysis.

**Research design and methods** All proteins with immunoglobulin V-set domain were screened in the human protein sequence database, and the corresponding genes were obtained in the gene sequence database. GSE154609 was downloaded from the GEO database, which contained peripheral blood CD14+ monocyte samples from patients with T1DM and healthy controls. The difference result and the similar genes were intersected. Analysis of gene ontology and Kyoto encyclopedia of genes and genomes pathways was used to predict potential functions using the R package 'cluster profiler'. The expression differences of intersected genes were analyzed in The Cancer Genome Atlas pancreatic cancer dataset and GTEx database using t-test. The correlation between the overall survival and disease-free progression of patients with pancreatic cancer was analyzed using Kaplan-Meier survival analysis.

**Results** 2068 proteins with immunoglobulin V-set domain similar to PD-1 and 307 corresponding genes were found. 1705 upregulated differentially expressed genes (DEGs) and 1335 downregulated DEGs in patients with T1DM compared with healthy controls were identified. A total of 21 genes were overlapped with the 307 PD-1 similarity genes, including 7 upregulated and 14 downregulated. Of these, mRNA levels of 13 genes were significantly increased in patients with pancreatic cancer. High expression of *MYOM3* and *HHLA2* was significantly correlated with shorter overall survival of patients with pancreatic cancer, while high expression of *FGFRL1*, *CD274*, and *SPEG* was significantly correlated with shorter disease-free survival of patients with pancreatic cancer.

**Conclusions** Genes encoding immunoglobulin V-set domain similar to PD-1 may contribute to the occurrence of T1DM. Of these genes, *MYOM3* and *SPEG* may serve as potential biomarkers for the prognosis of pancreatic cancer.

## INTRODUCTION

Programmed cell death protein-1 (PD-1) belongs to the CD28/CTLA-4 co-receptor family containing a single extracellular immunoglobulin variable (V) domain.<sup>1</sup> PD-L1

## WHAT IS ALREADY KNOWN ON THIS TOPIC

⇒ It is already known that programmed cell death protein-1 plays an important role in the development of type 1 diabetes mellitus (T1DM) and pancreatic cancer.

## WHAT THIS STUDY ADDS

⇒ This study identifies 63 genes corresponding to 483 proteins with immunoglobulin V-set domain and subcellular localization in patients with T1DM, which may contribute to the occurrence of T1DM. In addition, this study identifies potential prognostic biomarkers for pancreatic cancer, including *MYOM3*, *HHLA2*, *FGFRL1*, *CD274*, and *SPEG*, which were found to be significantly correlated with overall survival or disease-free progression of patients with pancreatic cancer.

## HOW THIS STUDY MIGHT AFFECT RESEARCH, PRACTICE OR POLICY

⇒ This study provides new insights into the potential mechanisms underlying T1DM and identifies potential biomarkers for the prognosis of pancreatic cancer. These findings may have implications for future research on the development of novel treatments for T1DM and the identification of prognostic biomarkers for pancreatic cancer. The results of this study could ultimately impact clinical practice and policy by improving patient outcomes through earlier detection and targeted treatment strategies.

is a ligand for PD-1 and is a member of the CD28/B7 family.<sup>2</sup> PD-1 is a critical immune checkpoint protein in human immune cells, which plays an important role in regulating immune responses and maintaining immune homeostasis by interacting with PD-L1.<sup>3</sup> PD-1 deficiency may lead to various autoimmune diseases.<sup>4</sup> Multiple studies have shown that the incidence of type 1 diabetes mellitus (T1DM) is significantly increased in the presence of PD-1 deficiency in pre-diabetic NOD mice.<sup>5</sup> In addition, PD-1/PD-L1 signaling pathway



is also involved in malignant tumorigenesis and immune escape.<sup>6</sup> It has been reported that the occurrence and immune escape of pancreatic cancer are related to the PD-1/PD-L1 pathway.<sup>7</sup> Previous studies have reported upregulation of PD-L1 in human pancreatic cancer samples.<sup>8</sup> It has also been shown that PD-L1 blockers can effectively inhibit pancreatic cancer in mouse models.<sup>9</sup> These results suggest that the PD-1/PD-L1 pathway plays an important role in pancreatic cancer.

Monocytes, the largest type of white blood cells and part of the innate immune system's phagocytic cells, have been shown to play a crucial role in the progression of cancer and autoimmune disorders. They are capable of inducing tumor cell killing via cytokines or phagocytosis induction and involved in the progression and regression of inflammation.<sup>10</sup> Notably, PD-1 expression was found to be elevated in the monocytes of patients with hepatocellular carcinoma and contributed to the suppression of CD8 T cell.<sup>11</sup> Individuals diagnosed with T1DM have been shown to exhibit elevated levels of pro-inflammatory monocytes and circulating inflammatory mediators.<sup>12</sup> The aforementioned evidence indicates that monocytes and PD-1/PD-L1 pathway have become crucial regulators in the progression of cancer and autoimmune diseases.

Given the significance of PD-1 pathway in T1DM and pancreatic cancer and the crucial role of monocytes in the progression of cancer and autoimmune disorders, this study aims to use bioinformatics analysis to identify proteins and their corresponding genes that share structural and sequential similarities with PD-1 in patients with T1DM. These identified proteins and genes could serve as potential targets for further investigation in future studies.

## MATERIALS AND METHODS

**Screening for proteins with similar structures to PD-1 protein**  
Human (GRCh38.p13) genome sequence database, protein sequence database and gene annotation file were downloaded from the National Center for Biotechnology Information ([https://www.ncbi.nlm.nih.gov/genome/?term=txid9606\(orgn\);](https://www.ncbi.nlm.nih.gov/genome/?term=txid9606(orgn);) (protein sequence: [https://ftp.ncbi.nlm.nih.gov/genomes/all/GCF/000/001/405/GCF\\_000001405.39\\_GRCh38.p13/GCF\\_000001405.39\\_GRCh38.p13\\_protein.faa.gz](https://ftp.ncbi.nlm.nih.gov/genomes/all/GCF/000/001/405/GCF_000001405.39_GRCh38.p13/GCF_000001405.39_GRCh38.p13_protein.faa.gz); gene annotation file: [https://ftp.ncbi.nlm.nih.gov/genomes/all/GCF/000/001/405/GCF\\_000001405.39\\_GRCh38.p13\\_genomic.gff.gz](https://ftp.ncbi.nlm.nih.gov/genomes/all/GCF/000/001/405/GCF_000001405.39_GRCh38.p13_genomic.gff.gz); genome sequence file: [https://ftp.ncbi.nlm.nih.gov/genomes/all/GCF/000/001/405/GCF\\_000001405.39\\_GRCh38.p13\\_genomic.fna.gz](https://ftp.ncbi.nlm.nih.gov/genomes/all/GCF/000/001/405/GCF_000001405.39_GRCh38.p13_genomic.fna.gz);

HMMER software: <https://www.ebi.ac.uk/Tools/hmmer/>; Pfam database: <http://Pfam.xfam.org/>; software parameters: –noali -E 1e-5 Pfam-A.hmm).

To identify the immunoglobulin V-set domain of PD-1, we used the Hmmscan program for Pfam annotation and applied a filtering criterion based on an E-value threshold of less than 1e-5.<sup>13</sup> All proteins with immunoglobulin V-set

domain similar to the PD-1 were then screened in human protein sequence database, and the corresponding genes were obtained in gene sequence database.

## Protein subcellular localization analysis

The subcellular distribution and functions of the obtained similar proteins were predicted using the Hum-mPLoc 3.0 database (<http://www.csbio.sjtu.edu.cn/bioinf/hum-mPLoc3/>).<sup>14</sup>

## Identification of differentially expressed genes in patients with T1DM

The GSE154609 dataset<sup>15</sup> containing 12 T1DM samples and 12 healthy controls was downloaded from the GEO database (<https://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE154609>) to identify differentially expressed genes (DEGs) in patients with T1DM using wilcox-test (R language, wilcox.test; R V.4.1.2 (<https://www.r-project.org/>)). Data were visualized using box plots. During comparison, filter according to the upper and lower limit algorithm of the box plot, that is, the upper limit of each group of data was Q3+1.5 IQR, the lower limit was Q1-1.5 IQR (IQR=Q3-Q1). After the difference result ( $p<0.05$ ) was obtained, the similar genes obtained in the first step were intersected. P value less than 0.05 was considered statistically significant.

## Gene ontology and Kyoto encyclopedia of genes and genomes

DEGs were subjected to gene ontology (GO) functional annotation (<http://www.geneontology.org/>) and Kyoto encyclopedia of genes and genomes (KEGG) pathway analysis (<http://www.kegg.jp/>). Statistical analysis of GO and KEGG enrichment data was carried out using the R package ‘cluster profiler’. A p value less than 0.05 was considered statistically significant.

## Prognosis and differential expression analysis in pancreatic cancer

To compare the mRNA levels of the genes related to both T1DM and PD-1 similarity, 179 pancreatic cancer samples and 4 normal pancreatic samples were downloaded from The Cancer Genome Atlas (TCGA) database. To increase the normal control sample size, 167 normal pancreatic samples were downloaded from the GTEx database. Expression differences of intersected genes were analyzed by t-test. Kaplan-Meier survival analysis was performed to assess the correlations of the genes related to both T1DM and PD-1 similarly with the prognosis (overall survival and disease-free progression) of patients with pancreatic cancer. A p value less than 0.05 was considered statistically significant.

## RESULTS

### Identification of proteins sharing sequential and structural similarity with PD-1

According to the structural similarity, the proteins with immunoglobulin V-set domain similar to PD-1 and their corresponding genes were screened in the Pfam

database. We found that 2068 proteins encoded by 307 genes may share structural and functional similarities with PD-1 (online supplemental tables 1–3). However, using the Hum-mPLoc bioinformatics tool, we found that only 483 of these proteins have subcellular localization information, which correspond to 63 genes. Eighty-two were located in the cytoplasm, 348 were located in the cell membrane, 14 were located in the nucleus, and 39 were located in the extracellular region (figure 1A and online supplemental table 4).

### Identification of DEGs in patients with T1DM and enrichment analysis

To identify the genes that might contribute to T1DM occurrence due to analogous pathway of PD-1 in T cells, we sought to find out the genes in the intersection between T1DM-related genes and the 307 genes encoding potential analogs (immunoglobulin V-set domain) of PD-1. In the GSE154609 dataset containing 12 peripheral blood CD14+ monocyte samples of patients with T1DM and 12 healthy controls, we identified 1705 upregulated DEGs and 1335 downregulated DEGs in patients with T1DM compared with healthy controls (online supplemental table 5). Among these DEGs, a total of 21 genes (figure 1B) were overlapped with the 307 PD-1 homologues, including 7 upregulated (figure 1C) and 14 downregulated (figure 1D) genes (online supplemental tables 6 and 7). The 1705 upregulated and 1335 downregulated DEGs were further subjected to GO annotation and KEGG pathway analysis. These genes were mainly annotated as receptor complex, external side of plasma membrane, and M band (figure 2A and online supplemental table 8). KEGG pathway analysis revealed that these genes were mostly enriched in the prostate cancer, central carbon metabolism in cancer, and EGFR tyrosine kinase inhibitor resistance pathways (figure 2B and online supplemental table 9).

### T1DM-related genes are highly expressed in pancreatic cancer and associated with the prognosis of pancreatic cancer

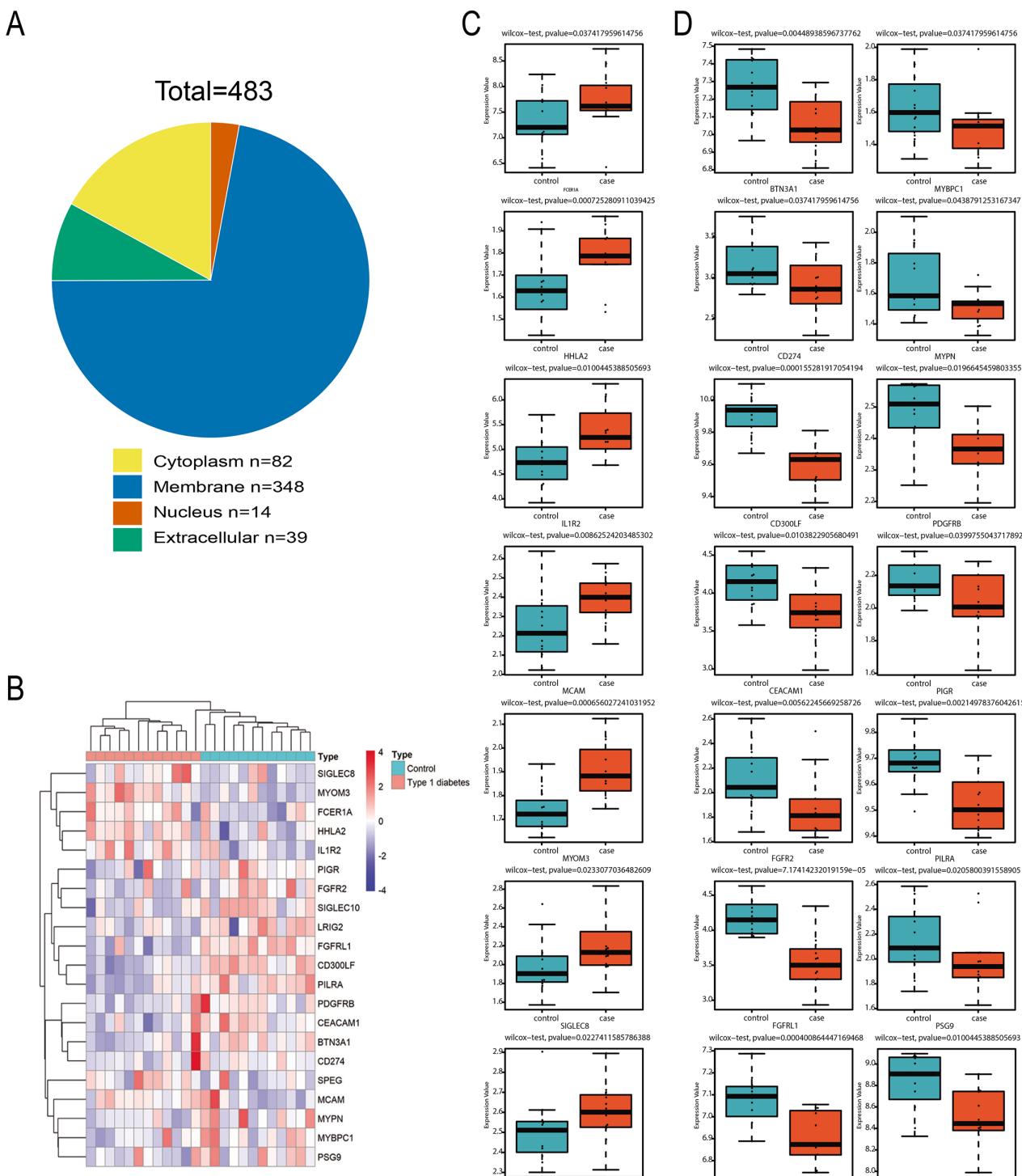
To investigate the clinical significance of the 21 common genes related to both both T1DM and PD-1 similarity, we compared their mRNA levels between pancreatic cancer tissue samples ( $n=179$ ) from the TCGA database and normal tissue samples from TCGA database ( $n=4$ ) and GTEx database ( $n=167$ ). As shown in figure 3A, compared with those in normal controls, the mRNA levels of *SIGLEC10*, *SPEG*, *BTN3A1*, *CD300LF*, *CEACAM1*, *FCER1A*, *HHLA2*, *IL1R2*, *MCAM*, *MYOM3*, *PDGFRB*, *PIGR*, and *PILRA* were significantly increased in patients with pancreatic cancer. Furthermore, high expression of *MYOM3* and *HHLA2* was significantly correlated with shorter overall survival of patients with pancreatic cancer (figure 3B) and that high expression of *FGFRL1*, *CD274*, and *SPEG* was significantly correlated with shorter disease-free survival of patients with pancreatic cancer (figure 3C). These results suggest that these genes may

serve as risk factors for T1DM onset and prognostic factors in patients with pancreatic cancer.

### DISCUSSION

PD-1 is a member of the CD28/CTLA-4 co-receptor family, sharing 25% sequence identity. It is recognized as a type I membrane protein possessing a singular extracellular immunoglobulin V domain.<sup>16</sup> PD-1 and PD-L1 interact using their V domains A'GFCC' β-sheets to form a pair of V domains in an Fv-like structure, similar to the V domains of antibodies, T cell receptors, or Fv paired (TCR) and CD8 to function.<sup>17</sup> Due to its significant involvement in the regulation of peripheral tolerance, a lack of PD-1 may contribute to the development of multiple autoimmune diseases.<sup>18</sup> Multiple studies have shown the presence of PD-1 deficiency in pre-diabetic NOD mice significantly increases the incidence of T1DM.<sup>19 20</sup> Antibodies specific for PD-1 or PD-L1 but not PD-L2 accelerate insulitis in NOD mice, and also induce T1DM within 10 days.<sup>21 22</sup> Not only do T cells act through the PD-1 pathway, but our study found that through gene encoding, a functionally similar protein was also present in peripheral blood mononuclear cells of T1DM.

The study found that islet macrophages (derived from monocytes) are located near blood vessels, and they communicate with cellular and acellular components of the blood through filopodia that extend into the vascular lumen. They also interact with β-cells to capture insulin and deliver it to self-reactive T cells, which are essential for immune responses.<sup>23</sup> This led us to wonder if monocytes could play the same role. On the one hand, multiple studies have shown that diabetes, through high blood glucose levels, alters monocyte/macrophage metabolism, leading to failure of innate immune and inflammatory processes, and dysregulation of macrophage-specific signal transduction.<sup>24–26 24</sup> On the other hand, Ying *et al* found that macrophages can protect and aggravate T1DM by increasing islet inflammation and affecting β-cell proliferation.<sup>25</sup> However, whether monocytes/macrophages affect T1DM through the PD-1 pathway has not been studied. Therefore, this aspect of research may be a direction in the future. Although the mechanisms of immune checkpoint inhibitor (ICI)-induced T1DM remain unclear, studies have linked the onset of T1DM with autoimmune responses.<sup>26</sup> Because the pathogenesis of ICI-induced T1DM is the same as that of T1DM, the PD-1 pathway may be blocked. In addition, epidemiological studies have suggested a close relationship between diabetes mellitus and pancreatic cancer.<sup>27</sup> Some researchers even suggest that new-onset diabetes may be an early manifestation of pancreatic cancer, which provides important clues for the early diagnosis of pancreatic cancer.<sup>28</sup> Meanwhile, several studies have reported that diabetes mellitus affects the prognosis of patients with pancreatic cancer.<sup>29</sup> However, the underlying molecular mechanism is still unclear. It is worth mentioning that pancreatic cancer evades the immune response by

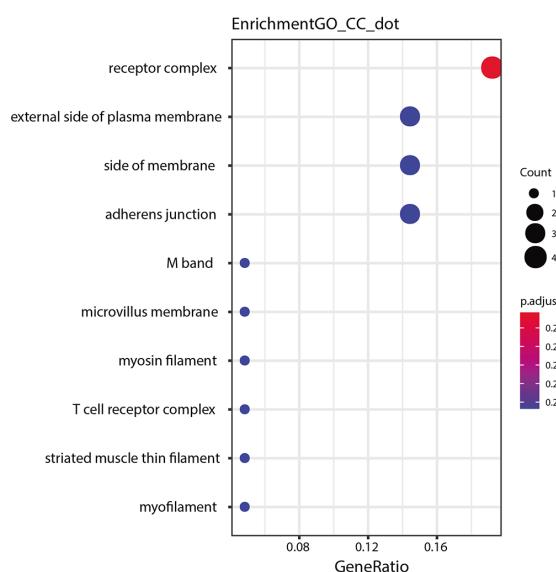


**Figure 1** Identification of differentially expressed genes (DEGs) in patients with type 1 diabetes mellitus (T1DM) compared with healthy controls. (A) Hum-mPLoc bioinformatics analysis was performed to predict the localization of proteins sharing sequential and structural similarity with programmed cell death protein-1. (B) The GSE154609 dataset containing 12 T1DM samples and 12 healthy controls was obtained from the GEO database (<https://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE154609>). The heat map shows 21 DEGs in patients with T1DM compared with healthy controls. (C) Box plots of seven significantly upregulated genes in diabetic samples. (D) Box plots of 14 significantly downregulated genes in diabetic samples.

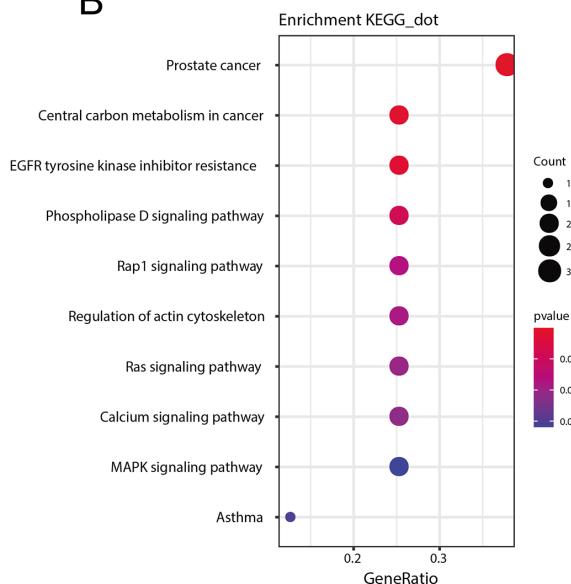
inducing the development of immunosuppressive T cells, thereby blocking the PD-1 pathway.<sup>8</sup> Based on the role of PD-1/PD-L1 pathway in T1DM and pancreatic cancer, in this article, we discuss these two diseases together.

In this study, we aimed to identify proteins and the corresponding genes sharing sequential and structural similarity with PD-1 in T1DM. We found 21 genes associated with both T1DM and PD-1 similarity which were

A



B

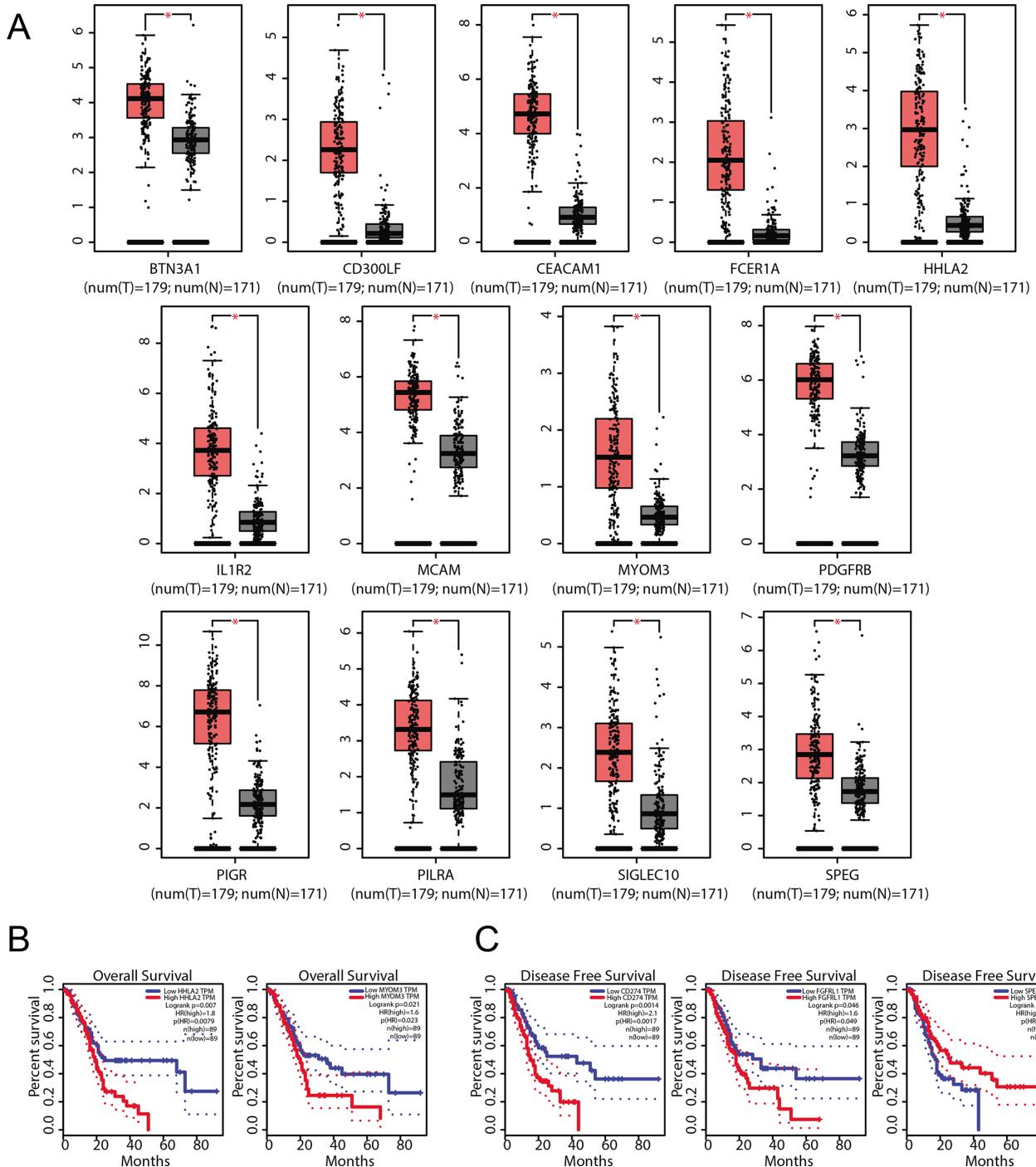


**Figure 2** Functional enrichment analysis of DEGs in patients with T1DM. A total of 985 upregulated genes and 1253 downregulated genes in patients with T1DM were subjected to gene ontology (GO) functional annotation (<http://www.geneontology.org/>) and Kyoto encyclopedia of genes and genomes (KEGG) pathway analysis (<http://www.kegg.jp/>). (A) Scatter plot (left) and directed acyclic graph (right) for GO term enrichment analysis. Rectangular nodes represent GO terms; oval nodes represent biological processes; yellow indicates  $p < 0.05$ ; red indicates  $p < 0.01$ . (B) A dot plot for KEGG enrichment analysis. Gene ratio=the numbers of DEGs annotated in a specific pathway/the numbers of all genes annotated. Top 10 pathway terms enriched are displayed in the figure. DEGs, differentially expressed genes; T1DM, type 1 diabetes mellitus.

screened from peripheral blood CD14+ monocyte samples of patients with T1DM. We identified 7 upregulated and 14 downregulated genes, out of which 13 genes, including *BTN3A1* and *CEACAM1*, were significantly upregulated in pancreatic cancer. High expression of *MYOM3*, *HHLA2*, *FGFRL1* and *CD274* and low expression of *SPEG* were significantly associated with poor prognosis of patients with pancreatic cancer. These genes may also be potential risk factors for T1DM and prognostic

factors for pancreatic cancer, and may serve as potential biomarkers for PD-1 inhibitor-induced T1DM.

Consistent with our results, previous researches have linked several genes to cancer, diabetes, and immune checkpoint pathways. For instance, *SIGLEC10*, a member of the Siglec family, is involved in the modulation of immune tolerance and is associated with the pathogenesis of autoimmune diseases, inflammatory reactions, and tumors.<sup>30,31</sup> Therapeutic drugs targeting Siglec antibodies



**Figure 3** The expression of T1DM-related genes in pancreatic cancer and the association with the prognosis of patients. The clinical characteristics and mRNA levels of the 21 T1DM-related genes of 179 patients with pancreatic cancer were collected from the TCGA database. The same information of healthy controls was collected from the TCGA database ( $n=4$ ) and GTEx database ( $n=167$ ). (A) The mRNA levels of *SIGLEC10*, *SPEG*, *BTN3A1*, *CD300LF*, *CEACAM1*, *FCER1A*, *HHLA2*, *IL1R2*, *MCAM*, *MYOM3*, *PDGFRB*, *PIGR*, and *PILRA* were compared between patients with pancreatic cancer and healthy controls. (B,C) Patients with pancreatic cancer were classified into low-expression and high-expression groups according to the mRNA levels of each DEG. Kaplan-Meier survival analysis was performed to assess the association of each DEG with the overall survival (B) and disease-free survival (C) of patients with pancreatic cancer. DEG, differentially expressed gene; T1DM, type 1 diabetes mellitus; TCGA, The Cancer Genome Atlas.

or glycosylation ligands have been developed and used in the treatment of various Siglec-associated diseases.<sup>32</sup> Additionally, butyrophilin (BTN) and butyrophilin-like (BTNL) families have been found to participate in the

progression of inflammatory diseases and tumors by modulating antigen-specific responses of  $\alpha\beta$ T and  $\gamma\delta$ T cells.<sup>33</sup> This suggests that targeting *SIGLEC10* through immunotherapy may hold promise for treating certain

diseases. Additionally, the extracellular domains of BTN and BTNL molecules share a structural similarity with the B7 family of co-stimulatory ligands, which includes PD-L1, B7-H3, and B7-H4. Consequently, BTN and BTNL are classified as members of this family.<sup>34</sup> Studies have shown that these families can play a role in the progression of inflammatory diseases and tumors by modulating the antigen-specific responses of  $\alpha\beta$ T and  $\gamma\delta$ -T cells.<sup>35 36</sup> For example, anti-BTN3A antibodies have shown efficacy in acute myeloid leukemia and pancreatic cancer both in vitro and in vivo.<sup>37</sup> *BTN3A1* homolog *BTN3A2* is related to gastric cancer and T1DM.<sup>38</sup> Carcinoembryonic antigen-related cell adhesion molecule 1 (*CEACAM1*), a glycoprotein belonging to the carcinoembryonic antigen cell family, plays a crucial role in tumor progression, immune regulation, and inflammation.<sup>39 40</sup> Additionally, *CEACAM1* is a crucial molecule in insulin signaling and metabolism.<sup>41</sup> Given its diverse functions, *CEACAM1* has the potential to emerge as a significant therapeutic target for both autoimmune disorders and cancer treatment in the future. *HHLA2* is a newly identified immune checkpoint protein that is rarely expressed in normal pancreatic tissue but widely expressed in pancreatic cancer lesions.<sup>42</sup> Several studies have highlighted a strong correlation between *HHLA2* expression and poor clinical outcomes in various types of cancer, including pancreatic cancer.<sup>42 43</sup> Furthermore, the inhibitory effects of *HHLA2* on CD4 and CD8 T cell activity suggest that targeting *HHLA2* could be a promising approach for the treatment of cancer and autoimmune disorders.<sup>44</sup> *IL1R2*, an interleukin-1 receptor family member, acts as a decoy receptor that competitively binds to IL1 $\beta$ , inhibiting its interaction with *IL1R1* and thereby impeding IL1 $\beta$  signaling in inflammatory conditions.<sup>45</sup> Overexpression of *IL1R2* has been associated with various cancers, as well as conditions such as arthritis, Alzheimer's disease, and diabetes.<sup>46</sup> *CD146*, also known as melanoma cell adhesion molecule (*MCAM*), shares homology with multiple cell adhesion molecules.<sup>47</sup> It is involved in critical biological processes such as signal transduction, cell migration, angiogenesis, and immune response.<sup>48</sup> Several investigations have reported a marked increase in CD146 $^+$  T cells at sites of inflammation in patients with autoimmune disorders.<sup>49</sup> In addition, our study identified potential new candidate genes, such as *MYOM3* and *SPEG*, that have not been associated with cancer and diabetes, and may serve as new potential candidates for future studies.

However, it is important to note the limitations of our study. First, whether monocytes can play a role in the PD-1 pathway of T cells, there is no relevant research, and further experiments are needed to verify our findings. Second, our samples were obtained from databases and may not fully represent the population characteristics in other regions.

Monocytes are known to interact with T cells to perform functions, such as in tuberculosis disease.<sup>50</sup> However, there is limited research on whether monocytes are also involved in the development of T1DM, pancreatic cancer

and ICI-induced fulminant T1DM through the PD-1 pathway. Here, we investigated whether monocytes would play a similar role to T cells and sought to identify the genes involved.

## CONCLUSIONS

In this study, we find the presence of PD-1 similarity genes in monocytes in patients with T1DM. These 21 similarity genes encode immunoglobulin V-set domain similar to PD-1. Our results suggest that these genes can promote the development of T1DM and contribute to the poor prognosis of pancreatic cancer.

**Acknowledgements** The authors acknowledge Zhiming Ma from the University of California, San Francisco, for editing the English text of this article.

**Contributors** ZM acted as the guarantor to design and supervise the study as well as revise the manuscript. Conceptualization—MZ. Methodology—CX and YH. Software—WenchuanZ. Formal analysis—YH. Investigation—CX. Resources—MZ. Data curation—YH, WenchuanZ and QL. Writing (original draft preparation)—YH, QL and WuZ. Writing (review and editing)—MZ and CX. Supervision—MZ. Project administration—MZ. Funding acquisition—MZ. All authors have read and agreed to the published version of the manuscript.

**Funding** This study was funded by the National Natural Science Foundation of China (grant no. 81773108).

**Disclaimer** The funders had no role in study design, data collection and analysis, decision to publish, or preparation of the manuscript.

**Competing interests** None declared.

**Patient consent for publication** Not required.

**Ethics approval** Not applicable.

**Provenance and peer review** Not commissioned; externally peer reviewed.

**Data availability statement** Data are available in a public, open access repository.

**Supplemental material** This content has been supplied by the author(s). It has not been vetted by BMJ Publishing Group Limited (BMJ) and may not have been peer-reviewed. Any opinions or recommendations discussed are solely those of the author(s) and are not endorsed by BMJ. BMJ disclaims all liability and responsibility arising from any reliance placed on the content. Where the content includes any translated material, BMJ does not warrant the accuracy and reliability of the translations (including but not limited to local regulations, clinical guidelines, terminology, drug names and drug dosages), and is not responsible for any error and/or omissions arising from translation and adaptation or otherwise.

**Open access** This is an open access article distributed in accordance with the Creative Commons Attribution Non Commercial (CC BY-NC 4.0) license, which permits others to distribute, remix, adapt, build upon this work non-commercially, and license their derivative works on different terms, provided the original work is properly cited, appropriate credit is given, any changes made indicated, and the use is non-commercial. See: <http://creativecommons.org/licenses/by-nc/4.0/>.

## ORCID iD

Mingming Zhang <http://orcid.org/0000-0002-5348-493X>

## REFERENCES

- 1 Okazaki T, Honjo T. PD-1 and PD-1 ligands: from discovery to clinical application. *Int Immunopharmacol* 2007;19:813–24.
- 2 Sun C, Mezzadra R, Schumacher TN. Regulation and function of the PD-L1 checkpoint. *Immunity* 2018;48:434–52.
- 3 Dermani FK, Samadi P, Rahmani G, et al. PD-1/PD-L1 immune checkpoint: potential target for cancer therapy. *J Cell Physiol* 2019;234:1313–25.
- 4 Sharpe AH, Freeman GJ. The B7-CD28 superfamily. *Nat Rev Immunol* 2002;2:116–26.
- 5 Jiang F, Yoshida T, Nakaki F, et al. Identification of QTLs that modify peripheral neuropathy in NOD.H2B-pcdc1 $^{-/-}$  mice. *Int Immunopharmacol* 2009;21:499–509.



- 6 Iwai Y, Ishida M, Tanaka Y, et al. Involvement of PD-L1 on tumor cells in the escape from host immune system and tumor immunotherapy by PD-L1 blockade. *Proc Natl Acad Sci U S A* 2002;99:12293–7.
- 7 Ma Y, Li J, Wang H, et al. Combination of PD-1 inhibitor and OX40 agonist induces tumor rejection and immune memory in mouse models of pancreatic cancer. *Gastroenterology* 2020;159:306–19.
- 8 Geng L, Huang D, Liu J, et al. B7-H1 up-regulated expression in human pancreatic carcinoma tissue associates with tumor progression. *J Cancer Res Clin Oncol* 2008;134:1021–7.
- 9 Okudaira K, Hokari R, Tsuzuki Y, et al. Blockade of B7-H1 or B7-DC induces an anti-tumor effect in a mouse pancreatic cancer model. *Int J Oncol* 2009;35:741–9.
- 10 Olingy CE, Dinh HQ, Hedrick CC. Monocyte heterogeneity and functions in cancer. *J Leukoc Biol* 2019;106:309–22.
- 11 Yun J, Yu G, Hu P, et al. PD-1 expression is elevated in monocytes from hepatocellular carcinoma patients and contributes to CD8 T cell suppression. *Immunol Res* 2020;68:436–44.
- 12 Devaraj S, Dasu MR, Rockwood J, et al. Increased toll-like receptor (TLR) 2 and TLR4 expression in monocytes from patients with type 1 diabetes: further evidence of a proinflammatory state. *J Clin Endocrinol Metab* 2008;93:578–83.
- 13 El-Gebali S, Mistry J, Bateman A, et al. The Pfam protein families database in 2019. *Nucleic Acids Res* 2019;47:D427–32.
- 14 Zhou H, Yang Y, Shen H-B, et al. Hum-Mploc 3.0: prediction enhancement of human protein subcellular localization through modeling the hidden correlations of gene ontology and functional domain features. *Bioinformatics* 2017;33:843–53.
- 15 Thiem K, van Dierendonck XAMH, Janssen AWM, et al. A high glycemic burden relates to functional and metabolic alterations of human monocytes in patients with type 1 diabetes. *Diabetes* 2020;69:2735–46.
- 16 Hui E, Cheung J, Zhu J, et al. T cell costimulatory receptor CD28 is a primary target for PD-1-mediated inhibition. *Science* 2017;355:1428–33.
- 17 Lin DY-W, Tanaka Y, Iwasaki M, et al. The PD-1/PD-L1 complex resembles the antigen-binding Fv domains of antibodies and T cell receptors. *Proc Natl Acad Sci U S A* 2008;105:3011–6.
- 18 Gremese E, Alivernini S, Ferraccioli ES, et al. Checkpoint inhibitors (CPI) and autoimmune chronic inflammatory diseases (ACIDs): tolerance and loss of tolerance in the occurrence of immuno-rheumatologic manifestations. *Clin Immunol* 2020;214:108395.
- 19 Quandt Z, Young A, Anderson M. Immune checkpoint inhibitor diabetes mellitus: a novel form of autoimmune diabetes. *Clin Exp Immunol* 2020;200:131–40.
- 20 Kyriacou A, Melson E, Chen W, et al. Is immune checkpoint inhibitor-associated diabetes the same as fulminant type 1 diabetes mellitus? *Clin Med (Lond)* 2020;20:417–23.
- 21 Ansari MJ, Salama AD, Chitnis T, et al. The programmed death-1 (PD-1) pathway regulates autoimmune diabetes in nonobese diabetic (NOD) mice. *J Exp Med* 2003;198:63–9.
- 22 Wang J, Yoshida T, Nakaki F, et al. Establishment of NOD-pdcd1<sup>-/-</sup> mice as an efficient animal model of type 1 diabetes. *Proc Natl Acad Sci U S A* 2005;102:11823–8.
- 23 Calderon B, Carrero JA, Miller MJ, et al. Cellular and molecular events in the localization of diabetogenic T cells to islets of Langerhans. *Proc Natl Acad Sci USA* 2011;108:1561–6.
- 24 Ayala TS, Tessaro FHG, Jannuzzi GP, et al. High glucose environments interfere with bone marrow-derived macrophage inflammatory mediator release, the TLR4 pathway and glucose metabolism. *Sci Rep* 2019;9:11447.
- 25 Ying W, Lee YS, Dong Y, et al. Expansion of islet-resident macrophages leads to inflammation affecting β cell proliferation and function in obesity. *Cell Metab* 2019;29:457–74.
- 26 Kotwal A, Haddox C, Block M, et al. Immune checkpoint inhibitors: an emerging cause of insulin-dependent diabetes. *BMJ Open Diabetes Res Care* 2019;7:e000591.
- 27 Pannala R, Leirness JB, Bamlet WR, et al. Prevalence and clinical profile of pancreatic cancer-associated diabetes mellitus. *Gastroenterology* 2008;134:981–7.
- 28 Pannala R, Basu A, Petersen GM, et al. New-onset diabetes: a potential clue to the early diagnosis of pancreatic cancer. *Lancet Oncol* 2009;10:88–95.
- 29 Cannon RM, LeGrand R, Chagpar RB, et al. Multi-institutional analysis of pancreatic adenocarcinoma demonstrating the effect of diabetes status on survival after resection. *HPB* 2012;14:228–35.
- 30 Stanczak MA, Siddiqui SS, Trefny MP, et al. Self-associated molecular patterns mediate cancer immune evasion by engaging siglecs on T cells. *J Clin Invest* 2018;128:4912–23.
- 31 van de Wall S, Santegoets KCM, van Houtum EJH, et al. Sialoglycans and siglecs can shape the tumor immune microenvironment. *Trends Immunol* 2020;41:274–85.
- 32 Wang J, Sun J, Liu LN, et al. Siglec-15 as an immune suppressor and potential target for normalization cancer immunotherapy. *Nat Med* 2019;25:656–66.
- 33 Barkal AA, Brewer RE, Markovic M, et al. CD24 signalling through macrophage Siglec-10 is a target for cancer immunotherapy. *Nature* 2019;572:392–6.
- 34 Rhodes DA, Reith W, Trowsdale J. Regulation of immunity by butyrophilins. *Annu Rev Immunol* 2016;34:151–72.
- 35 Vavassori S, Kumar A, Wan GS, et al. Butyrophilin 3A1 binds phosphorylated antigens and stimulates human γδ T cells. *Nat Immunol* 2013;14:908–16.
- 36 Payne KK, Mine JA, Biswas S, et al. BTN3A1 governs antitumor responses by coordinating αβ and γδ T cells. *Science* 2020;369:942–9.
- 37 Blazquez J-L, Benyamine A, Pasero C, et al. New insights into the regulation of γδ T cells by BTN3A and other btn/btnl in tumor immunity. *Front Immunol* 2018;9:1601.
- 38 Zhu M, Yan C, Ren C, et al. Exome array analysis identifies variants in SPOCD1 and BTN3A2 that affect risk for gastric cancer. *Gastroenterology* 2017;152:2011–21.
- 39 Beauchemin N, Arabzadeh A. Carcinoembryonic antigen-related cell adhesion molecules (CEACAMs) in cancer progression and metastasis. *Cancer Metastasis Rev* 2013;32:643–71.
- 40 Huang Y-H, Zhu C, Kondo Y, et al. CEACAM1 regulates TIM-3-mediated tolerance and exhaustion. *Nature* 2015;517:386–90.
- 41 Poy MN, Yang Y, Rezaei K, et al. CEACAM1 regulates insulin clearance in liver. *Nat Genet* 2002;30:270–6.
- 42 Yan H, Qiu W, Koehne de Gonzalez AK, et al. HHLA2 is a novel immune checkpoint protein in pancreatic ductal adenocarcinoma and predicts post-surgical survival. *Cancer Letters* 2019;442:333–40.
- 43 Zhou Q-H, Li K-W, Chen X, et al. HHLA2 and PD-L1 co-expression predicts poor prognosis in patients with clear cell renal cell carcinoma. *J Immunother Cancer* 2020;8:e000157.
- 44 Zhao R, Chinai JM, Buhl S, et al. HHLA2 is a member of the B7 family and inhibits human CD4 and CD8 T-cell function. *Proc Natl Acad Sci U S A* 2013;110:9879–84.
- 45 Molgora M, Supino D, Mantovani A, et al. Tuning inflammation and immunity by the negative regulators IL-1R2 and IL-1R8. *Immunol Rev* 2018;281:233–47.
- 46 Peters VA, Joesting JJ, Freund GG. IL-1 receptor 2 (IL-1R2) and its role in immune regulation. *Brain Behav Immun* 2013;32:1–8.
- 47 Johnson JP, Rothbächer U, Sers C. The progression associated antigen MUC18: a unique member of the immunoglobulin supergene family. *Melanoma Res* 1993;3:337–40.
- 48 Wang Z, Yan X. CD146, a multi-functional molecule beyond adhesion. *Cancer Letters* 2013;330:150–62.
- 49 Dagur PK, McCoy JP. Endothelial-binding, proinflammatory T cells identified by MCAM (CD146) expression: characterization and role in human autoimmune diseases. *Autoimmun Rev* 2015;14:415–22.
- 50 Habtamu M, Abrahamsen G, Aseffa A, et al. High-throughput analysis of T cell-monocyte interaction in human tuberculosis. *Clin Exp Immunol* 2020;201:187–99.

ONTOLOGY	ID	GeneRatio	BgRatio	pvalue	p. adjust	qvalue
BP	GO:0002768	5/21	344/11512	0.0003173	0.210148357	0.172136927
BP	GO:0032692	2/21	23/11512	0.0007836	0.210148357	0.172136927
BP	GO:0055003	2/21	24/11512	0.0008539	0.210148357	0.172136927
BP	GO:0002764	5/21	477/11512	0.001402	0.210148357	0.172136927
BP	GO:0042692	4/21	289/11512	0.0016612	0.210148357	0.172136927
BP	GO:0050798	2/21	34/11512	0.0017166	0.210148357	0.172136927
BP	GO:0050852	3/21	175/11512	0.0037545	0.210148357	0.172136927
BP	GO:0048008	2/21	51/11512	0.0038292	0.210148357	0.172136927
BP	GO:0048738	3/21	181/11512	0.0041274	0.210148357	0.172136927
BP	GO:0010518	2/21	53/11512	0.0041294	0.210148357	0.172136927
BP	GO:0055008	2/21	59/11512	0.0050937	0.210148357	0.172136927
BP	GO:0060193	2/21	61/11512	0.005436	0.210148357	0.172136927
BP	GO:0010517	2/21	62/11512	0.0056111	0.210148357	0.172136927
BP	GO:0030239	2/21	63/11512	0.0057887	0.210148357	0.172136927
BP	GO:0050851	3/21	214/11512	0.0065799	0.210148357	0.172136927
BP	GO:0055013	2/21	69/11512	0.006908	0.210148357	0.172136927
BP	GO:0060415	2/21	69/11512	0.006908	0.210148357	0.172136927
BP	GO:0001570	2/21	70/11512	0.0071034	0.210148357	0.172136927
BP	GO:0001525	4/21	439/11512	0.0074513	0.210148357	0.172136927
BP	GO:0032652	2/21	72/11512	0.0075017	0.210148357	0.172136927
BP	GO:0055006	2/21	73/11512	0.0077045	0.210148357	0.172136927
BP	GO:0048644	2/21	74/11512	0.0079099	0.210148357	0.172136927
BP	GO:1903035	2/21	78/11512	0.0087559	0.210148357	0.172136927
BP	GO:0070372	3/21	238/11512	0.0088131	0.210148357	0.172136927
BP	GO:0032612	2/21	80/11512	0.0091935	0.210148357	0.172136927
BP	GO:0048661	2/21	81/11512	0.0094159	0.210148357	0.172136927
BP	GO:0042060	4/21	473/11512	0.0096526	0.210148357	0.172136927
BP	GO:0060191	2/21	84/11512	0.0100976	0.210148357	0.172136927
BP	GO:0070371	3/21	253/11512	0.0104104	0.210148357	0.172136927
BP	GO:0010927	2/21	96/11512	0.0130363	0.210148357	0.172136927
BP	GO:0032526	2/21	97/11512	0.0132962	0.210148357	0.172136927
BP	GO:0032102	3/21	279/11512	0.013558	0.210148357	0.172136927
BP	GO:0055007	2/21	98/11512	0.0135584	0.210148357	0.172136927
BP	GO:0007173	2/21	102/11512	0.0146296	0.210148357	0.172136927
BP	GO:0022612	2/21	110/11512	0.0168786	0.210148357	0.172136927
BP	GO:0014066	2/21	111/11512	0.0171695	0.210148357	0.172136927
BP	GO:0050680	2/21	111/11512	0.0171695	0.210148357	0.172136927
BP	GO:0014706	3/21	308/11512	0.0176506	0.210148357	0.172136927
BP	GO:0031034	1/21	10/11512	0.0180998	0.210148357	0.172136927
BP	GO:0036445	1/21	10/11512	0.0180998	0.210148357	0.172136927
BP	GO:0050711	1/21	10/11512	0.0180998	0.210148357	0.172136927
BP	GO:0055057	1/21	10/11512	0.0180998	0.210148357	0.172136927
BP	GO:0060174	1/21	10/11512	0.0180998	0.210148357	0.172136927
BP	GO:0060601	1/21	10/11512	0.0180998	0.210148357	0.172136927
BP	GO:0060736	1/21	10/11512	0.0180998	0.210148357	0.172136927
BP	GO:0061042	1/21	10/11512	0.0180998	0.210148357	0.172136927
BP	GO:0072110	1/21	10/11512	0.0180998	0.210148357	0.172136927
BP	GO:0072537	1/21	10/11512	0.0180998	0.210148357	0.172136927
BP	GO:0090331	1/21	10/11512	0.0180998	0.210148357	0.172136927
BP	GO:2001214	1/21	10/11512	0.0180998	0.210148357	0.172136927

BP	GO:0002429	3/21	316/11512	0.0188893	0.210148357	0.172136927
BP	GO:0007517	3/21	317/11512	0.0190475	0.210148357	0.172136927
BP	GO:0030240	1/21	11/11512	0.0198926	0.210148357	0.172136927
BP	GO:0031033	1/21	11/11512	0.0198926	0.210148357	0.172136927
BP	GO:0034111	1/21	11/11512	0.0198926	0.210148357	0.172136927
BP	GO:0060525	1/21	11/11512	0.0198926	0.210148357	0.172136927
BP	GO:0060670	1/21	11/11512	0.0198926	0.210148357	0.172136927
BP	GO:0060742	1/21	11/11512	0.0198926	0.210148357	0.172136927
BP	GO:0070571	1/21	11/11512	0.0198926	0.210148357	0.172136927
BP	GO:0060537	3/21	323/11512	0.0200125	0.210148357	0.172136927
BP	GO:0038127	2/21	123/11512	0.0208266	0.210148357	0.172136927
BP	GO:0035051	2/21	124/11512	0.021145	0.210148357	0.172136927
BP	GO:0048660	2/21	124/11512	0.021145	0.210148357	0.172136927
BP	GO:0002834	1/21	12/11512	0.0216822	0.210148357	0.172136927
BP	GO:0002837	1/21	12/11512	0.0216822	0.210148357	0.172136927
BP	GO:0030852	1/21	12/11512	0.0216822	0.210148357	0.172136927
BP	GO:0043116	1/21	12/11512	0.0216822	0.210148357	0.172136927
BP	GO:0043301	1/21	12/11512	0.0216822	0.210148357	0.172136927
BP	GO:0045953	1/21	12/11512	0.0216822	0.210148357	0.172136927
BP	GO:0060442	1/21	12/11512	0.0216822	0.210148357	0.172136927
BP	GO:2000345	1/21	12/11512	0.0216822	0.210148357	0.172136927
BP	GO:0048659	2/21	126/11512	0.0217878	0.210148357	0.172136927
BP	GO:0014065	2/21	131/11512	0.0234304	0.210148357	0.172136927
BP	GO:0002716	1/21	13/11512	0.0234687	0.210148357	0.172136927
BP	GO:0014866	1/21	13/11512	0.0234687	0.210148357	0.172136927
BP	GO:0035791	1/21	13/11512	0.0234687	0.210148357	0.172136927
BP	GO:0060572	1/21	13/11512	0.0234687	0.210148357	0.172136927
BP	GO:0071599	1/21	13/11512	0.0234687	0.210148357	0.172136927
BP	GO:0072075	1/21	13/11512	0.0234687	0.210148357	0.172136927
BP	GO:1900016	1/21	13/11512	0.0234687	0.210148357	0.172136927
BP	GO:0060977	1/21	14/11512	0.025252	0.210148357	0.172136927
BP	GO:0072216	1/21	14/11512	0.025252	0.210148357	0.172136927
BP	GO:2001212	1/21	14/11512	0.025252	0.210148357	0.172136927
BP	GO:0055002	2/21	137/11512	0.0254674	0.210148357	0.172136927
BP	GO:0002418	1/21	15/11512	0.0270323	0.210148357	0.172136927
BP	GO:0031069	1/21	15/11512	0.0270323	0.210148357	0.172136927
BP	GO:0032516	1/21	15/11512	0.0270323	0.210148357	0.172136927
BP	GO:0045056	1/21	15/11512	0.0270323	0.210148357	0.172136927
BP	GO:0045717	1/21	15/11512	0.0270323	0.210148357	0.172136927
BP	GO:0048739	1/21	15/11512	0.0270323	0.210148357	0.172136927
BP	GO:0060973	1/21	15/11512	0.0270323	0.210148357	0.172136927
BP	GO:0072109	1/21	15/11512	0.0270323	0.210148357	0.172136927
BP	GO:0072224	1/21	15/11512	0.0270323	0.210148357	0.172136927
BP	GO:0051897	2/21	146/11512	0.0286542	0.210148357	0.172136927
BP	GO:0001911	1/21	16/11512	0.0288095	0.210148357	0.172136927
BP	GO:0048557	1/21	16/11512	0.0288095	0.210148357	0.172136927
BP	GO:0061298	1/21	16/11512	0.0288095	0.210148357	0.172136927
BP	GO:0072074	1/21	16/11512	0.0288095	0.210148357	0.172136927
BP	GO:0072574	1/21	16/11512	0.0288095	0.210148357	0.172136927
BP	GO:0072575	1/21	16/11512	0.0288095	0.210148357	0.172136927
BP	GO:0090330	1/21	16/11512	0.0288095	0.210148357	0.172136927

BP	GO:2000010	1/21	16/11512	0.0288095	0.210148357	0.172136927
BP	GO:0055001	2/21	147/11512	0.0290178	0.210148357	0.172136927
BP	GO:1903034	2/21	149/11512	0.0297507	0.210148357	0.172136927
BP	GO:0048839	2/21	151/11512	0.030491	0.210148357	0.172136927
BP	GO:0002710	1/21	17/11512	0.0305836	0.210148357	0.172136927
BP	GO:0003094	1/21	17/11512	0.0305836	0.210148357	0.172136927
BP	GO:0010544	1/21	17/11512	0.0305836	0.210148357	0.172136927
BP	GO:0048103	1/21	17/11512	0.0305836	0.210148357	0.172136927
BP	GO:0060602	1/21	17/11512	0.0305836	0.210148357	0.172136927
BP	GO:0072576	1/21	17/11512	0.0305836	0.210148357	0.172136927
BP	GO:0030324	2/21	153/11512	0.0312387	0.210148357	0.172136927
BP	GO:0035265	2/21	154/11512	0.0316153	0.210148357	0.172136927
BP	GO:0002347	1/21	18/11512	0.0323546	0.210148357	0.172136927
BP	GO:0036120	1/21	18/11512	0.0323546	0.210148357	0.172136927
BP	GO:0048730	1/21	18/11512	0.0323546	0.210148357	0.172136927
BP	GO:0090280	1/21	18/11512	0.0323546	0.210148357	0.172136927
BP	GO:0097205	1/21	18/11512	0.0323546	0.210148357	0.172136927
BP	GO:0030323	2/21	157/11512	0.0327561	0.210148357	0.172136927
BP	GO:0042098	2/21	157/11512	0.0327561	0.210148357	0.172136927
BP	GO:0042110	3/21	392/11512	0.0330592	0.210148357	0.172136927
BP	GO:0048015	2/21	159/11512	0.0335256	0.210148357	0.172136927
BP	GO:0033688	1/21	19/11512	0.0341225	0.210148357	0.172136927
BP	GO:0036119	1/21	19/11512	0.0341225	0.210148357	0.172136927
BP	GO:0042104	1/21	19/11512	0.0341225	0.210148357	0.172136927
BP	GO:0050860	1/21	19/11512	0.0341225	0.210148357	0.172136927
BP	GO:0055093	1/21	19/11512	0.0341225	0.210148357	0.172136927
BP	GO:0072111	1/21	19/11512	0.0341225	0.210148357	0.172136927
BP	GO:0048017	2/21	161/11512	0.0343024	0.210148357	0.172136927
BP	GO:0021846	1/21	20/11512	0.0358874	0.210148357	0.172136927
BP	GO:0031342	1/21	20/11512	0.0358874	0.210148357	0.172136927
BP	GO:0051043	1/21	20/11512	0.0358874	0.210148357	0.172136927
BP	GO:0060055	1/21	20/11512	0.0358874	0.210148357	0.172136927
BP	GO:0060713	1/21	20/11512	0.0358874	0.210148357	0.172136927
BP	GO:0072643	1/21	20/11512	0.0358874	0.210148357	0.172136927
BP	GO:0031032	2/21	168/11512	0.0370765	0.210148357	0.172136927
BP	GO:0015721	1/21	21/11512	0.0376492	0.210148357	0.172136927
BP	GO:0033687	1/21	21/11512	0.0376492	0.210148357	0.172136927
BP	GO:0034110	1/21	21/11512	0.0376492	0.210148357	0.172136927
BP	GO:0048679	1/21	21/11512	0.0376492	0.210148357	0.172136927
BP	GO:0060384	1/21	21/11512	0.0376492	0.210148357	0.172136927
BP	GO:0060445	1/21	21/11512	0.0376492	0.210148357	0.172136927
BP	GO:0060571	1/21	21/11512	0.0376492	0.210148357	0.172136927
BP	GO:0072273	1/21	21/11512	0.0376492	0.210148357	0.172136927
BP	GO:0031348	2/21	170/11512	0.0378848	0.210148357	0.172136927
BP	GO:0038093	2/21	170/11512	0.0378848	0.210148357	0.172136927
BP	GO:1903531	2/21	170/11512	0.0378848	0.210148357	0.172136927
BP	GO:0043583	2/21	172/11512	0.0386999	0.210148357	0.172136927
BP	GO:0001580	1/21	22/11512	0.0394079	0.210148357	0.172136927
BP	GO:0002385	1/21	22/11512	0.0394079	0.210148357	0.172136927
BP	GO:0010640	1/21	22/11512	0.0394079	0.210148357	0.172136927
BP	GO:0045922	1/21	22/11512	0.0394079	0.210148357	0.172136927

BP	GO:0072215	1/21	22/11512	0.0394079	0.210148357	0.172136927
BP	GO:1903306	1/21	22/11512	0.0394079	0.210148357	0.172136927
BP	GO:0060541	2/21	174/11512	0.0395218	0.210148357	0.172136927
BP	GO:0033002	2/21	175/11512	0.0399353	0.210148357	0.172136927
BP	GO:0070374	2/21	175/11512	0.0399353	0.210148357	0.172136927
BP	GO:0035025	1/21	23/11512	0.0411635	0.210148357	0.172136927
BP	GO:0044319	1/21	23/11512	0.0411635	0.210148357	0.172136927
BP	GO:0050912	1/21	23/11512	0.0411635	0.210148357	0.172136927
BP	GO:0060669	1/21	23/11512	0.0411635	0.210148357	0.172136927
BP	GO:0072012	1/21	23/11512	0.0411635	0.210148357	0.172136927
BP	GO:0090505	1/21	23/11512	0.0411635	0.210148357	0.172136927
BP	GO:0002053	1/21	24/11512	0.0429161	0.210148357	0.172136927
BP	GO:0003401	1/21	24/11512	0.0429161	0.210148357	0.172136927
BP	GO:0010714	1/21	24/11512	0.0429161	0.210148357	0.172136927
BP	GO:0032967	1/21	24/11512	0.0429161	0.210148357	0.172136927
BP	GO:0036296	1/21	24/11512	0.0429161	0.210148357	0.172136927
BP	GO:0051150	1/21	24/11512	0.0429161	0.210148357	0.172136927
BP	GO:0060045	1/21	24/11512	0.0429161	0.210148357	0.172136927
BP	GO:0060441	1/21	24/11512	0.0429161	0.210148357	0.172136927
BP	GO:0060740	1/21	24/11512	0.0429161	0.210148357	0.172136927
BP	GO:0090504	1/21	24/11512	0.0429161	0.210148357	0.172136927
BP	GO:0050663	2/21	186/11512	0.0445931	0.210148357	0.172136927
BP	GO:0002251	1/21	25/11512	0.0446657	0.210148357	0.172136927
BP	GO:0003148	1/21	25/11512	0.0446657	0.210148357	0.172136927
BP	GO:0010922	1/21	25/11512	0.0446657	0.210148357	0.172136927
BP	GO:0021884	1/21	25/11512	0.0446657	0.210148357	0.172136927
BP	GO:0050858	1/21	25/11512	0.0446657	0.210148357	0.172136927
BP	GO:0050913	1/21	25/11512	0.0446657	0.210148357	0.172136927
BP	GO:0061437	1/21	25/11512	0.0446657	0.210148357	0.172136927
BP	GO:0061440	1/21	25/11512	0.0446657	0.210148357	0.172136927
BP	GO:0070570	1/21	25/11512	0.0446657	0.210148357	0.172136927
BP	GO:0030851	1/21	26/11512	0.0464122	0.215365106	0.176410075
BP	GO:0060512	1/21	26/11512	0.0464122	0.215365106	0.176410075
BP	GO:0002757	3/21	449/11512	0.0465319	0.215365106	0.176410075
BP	GO:0051048	2/21	191/11512	0.046775	0.215365106	0.176410075
BP	GO:0050865	3/21	454/11512	0.0478281	0.217078536	0.177813581
BP	GO:0051896	2/21	194/11512	0.0481031	0.217078536	0.177813581
BP	GO:0003338	1/21	27/11512	0.0481556	0.217078536	0.177813581
BP	GO:0010092	1/21	27/11512	0.0481556	0.217078536	0.177813581
BP	GO:0046777	2/21	200/11512	0.0508009	0.22566698	0.184848556
BP	GO:0007507	3/21	468/11512	0.0515539	0.22566698	0.184848556
BP	GO:0010543	1/21	29/11512	0.0516334	0.22566698	0.184848556
BP	GO:0035909	1/21	29/11512	0.0516334	0.22566698	0.184848556
BP	GO:0043552	1/21	29/11512	0.0516334	0.22566698	0.184848556
BP	GO:0048333	1/21	29/11512	0.0516334	0.22566698	0.184848556
BP	GO:0001914	1/21	30/11512	0.0533678	0.226353114	0.185410583
BP	GO:0017145	1/21	30/11512	0.0533678	0.226353114	0.185410583
BP	GO:0038084	1/21	30/11512	0.0533678	0.226353114	0.185410583
BP	GO:0045601	1/21	30/11512	0.0533678	0.226353114	0.185410583
BP	GO:0045920	1/21	30/11512	0.0533678	0.226353114	0.185410583
BP	GO:0046006	1/21	30/11512	0.0533678	0.226353114	0.185410583

BP	GO:0010955	1/21	31/11512	0. 0550991	0. 226623854	0. 185632352
BP	GO:0048566	1/21	31/11512	0. 0550991	0. 226623854	0. 185632352
BP	GO:0055023	1/21	31/11512	0. 0550991	0. 226623854	0. 185632352
BP	GO:0060603	1/21	31/11512	0. 0550991	0. 226623854	0. 185632352
BP	GO:1903318	1/21	31/11512	0. 0550991	0. 226623854	0. 185632352
BP	GO:0007435	1/21	32/11512	0. 0568275	0. 226623854	0. 185632352
BP	GO:0010464	1/21	32/11512	0. 0568275	0. 226623854	0. 185632352
BP	GO:0032965	1/21	32/11512	0. 0568275	0. 226623854	0. 185632352
BP	GO:0110111	1/21	32/11512	0. 0568275	0. 226623854	0. 185632352
BP	GO:0003007	2/21	214/11512	0. 0573054	0. 226623854	0. 185632352
BP	GO:2000027	2/21	214/11512	0. 0573054	0. 226623854	0. 185632352
BP	GO:0043114	1/21	33/11512	0. 0585528	0. 226623854	0. 185632352
BP	GO:0060428	1/21	33/11512	0. 0585528	0. 226623854	0. 185632352
BP	GO:0072210	1/21	33/11512	0. 0585528	0. 226623854	0. 185632352
BP	GO:0090218	1/21	33/11512	0. 0585528	0. 226623854	0. 185632352
BP	GO:0090279	1/21	33/11512	0. 0585528	0. 226623854	0. 185632352
BP	GO:1900015	1/21	33/11512	0. 0585528	0. 226623854	0. 185632352
BP	GO:2001222	1/21	33/11512	0. 0585528	0. 226623854	0. 185632352
BP	GO:0043491	2/21	217/11512	0. 0587361	0. 226623854	0. 185632352
BP	GO:0060485	2/21	217/11512	0. 0587361	0. 226623854	0. 185632352
BP	GO:0002707	1/21	34/11512	0. 0602751	0. 226623854	0. 185632352
BP	GO:0034405	1/21	34/11512	0. 0602751	0. 226623854	0. 185632352
BP	GO:0035307	1/21	34/11512	0. 0602751	0. 226623854	0. 185632352
BP	GO:0042269	1/21	34/11512	0. 0602751	0. 226623854	0. 185632352
BP	GO:0048286	1/21	34/11512	0. 0602751	0. 226623854	0. 185632352
BP	GO:2000008	1/21	34/11512	0. 0602751	0. 226623854	0. 185632352
BP	GO:0002715	1/21	35/11512	0. 0619944	0. 226673273	0. 185672832
BP	GO:0007431	1/21	35/11512	0. 0619944	0. 226673273	0. 185672832
BP	GO:0060421	1/21	35/11512	0. 0619944	0. 226673273	0. 185672832
BP	GO:0051146	2/21	224/11512	0. 0621234	0. 226673273	0. 185672832
BP	GO:0002534	1/21	36/11512	0. 0637107	0. 226673273	0. 185672832
BP	GO:0002823	1/21	36/11512	0. 0637107	0. 226673273	0. 185672832
BP	GO:0003416	1/21	36/11512	0. 0637107	0. 226673273	0. 185672832
BP	GO:0010712	1/21	36/11512	0. 0637107	0. 226673273	0. 185672832
BP	GO:0014911	1/21	36/11512	0. 0637107	0. 226673273	0. 185672832
BP	GO:0030049	1/21	36/11512	0. 0637107	0. 226673273	0. 185672832
BP	GO:0033275	1/21	36/11512	0. 0637107	0. 226673273	0. 185672832
BP	GO:0050704	1/21	36/11512	0. 0637107	0. 226673273	0. 185672832
BP	GO:0060412	1/21	36/11512	0. 0637107	0. 226673273	0. 185672832
BP	GO:0001974	1/21	37/11512	0. 065424	0. 228592224	0. 187244685
BP	GO:0002762	1/21	37/11512	0. 065424	0. 228592224	0. 187244685
BP	GO:0006509	1/21	37/11512	0. 065424	0. 228592224	0. 187244685
BP	GO:0090184	1/21	37/11512	0. 065424	0. 228592224	0. 187244685
BP	GO:0001818	2/21	231/11512	0. 0655776	0. 228592224	0. 187244685
BP	GO:0046651	2/21	234/11512	0. 0670778	0. 229375795	0. 187886524
BP	GO:0002832	1/21	38/11512	0. 0671344	0. 229375795	0. 187886524
BP	GO:0050856	1/21	38/11512	0. 0671344	0. 229375795	0. 187886524
BP	GO:0060043	1/21	38/11512	0. 0671344	0. 229375795	0. 187886524
BP	GO:0060976	1/21	38/11512	0. 0671344	0. 229375795	0. 187886524
BP	GO:0032943	2/21	236/11512	0. 0680845	0. 231534109	0. 189654445
BP	GO:0010863	1/21	39/11512	0. 0688417	0. 231534109	0. 189654445

BP	GO:0048701	1/21	39/11512	0.0688417	0.231534109	0.189654445
BP	GO:0098868	1/21	39/11512	0.0688417	0.231534109	0.189654445
BP	GO:0050909	1/21	40/11512	0.0705461	0.234935308	0.192440438
BP	GO:0055025	1/21	40/11512	0.0705461	0.234935308	0.192440438
BP	GO:0001822	2/21	242/11512	0.0711355	0.234935308	0.192440438
BP	GO:0002820	1/21	41/11512	0.0722475	0.234935308	0.192440438
BP	GO:0032964	1/21	41/11512	0.0722475	0.234935308	0.192440438
BP	GO:0050701	1/21	41/11512	0.0722475	0.234935308	0.192440438
BP	GO:0051055	1/21	41/11512	0.0722475	0.234935308	0.192440438
BP	GO:1900274	1/21	41/11512	0.0722475	0.234935308	0.192440438
BP	GO:0001913	1/21	42/11512	0.073946	0.234935308	0.192440438
BP	GO:0010463	1/21	42/11512	0.073946	0.234935308	0.192440438
BP	GO:0021879	1/21	42/11512	0.073946	0.234935308	0.192440438
BP	GO:0031103	1/21	42/11512	0.073946	0.234935308	0.192440438
BP	GO:0042304	1/21	42/11512	0.073946	0.234935308	0.192440438
BP	GO:0060425	1/21	42/11512	0.073946	0.234935308	0.192440438
BP	GO:0060443	1/21	42/11512	0.073946	0.234935308	0.192440438
BP	GO:0002011	1/21	43/11512	0.0756414	0.235116517	0.19258887
BP	GO:0002067	1/21	43/11512	0.0756414	0.235116517	0.19258887
BP	GO:0035272	1/21	43/11512	0.0756414	0.235116517	0.19258887
BP	GO:0043300	1/21	43/11512	0.0756414	0.235116517	0.19258887
BP	GO:0060711	1/21	43/11512	0.0756414	0.235116517	0.19258887
BP	GO:1903727	1/21	43/11512	0.0756414	0.235116517	0.19258887
BP	GO:0002704	1/21	44/11512	0.077334	0.236247416	0.193515213
BP	GO:0048546	1/21	44/11512	0.077334	0.236247416	0.193515213
BP	GO:0072001	2/21	254/11512	0.0773719	0.236247416	0.193515213
BP	GO:1903037	2/21	254/11512	0.0773719	0.236247416	0.193515213
BP	GO:0070661	2/21	256/11512	0.0784282	0.236247416	0.193515213
BP	GO:0030850	1/21	45/11512	0.0790235	0.236247416	0.193515213
BP	GO:0035306	1/21	45/11512	0.0790235	0.236247416	0.193515213
BP	GO:0043551	1/21	45/11512	0.0790235	0.236247416	0.193515213
BP	GO:0045214	1/21	45/11512	0.0790235	0.236247416	0.193515213
BP	GO:0046622	1/21	45/11512	0.0790235	0.236247416	0.193515213
BP	GO:0055010	1/21	45/11512	0.0790235	0.236247416	0.193515213
BP	GO:0045840	1/21	46/11512	0.0807101	0.238802193	0.195607885
BP	GO:0051145	1/21	46/11512	0.0807101	0.238802193	0.195607885
BP	GO:0060038	1/21	46/11512	0.0807101	0.238802193	0.195607885
BP	GO:0050863	2/21	262/11512	0.0816252	0.239665836	0.196315313
BP	GO:0007405	1/21	47/11512	0.0823938	0.239665836	0.196315313
BP	GO:0035924	1/21	47/11512	0.0823938	0.239665836	0.196315313
BP	GO:0042267	1/21	47/11512	0.0823938	0.239665836	0.196315313
BP	GO:0043113	1/21	47/11512	0.0823938	0.239665836	0.196315313
BP	GO:0001895	1/21	48/11512	0.0840746	0.239696053	0.196340064
BP	GO:0001960	1/21	48/11512	0.0840746	0.239696053	0.196340064
BP	GO:0031295	1/21	48/11512	0.0840746	0.239696053	0.196340064
BP	GO:0035904	1/21	48/11512	0.0840746	0.239696053	0.196340064
BP	GO:0045824	1/21	48/11512	0.0840746	0.239696053	0.196340064
BP	GO:0048146	1/21	48/11512	0.0840746	0.239696053	0.196340064
BP	GO:0045861	2/21	269/11512	0.085407	0.239716896	0.196357137
BP	GO:0002228	1/21	49/11512	0.0857524	0.239716896	0.196357137
BP	GO:0009880	1/21	49/11512	0.0857524	0.239716896	0.196357137

BP	GO:0031102	1/21	49/11512	0.0857524	0.239716896	0.196357137
BP	GO:0031294	1/21	49/11512	0.0857524	0.239716896	0.196357137
BP	GO:0033619	1/21	49/11512	0.0857524	0.239716896	0.196357137
BP	GO:0030195	1/21	50/11512	0.0874273	0.241265639	0.197625745
BP	GO:0048645	1/21	50/11512	0.0874273	0.241265639	0.197625745
BP	GO:0060688	1/21	50/11512	0.0874273	0.241265639	0.197625745
BP	GO:0090183	1/21	50/11512	0.0874273	0.241265639	0.197625745
BP	GO:0021872	1/21	51/11512	0.0890992	0.243537901	0.199487002
BP	GO:0050819	1/21	51/11512	0.0890992	0.243537901	0.199487002
BP	GO:1900047	1/21	51/11512	0.0890992	0.243537901	0.199487002
BP	GO:0050678	2/21	278/11512	0.0903488	0.244988984	0.200675615
BP	GO:0003229	1/21	52/11512	0.0907683	0.244988984	0.200675615
BP	GO:0060761	1/21	52/11512	0.0907683	0.244988984	0.200675615
BP	GO:0070527	1/21	52/11512	0.0907683	0.244988984	0.200675615
BP	GO:0050867	2/21	280/11512	0.0914587	0.24563588	0.201205501
BP	GO:0008589	1/21	53/11512	0.0924344	0.24563588	0.201205501
BP	GO:0034394	1/21	53/11512	0.0924344	0.24563588	0.201205501
BP	GO:0046579	1/21	53/11512	0.0924344	0.24563588	0.201205501
BP	GO:0050854	1/21	53/11512	0.0924344	0.24563588	0.201205501
BP	GO:0043550	1/21	54/11512	0.0940976	0.247411113	0.202659632
BP	GO:0050710	1/21	54/11512	0.0940976	0.247411113	0.202659632
BP	GO:0055021	1/21	54/11512	0.0940976	0.247411113	0.202659632
BP	GO:0007159	2/21	285/11512	0.0942519	0.247411113	0.202659632
BP	GO:0046677	2/21	289/11512	0.0965048	0.251121666	0.205699023
BP	GO:0001655	2/21	290/11512	0.0970705	0.251121666	0.205699023
BP	GO:0032835	1/21	56/11512	0.0974154	0.251121666	0.205699023
BP	GO:0048747	1/21	56/11512	0.0974154	0.251121666	0.205699023
BP	GO:0051785	1/21	56/11512	0.0974154	0.251121666	0.205699023
BP	GO:1904888	1/21	56/11512	0.0974154	0.251121666	0.205699023
BP	GO:0001707	1/21	58/11512	0.1007215	0.256571737	0.210163291
BP	GO:0014910	1/21	58/11512	0.1007215	0.256571737	0.210163291
BP	GO:1903670	1/21	58/11512	0.1007215	0.256571737	0.210163291
BP	GO:2000573	1/21	58/11512	0.1007215	0.256571737	0.210163291
BP	GO:0002532	1/21	59/11512	0.1023703	0.258477495	0.211724337
BP	GO:0014855	1/21	59/11512	0.1023703	0.258477495	0.211724337
BP	GO:0051057	1/21	59/11512	0.1023703	0.258477495	0.211724337
BP	GO:0048332	1/21	60/11512	0.1040162	0.260342806	0.213252253
BP	GO:0048844	1/21	60/11512	0.1040162	0.260342806	0.213252253
BP	GO:0060420	1/21	60/11512	0.1040162	0.260342806	0.213252253
BP	GO:0003281	1/21	61/11512	0.1056592	0.261450699	0.214159751
BP	GO:0045844	1/21	61/11512	0.1056592	0.261450699	0.214159751
BP	GO:0048636	1/21	61/11512	0.1056592	0.261450699	0.214159751
BP	GO:0001101	2/21	305/11512	0.1056735	0.261450699	0.214159751
BP	GO:1901863	1/21	62/11512	0.1072993	0.264209554	0.216419587
BP	GO:0045787	2/21	308/11512	0.1074195	0.264209554	0.216419587
BP	GO:0043627	1/21	63/11512	0.1089366	0.264209554	0.216419587
BP	GO:0045638	1/21	63/11512	0.1089366	0.264209554	0.216419587
BP	GO:0050907	1/21	63/11512	0.1089366	0.264209554	0.216419587
BP	GO:0071300	1/21	63/11512	0.1089366	0.264209554	0.216419587
BP	GO:0072028	1/21	63/11512	0.1089366	0.264209554	0.216419587
BP	GO:0002709	1/21	64/11512	0.110571	0.265185562	0.217219055

BP	GO:0014909	1/21	64/11512	0.110571	0.265185562	0.217219055
BP	GO:0045833	1/21	64/11512	0.110571	0.265185562	0.217219055
BP	GO:0048678	1/21	64/11512	0.110571	0.265185562	0.217219055
BP	GO:0018108	2/21	314/11512	0.1109358	0.265321515	0.217330418
BP	GO:0018212	2/21	316/11512	0.112115	0.266133287	0.217995357
BP	GO:0001910	1/21	65/11512	0.1122025	0.266133287	0.217995357
BP	GO:0021675	1/21	65/11512	0.1122025	0.266133287	0.217995357
BP	GO:0003208	1/21	66/11512	0.1138312	0.26778332	0.219346934
BP	GO:0060411	1/21	66/11512	0.1138312	0.26778332	0.219346934
BP	GO:0061180	1/21	66/11512	0.1138312	0.26778332	0.219346934
BP	GO:0001942	1/21	67/11512	0.1154571	0.268671775	0.220074686
BP	GO:0034103	1/21	67/11512	0.1154571	0.268671775	0.220074686
BP	GO:0070509	1/21	67/11512	0.1154571	0.268671775	0.220074686
BP	GO:0098773	1/21	67/11512	0.1154571	0.268671775	0.220074686
BP	GO:0030901	1/21	68/11512	0.1170801	0.270257298	0.221373421
BP	GO:0034109	1/21	68/11512	0.1170801	0.270257298	0.221373421
BP	GO:0110110	1/21	68/11512	0.1170801	0.270257298	0.221373421
BP	GO:0021954	1/21	69/11512	0.1187003	0.271090041	0.222055539
BP	GO:0022404	1/21	69/11512	0.1187003	0.271090041	0.222055539
BP	GO:0022405	1/21	69/11512	0.1187003	0.271090041	0.222055539
BP	GO:0061045	1/21	69/11512	0.1187003	0.271090041	0.222055539
BP	GO:0050673	2/21	330/11512	0.1204646	0.274391587	0.224759904
BP	GO:0019216	2/21	332/11512	0.1216705	0.275547459	0.225706703
BP	GO:0003151	1/21	71/11512	0.1219322	0.275547459	0.225706703
BP	GO:0055024	1/21	71/11512	0.1219322	0.275547459	0.225706703
BP	GO:0042058	1/21	72/11512	0.1235438	0.277731731	0.227495886
BP	GO:1903725	1/21	72/11512	0.1235438	0.277731731	0.227495886
BP	GO:0022407	2/21	337/11512	0.1246992	0.27959907	0.229025462
BP	GO:0051781	1/21	73/11512	0.1251527	0.279887008	0.229261318
BP	GO:0048145	1/21	74/11512	0.1267588	0.281938077	0.230941392
BP	GO:0055017	1/21	74/11512	0.1267588	0.281938077	0.230941392
BP	GO:0014812	1/21	75/11512	0.1283621	0.281938077	0.230941392
BP	GO:0019217	1/21	75/11512	0.1283621	0.281938077	0.230941392
BP	GO:0030193	1/21	75/11512	0.1283621	0.281938077	0.230941392
BP	GO:0048144	1/21	75/11512	0.1283621	0.281938077	0.230941392
BP	GO:0060993	1/21	75/11512	0.1283621	0.281938077	0.230941392
BP	GO:0009791	1/21	76/11512	0.1299625	0.283285361	0.232044981
BP	GO:0042472	1/21	76/11512	0.1299625	0.283285361	0.232044981
BP	GO:1900046	1/21	76/11512	0.1299625	0.283285361	0.232044981
BP	GO:0050818	1/21	77/11512	0.1315602	0.286043684	0.234304381
BP	GO:0001656	1/21	78/11512	0.133155	0.286616186	0.234773329
BP	GO:0001892	1/21	78/11512	0.133155	0.286616186	0.234773329
BP	GO:0042102	1/21	78/11512	0.133155	0.286616186	0.234773329
BP	GO:1901184	1/21	78/11512	0.133155	0.286616186	0.234773329
BP	GO:0051249	2/21	353/11512	0.134518	0.288600119	0.23639841
BP	GO:0048704	1/21	79/11512	0.1347471	0.288600119	0.23639841
BP	GO:0060419	1/21	80/11512	0.1363364	0.290558474	0.23800254
BP	GO:0060840	1/21	80/11512	0.1363364	0.290558474	0.23800254
BP	GO:0014068	1/21	81/11512	0.1379229	0.292459249	0.239559504
BP	GO:1902106	1/21	81/11512	0.1379229	0.292459249	0.239559504
BP	GO:0002250	2/21	359/11512	0.1382473	0.292459249	0.239559504

BP	GO:0031341	1/21	83/11512	0. 1410876	0. 29773628	0. 243882032
BP	GO:0042303	1/21	84/11512	0. 1426658	0. 298869163	0. 24481
BP	GO:0042633	1/21	84/11512	0. 1426658	0. 298869163	0. 24481
BP	GO:0046620	1/21	84/11512	0. 1426658	0. 298869163	0. 24481
BP	GO:0001657	1/21	85/11512	0. 1442412	0. 300706227	0. 246314777
BP	GO:2000379	1/21	85/11512	0. 1442412	0. 300706227	0. 246314777
BP	GO:0048608	2/21	370/11512	0. 1451469	0. 301068928	0. 246611873
BP	GO:0062014	1/21	86/11512	0. 1458139	0. 301068928	0. 246611873
BP	GO:0072163	1/21	86/11512	0. 1458139	0. 301068928	0. 246611873
BP	GO:0072164	1/21	86/11512	0. 1458139	0. 301068928	0. 246611873
BP	GO:0061458	2/21	373/11512	0. 1470421	0. 302878594	0. 248094208
BP	GO:0002286	1/21	88/11512	0. 148951	0. 305349475	0. 250118159
BP	GO:0043666	1/21	88/11512	0. 148951	0. 305349475	0. 250118159
BP	GO:0001823	1/21	89/11512	0. 1505154	0. 306915608	0. 251401011
BP	GO:0008543	1/21	89/11512	0. 1505154	0. 306915608	0. 251401011
BP	GO:0051051	2/21	381/11512	0. 1521229	0. 306915608	0. 251401011
BP	GO:0001909	1/21	91/11512	0. 153636	0. 306915608	0. 251401011
BP	GO:0006023	1/21	91/11512	0. 153636	0. 306915608	0. 251401011
BP	GO:0006024	1/21	91/11512	0. 153636	0. 306915608	0. 251401011
BP	GO:0009593	1/21	91/11512	0. 153636	0. 306915608	0. 251401011
BP	GO:0032609	1/21	91/11512	0. 153636	0. 306915608	0. 251401011
BP	GO:0042471	1/21	91/11512	0. 153636	0. 306915608	0. 251401011
BP	GO:0045446	1/21	91/11512	0. 153636	0. 306915608	0. 251401011
BP	GO:0050868	1/21	91/11512	0. 153636	0. 306915608	0. 251401011
BP	GO:0070498	1/21	92/11512	0. 1551923	0. 308592463	0. 252774558
BP	GO:2000278	1/21	92/11512	0. 1551923	0. 308592463	0. 252774558
BP	GO:0007229	1/21	93/11512	0. 1567458	0. 310463143	0. 254306871
BP	GO:0048732	2/21	389/11512	0. 1572411	0. 310463143	0. 254306871
BP	GO:0002456	1/21	94/11512	0. 1582965	0. 310463143	0. 254306871
BP	GO:0002761	1/21	94/11512	0. 1582965	0. 310463143	0. 254306871
BP	GO:0007224	1/21	94/11512	0. 1582965	0. 310463143	0. 254306871
BP	GO:0031623	1/21	94/11512	0. 1582965	0. 310463143	0. 254306871
BP	GO:0002040	1/21	95/11512	0. 1598446	0. 310668625	0. 254475187
BP	GO:0003279	1/21	95/11512	0. 1598446	0. 310668625	0. 254475187
BP	GO:0060349	1/21	95/11512	0. 1598446	0. 310668625	0. 254475187
BP	GO:0072089	1/21	95/11512	0. 1598446	0. 310668625	0. 254475187
BP	GO:0002065	1/21	96/11512	0. 16139	0. 311562214	0. 255207144
BP	GO:0021761	1/21	96/11512	0. 16139	0. 311562214	0. 255207144
BP	GO:0030282	1/21	96/11512	0. 16139	0. 311562214	0. 255207144
BP	GO:0032963	1/21	97/11512	0. 1629326	0. 313136078	0. 256496329
BP	GO:0045667	1/21	97/11512	0. 1629326	0. 313136078	0. 256496329
BP	GO:0001704	1/21	98/11512	0. 1644725	0. 315391651	0. 258343916
BP	GO:0007606	1/21	101/11512	0. 1690762	0. 322067682	0. 263812393
BP	GO:0070613	1/21	101/11512	0. 1690762	0. 322067682	0. 263812393
BP	GO:1903038	1/21	101/11512	0. 1690762	0. 322067682	0. 263812393
BP	GO:0070252	1/21	102/11512	0. 1706054	0. 324263159	0. 265610754
BP	GO:1903317	1/21	103/11512	0. 1721318	0. 325147438	0. 266335086
BP	GO:0050709	1/21	104/11512	0. 1736557	0. 325147438	0. 266335086
BP	GO:0043312	2/21	416/11512	0. 1747662	0. 325147438	0. 266335086
BP	GO:0007156	1/21	105/11512	0. 1751768	0. 325147438	0. 266335086
BP	GO:0042177	1/21	105/11512	0. 1751768	0. 325147438	0. 266335086

BP	GO:0051928	1/21	105/11512	0.1751768	0.325147438	0.266335086
BP	GO:0072175	1/21	105/11512	0.1751768	0.325147438	0.266335086
BP	GO:0003014	1/21	106/11512	0.1766953	0.325147438	0.266335086
BP	GO:0003158	1/21	106/11512	0.1766953	0.325147438	0.266335086
BP	GO:0007498	1/21	106/11512	0.1766953	0.325147438	0.266335086
BP	GO:0035304	1/21	106/11512	0.1766953	0.325147438	0.266335086
BP	GO:0048706	1/21	106/11512	0.1766953	0.325147438	0.266335086
BP	GO:0050671	1/21	106/11512	0.1766953	0.325147438	0.266335086
BP	GO:0050906	1/21	106/11512	0.1766953	0.325147438	0.266335086
BP	GO:0002283	2/21	419/11512	0.1767352	0.325147438	0.266335086
BP	GO:0002694	2/21	420/11512	0.1773924	0.325660702	0.266755511
BP	GO:0032946	1/21	107/11512	0.1782111	0.325966452	0.267005957
BP	GO:0001837	1/21	108/11512	0.1797243	0.325966452	0.267005957
BP	GO:0002698	1/21	109/11512	0.1812348	0.325966452	0.267005957
BP	GO:0003231	1/21	109/11512	0.1812348	0.325966452	0.267005957
BP	GO:0007605	1/21	109/11512	0.1812348	0.325966452	0.267005957
BP	GO:0035023	1/21	109/11512	0.1812348	0.325966452	0.267005957
BP	GO:0038095	1/21	109/11512	0.1812348	0.325966452	0.267005957
BP	GO:0042476	1/21	109/11512	0.1812348	0.325966452	0.267005957
BP	GO:0050728	1/21	109/11512	0.1812348	0.325966452	0.267005957
BP	GO:0061564	2/21	426/11512	0.1813449	0.325966452	0.267005957
BP	GO:0042119	2/21	427/11512	0.1820051	0.32647164	0.267419768
BP	GO:0002446	2/21	428/11512	0.1826657	0.326975472	0.267832467
BP	GO:0002792	1/21	111/11512	0.1842478	0.327763192	0.268477705
BP	GO:0002831	1/21	111/11512	0.1842478	0.327763192	0.268477705
BP	GO:1903707	1/21	111/11512	0.1842478	0.327763192	0.268477705
BP	GO:0036230	2/21	432/11512	0.1853124	0.328977278	0.269472188
BP	GO:0070665	1/21	112/11512	0.1857504	0.329076332	0.269553325
BP	GO:0030335	2/21	434/11512	0.1866381	0.329970098	0.270285428
BP	GO:0044344	1/21	114/11512	0.1887476	0.333015813	0.272780237
BP	GO:0003206	1/21	115/11512	0.1902423	0.333731927	0.273366821
BP	GO:0016202	1/21	115/11512	0.1902423	0.333731927	0.273366821
BP	GO:0045471	1/21	116/11512	0.1917344	0.333731927	0.273366821
BP	GO:0035148	1/21	117/11512	0.1932238	0.333731927	0.273366821
BP	GO:0048565	1/21	117/11512	0.1932238	0.333731927	0.273366821
BP	GO:0048634	1/21	117/11512	0.1932238	0.333731927	0.273366821
BP	GO:0002009	2/21	444/11512	0.1932898	0.333731927	0.273366821
BP	GO:0007423	2/21	444/11512	0.1932898	0.333731927	0.273366821
BP	GO:1901861	1/21	118/11512	0.1947106	0.333731927	0.273366821
BP	GO:0043410	2/21	447/11512	0.1952924	0.333731927	0.273366821
BP	GO:2000147	2/21	448/11512	0.1959606	0.333731927	0.273366821
BP	GO:0060041	1/21	119/11512	0.1961948	0.333731927	0.273366821
BP	GO:0016331	1/21	120/11512	0.1976764	0.333731927	0.273366821
BP	GO:0051147	1/21	120/11512	0.1976764	0.333731927	0.273366821
BP	GO:0061351	1/21	120/11512	0.1976764	0.333731927	0.273366821
BP	GO:0090263	1/21	120/11512	0.1976764	0.333731927	0.273366821
BP	GO:0009636	2/21	451/11512	0.1979674	0.333731927	0.273366821
BP	GO:0001889	1/21	121/11512	0.1991554	0.333731927	0.273366821
BP	GO:0008584	1/21	121/11512	0.1991554	0.333731927	0.273366821
BP	GO:0071774	1/21	121/11512	0.1991554	0.333731927	0.273366821
BP	GO:0072006	1/21	121/11512	0.1991554	0.333731927	0.273366821

BP	GO:0072073	1/21	121/11512	0.1991554	0.333731927	0.273366821
BP	GO:0007600	2/21	454/11512	0.1999772	0.333731927	0.273366821
BP	GO:0002822	1/21	122/11512	0.2006318	0.333731927	0.273366821
BP	GO:0030048	1/21	122/11512	0.2006318	0.333731927	0.273366821
BP	GO:0045834	1/21	122/11512	0.2006318	0.333731927	0.273366821
BP	GO:0046546	1/21	122/11512	0.2006318	0.333731927	0.273366821
BP	GO:0051250	1/21	122/11512	0.2006318	0.333731927	0.273366821
BP	GO:0032355	1/21	123/11512	0.2021056	0.333731927	0.273366821
BP	GO:0035107	1/21	123/11512	0.2021056	0.333731927	0.273366821
BP	GO:0035108	1/21	123/11512	0.2021056	0.333731927	0.273366821
BP	GO:0050921	1/21	123/11512	0.2021056	0.333731927	0.273366821
BP	GO:0061008	1/21	124/11512	0.2035769	0.333731927	0.273366821
BP	GO:0051272	2/21	460/11512	0.2040055	0.333731927	0.273366821
BP	GO:0043299	2/21	461/11512	0.2046779	0.333731927	0.273366821
BP	GO:0002706	1/21	125/11512	0.2050455	0.333731927	0.273366821
BP	GO:0030856	1/21	125/11512	0.2050455	0.333731927	0.273366821
BP	GO:0042542	1/21	125/11512	0.2050455	0.333731927	0.273366821
BP	GO:0050954	1/21	125/11512	0.2050455	0.333731927	0.273366821
BP	GO:0051668	1/21	125/11512	0.2050455	0.333731927	0.273366821
BP	GO:0055123	1/21	125/11512	0.2050455	0.333731927	0.273366821
BP	GO:0001764	1/21	126/11512	0.2065116	0.334079347	0.2736514
BP	GO:0061041	1/21	126/11512	0.2065116	0.334079347	0.2736514
BP	GO:0006633	1/21	127/11512	0.2079751	0.334079347	0.2736514
BP	GO:0010921	1/21	127/11512	0.2079751	0.334079347	0.2736514
BP	GO:0015718	1/21	127/11512	0.2079751	0.334079347	0.2736514
BP	GO:0030879	1/21	127/11512	0.2079751	0.334079347	0.2736514
BP	GO:0045931	1/21	127/11512	0.2079751	0.334079347	0.2736514
BP	GO:0002275	2/21	470/11512	0.2107435	0.337509325	0.276460967
BP	GO:0050777	1/21	129/11512	0.2108943	0.337509325	0.276460967
BP	GO:0009306	2/21	472/11512	0.2120945	0.33795462	0.276825717
BP	GO:0040017	2/21	472/11512	0.2120945	0.33795462	0.276825717
BP	GO:0042129	1/21	130/11512	0.2123501	0.33795462	0.276825717
BP	GO:0002444	2/21	475/11512	0.214123	0.340147377	0.27862185
BP	GO:0048754	1/21	132/11512	0.215254	0.340263026	0.278716581
BP	GO:0051302	1/21	132/11512	0.215254	0.340263026	0.278716581
BP	GO:0001890	1/21	133/11512	0.2167021	0.340263026	0.278716581
BP	GO:0010977	1/21	133/11512	0.2167021	0.340263026	0.278716581
BP	GO:1903305	1/21	133/11512	0.2167021	0.340263026	0.278716581
BP	GO:0001906	1/21	134/11512	0.2181477	0.340263026	0.278716581
BP	GO:0001959	1/21	134/11512	0.2181477	0.340263026	0.278716581
BP	GO:0030203	1/21	134/11512	0.2181477	0.340263026	0.278716581
BP	GO:0031214	1/21	134/11512	0.2181477	0.340263026	0.278716581
BP	GO:0046488	1/21	134/11512	0.2181477	0.340263026	0.278716581
BP	GO:0002819	1/21	136/11512	0.2210313	0.344137286	0.281890069
BP	GO:0007088	1/21	137/11512	0.2224692	0.345750923	0.283211832
BP	GO:0002244	1/21	138/11512	0.2239047	0.346730083	0.284013883
BP	GO:0006022	1/21	138/11512	0.2239047	0.346730083	0.284013883
BP	GO:0010594	1/21	139/11512	0.2253376	0.34769833	0.284806994
BP	GO:0030168	1/21	139/11512	0.2253376	0.34769833	0.284806994
BP	GO:0046661	1/21	140/11512	0.226768	0.3492795	0.286102164
BP	GO:0051224	1/21	141/11512	0.2281959	0.350851155	0.287389539

BP	GO:0021953	1/21	142/11512 0.2296212	0.352413352	0.288669168
BP	GO:0002790	2/21	499/11512 0.2304286	0.353023236	0.289168737
BP	GO:0022408	1/21	143/11512 0.2310441	0.353337434	0.289426103
BP	GO:0060759	1/21	144/11512 0.2324645	0.354879265	0.290689049
BP	GO:0002695	1/21	145/11512 0.2338823	0.355782127	0.291428602
BP	GO:1904950	1/21	145/11512 0.2338823	0.355782127	0.291428602
BP	GO:0002285	1/21	146/11512 0.2352977	0.356048005	0.291646388
BP	GO:0048736	1/21	146/11512 0.2352977	0.356048005	0.291646388
BP	GO:0060173	1/21	146/11512 0.2352977	0.356048005	0.291646388
BP	GO:0030177	1/21	147/11512 0.2367106	0.357557545	0.292882885
BP	GO:0003205	1/21	148/11512 0.238121	0.357804793	0.29308541
BP	GO:0010565	1/21	148/11512 0.238121	0.357804793	0.29308541
BP	GO:0048639	1/21	148/11512 0.238121	0.357804793	0.29308541
BP	GO:0007369	1/21	150/11512 0.2409343	0.360772921	0.295516666
BP	GO:0048771	1/21	150/11512 0.2409343	0.360772921	0.295516666
BP	GO:0051783	1/21	154/11512 0.2465313	0.368512957	0.301856692
BP	GO:0003018	1/21	156/11512 0.2493151	0.370743128	0.303683472
BP	GO:0031345	1/21	156/11512 0.2493151	0.370743128	0.303683472
BP	GO:0071347	1/21	156/11512 0.2493151	0.370743128	0.303683472
BP	GO:0035303	1/21	157/11512 0.2507033	0.371524114	0.304323194
BP	GO:0046890	1/21	157/11512 0.2507033	0.371524114	0.304323194
BP	GO:2000377	1/21	159/11512 0.2534723	0.374982261	0.307155835
BP	GO:0043112	1/21	160/11512 0.2548532	0.375196342	0.307331193
BP	GO:1904018	1/21	160/11512 0.2548532	0.375196342	0.307331193
BP	GO:0007266	1/21	161/11512 0.2562316	0.375196342	0.307331193
BP	GO:0030278	1/21	161/11512 0.2562316	0.375196342	0.307331193
BP	GO:0050679	1/21	161/11512 0.2562316	0.375196342	0.307331193
BP	GO:0071897	1/21	161/11512 0.2562316	0.375196342	0.307331193
BP	GO:0061138	1/21	162/11512 0.2576077	0.376570793	0.308457035
BP	GO:0050707	1/21	163/11512 0.2589813	0.37729756	0.309052344
BP	GO:0050866	1/21	163/11512 0.2589813	0.37729756	0.309052344
BP	GO:0031099	1/21	166/11512 0.2630875	0.382632344	0.313422178
BP	GO:0002573	1/21	169/11512 0.2671721	0.387917664	0.317751494
BP	GO:0001763	1/21	173/11512 0.2725847	0.393784239	0.322556929
BP	GO:0002703	1/21	173/11512 0.2725847	0.393784239	0.322556929
BP	GO:0048762	1/21	173/11512 0.2725847	0.393784239	0.322556929
BP	GO:0007565	1/21	174/11512 0.2739319	0.395067558	0.323608123
BP	GO:0050670	1/21	175/11512 0.2752767	0.395681489	0.324111006
BP	GO:0050870	1/21	175/11512 0.2752767	0.395681489	0.324111006
BP	GO:0032944	1/21	176/11512 0.2766191	0.396948415	0.325148772
BP	GO:0060348	1/21	177/11512 0.2779592	0.398136769	0.326122177
BP	GO:0001649	1/21	178/11512 0.2792969	0.398136769	0.326122177
BP	GO:0001894	1/21	178/11512 0.2792969	0.398136769	0.326122177
BP	GO:0070555	1/21	178/11512 0.2792969	0.398136769	0.326122177
BP	GO:0045637	1/21	179/11512 0.2806322	0.39937907	0.327139773
BP	GO:0032869	1/21	180/11512 0.2819652	0.399953934	0.327610656
BP	GO:0043542	1/21	180/11512 0.2819652	0.399953934	0.327610656
BP	GO:0006469	1/21	181/11512 0.2832958	0.401180449	0.32861532
BP	GO:0017157	1/21	182/11512 0.2846241	0.402399615	0.329613964
BP	GO:0008406	1/21	183/11512 0.2859501	0.402950899	0.330065533
BP	GO:0071229	1/21	183/11512 0.2859501	0.402950899	0.330065533

BP	GO:0098742	1/21	185/11512	0.2885949	0.406013438	0.332574123
BP	GO:0070663	1/21	186/11512	0.2899138	0.407203625	0.333549029
BP	GO:0045137	1/21	188/11512	0.2925447	0.409562609	0.335481323
BP	GO:0045665	1/21	188/11512	0.2925447	0.409562609	0.335481323
BP	GO:0050920	1/21	189/11512	0.2938567	0.410065797	0.335893495
BP	GO:1903039	1/21	189/11512	0.2938567	0.410065797	0.335893495
BP	GO:0051054	1/21	190/11512	0.2951663	0.41122685	0.336844538
BP	GO:0046578	1/21	192/11512	0.2977786	0.414196146	0.33927675
BP	GO:0010632	1/21	196/11512	0.3029757	0.419392381	0.343533096
BP	GO:0015850	1/21	196/11512	0.3029757	0.419392381	0.343533096
BP	GO:0048705	1/21	196/11512	0.3029757	0.419392381	0.343533096
BP	GO:0060560	1/21	197/11512	0.3042692	0.420506878	0.344446003
BP	GO:0033673	1/21	198/11512	0.3055604	0.421614647	0.3453534
BP	GO:0000302	1/21	200/11512	0.3081361	0.423810156	0.347151787
BP	GO:0044706	1/21	200/11512	0.3081361	0.423810156	0.347151787
BP	GO:0071560	1/21	205/11512	0.3145354	0.431921822	0.353796223
BP	GO:0042180	1/21	206/11512	0.3158085	0.432291108	0.354098713
BP	GO:0051924	1/21	206/11512	0.3158085	0.432291108	0.354098713
BP	GO:0090596	1/21	208/11512	0.3183479	0.435075466	0.356379439
BP	GO:0031330	1/21	209/11512	0.3196142	0.436113884	0.357230029
BP	GO:0097305	1/21	210/11512	0.3208783	0.437145964	0.358075428
BP	GO:0045165	1/21	211/11512	0.3221402	0.437480618	0.35834955
BP	GO:0071559	1/21	211/11512	0.3221402	0.437480618	0.35834955
BP	GO:0051348	1/21	216/11512	0.3284161	0.445301177	0.364755533
BP	GO:0140014	1/21	219/11512	0.332155	0.44948848	0.368185441
BP	GO:0045927	1/21	220/11512	0.3333969	0.44948848	0.368185441
BP	GO:0048863	1/21	220/11512	0.3333969	0.44948848	0.368185441
BP	GO:0006898	1/21	221/11512	0.3346366	0.44948848	0.368185441
BP	GO:0016485	1/21	221/11512	0.3346366	0.44948848	0.368185441
BP	GO:1902105	1/21	221/11512	0.3346366	0.44948848	0.368185441
BP	GO:0002449	1/21	222/11512	0.3358741	0.449747441	0.368397562
BP	GO:0022409	1/21	222/11512	0.3358741	0.449747441	0.368397562
BP	GO:0060828	1/21	223/11512	0.3371094	0.450700631	0.369178339
BP	GO:0043406	1/21	225/11512	0.3395735	0.4532911	0.371300247
BP	GO:0002460	1/21	228/11512	0.3432532	0.455379063	0.373010542
BP	GO:0007548	1/21	228/11512	0.3432532	0.455379063	0.373010542
BP	GO:0043270	1/21	228/11512	0.3432532	0.455379063	0.373010542
BP	GO:0072593	1/21	228/11512	0.3432532	0.455379063	0.373010542
BP	GO:0061448	1/21	229/11512	0.3444754	0.455596552	0.373188691
BP	GO:0090068	1/21	229/11512	0.3444754	0.455596552	0.373188691
BP	GO:0032868	1/21	230/11512	0.3456955	0.456508946	0.373936052
BP	GO:0048562	1/21	232/11512	0.3481292	0.458316827	0.375416925
BP	GO:0051251	1/21	232/11512	0.3481292	0.458316827	0.375416925
BP	GO:0007162	1/21	233/11512	0.3493427	0.459212374	0.376150487
BP	GO:0051606	1/21	237/11512	0.3541756	0.464855503	0.380772892
BP	GO:0006650	1/21	239/11512	0.3565792	0.46729788	0.382773494
BP	GO:0050768	1/21	241/11512	0.3589743	0.469721684	0.384758883
BP	GO:0009895	1/21	242/11512	0.3601686	0.470569355	0.385453228
BP	GO:0006470	1/21	244/11512	0.362551	0.472964254	0.38741494
BP	GO:0043588	1/21	247/11512	0.3661087	0.476882871	0.390624761
BP	GO:0010631	1/21	249/11512	0.36847	0.479233593	0.392550287

BP	GO:0090132	1/21	251/11512	0.3708229	0.481566342	0.394461091
BP	GO:0045765	1/21	253/11512	0.3731674	0.483881238	0.396357271
BP	GO:0060326	1/21	257/11512	0.3778316	0.488457935	0.400106139
BP	GO:0090130	1/21	257/11512	0.3778316	0.488457935	0.400106139
BP	GO:0051961	1/21	258/11512	0.3789924	0.489224122	0.400733739
BP	GO:0015849	1/21	259/11512	0.3801512	0.489252942	0.400757346
BP	GO:0046942	1/21	259/11512	0.3801512	0.489252942	0.400757346
BP	GO:0032103	1/21	263/11512	0.3847659	0.49445288	0.405016724
BP	GO:0043010	1/21	265/11512	0.3870609	0.496649085	0.406815682
BP	GO:0051056	1/21	266/11512	0.3882054	0.496649085	0.406815682
BP	GO:0060070	1/21	266/11512	0.3882054	0.496649085	0.406815682
BP	GO:0060562	1/21	267/11512	0.3893478	0.497371602	0.407407511
BP	GO:0002696	1/21	268/11512	0.3904882	0.498089388	0.407995464
BP	GO:0051604	1/21	270/11512	0.3927629	0.500249783	0.409765089
BP	GO:0032956	1/21	272/11512	0.3950295	0.502393512	0.411521062
BP	GO:0003002	1/21	273/11512	0.3961598	0.503087878	0.412089832
BP	GO:0071375	1/21	274/11512	0.3972881	0.503777648	0.412654837
BP	GO:0006869	1/21	275/11512	0.3984143	0.504462847	0.413216098
BP	GO:0007568	1/21	276/11512	0.3995386	0.505143499	0.413773635
BP	GO:0010721	1/21	277/11512	0.4006608	0.505819629	0.414327467
BP	GO:0032496	1/21	279/11512	0.4028994	0.507821125	0.415966934
BP	GO:0030111	1/21	280/11512	0.4040156	0.507821125	0.415966934
BP	GO:1901342	1/21	280/11512	0.4040156	0.507821125	0.415966934
BP	GO:0048638	1/21	281/11512	0.4051299	0.508479404	0.416506145
BP	GO:1903829	1/21	282/11512	0.4062422	0.509133281	0.417041749
BP	GO:0072330	1/21	283/11512	0.4073526	0.509782778	0.417573765
BP	GO:0071902	1/21	284/11512	0.4084609	0.510427918	0.418102213
BP	GO:0008544	1/21	286/11512	0.4106717	0.512446822	0.41975594
BP	GO:0002237	1/21	289/11512	0.4139731	0.515073435	0.421907453
BP	GO:0043405	1/21	289/11512	0.4139731	0.515073435	0.421907453
BP	GO:0006631	1/21	292/11512	0.4172569	0.518410039	0.424640536
BP	GO:0007596	1/21	293/11512	0.4183476	0.519016205	0.425137059
BP	GO:0050817	1/21	296/11512	0.421608	0.522308604	0.427833932
BP	GO:0007599	1/21	297/11512	0.4226909	0.522897829	0.428316579
BP	GO:0001654	1/21	300/11512	0.4259282	0.52614656	0.430977683
BP	GO:0010876	1/21	301/11512	0.4270034	0.526719094	0.431446657
BP	GO:0150063	1/21	303/11512	0.4291481	0.528607334	0.432993354
BP	GO:0000280	1/21	305/11512	0.4312852	0.529864403	0.434023045
BP	GO:0006936	1/21	306/11512	0.4323509	0.529864403	0.434023045
BP	GO:0046486	1/21	306/11512	0.4323509	0.529864403	0.434023045
BP	GO:0001701	1/21	307/11512	0.4334146	0.529864403	0.434023045
BP	GO:0010959	1/21	308/11512	0.4344765	0.529864403	0.434023045
BP	GO:0032970	1/21	308/11512	0.4344765	0.529864403	0.434023045
BP	GO:0048880	1/21	308/11512	0.4344765	0.529864403	0.434023045
BP	GO:0042176	1/21	310/11512	0.4365946	0.531694372	0.435522011
BP	GO:0007015	1/21	311/11512	0.4376508	0.532227834	0.435958981
BP	GO:0030900	1/21	315/11512	0.4418567	0.53658482	0.43952788
BP	GO:0050727	1/21	316/11512	0.4429035	0.537098495	0.439948642
BP	GO:0006644	1/21	322/11512	0.4491452	0.543901519	0.445521141
BP	GO:0030099	1/21	324/11512	0.4512109	0.545635605	0.446941568
BP	GO:0001933	1/21	327/11512	0.4542956	0.548595375	0.449365977

BP	GO:0001503	1/21	330/11512	0.4573638	0.550755568	0.451135437
BP	GO:1901653	1/21	330/11512	0.4573638	0.550755568	0.451135437
BP	GO:0048285	1/21	336/11512	0.463451	0.557306303	0.456501281
BP	GO:0051052	1/21	339/11512	0.4664702	0.560154545	0.458834336
BP	GO:0001667	1/21	341/11512	0.4684739	0.560995912	0.459523517
BP	GO:0002697	1/21	341/11512	0.4684739	0.560995912	0.459523517
BP	GO:0001558	1/21	342/11512	0.4694731	0.561411626	0.459864037
BP	GO:0007389	1/21	344/11512	0.4714662	0.563012999	0.461175755
BP	GO:0060249	1/21	347/11512	0.4744424	0.565782364	0.463444201
BP	GO:0070482	1/21	348/11512	0.4754309	0.565786974	0.463447976
BP	GO:0006816	1/21	349/11512	0.4764176	0.565786974	0.463447976
BP	GO:0045785	1/21	349/11512	0.4764176	0.565786974	0.463447976
BP	GO:0048568	1/21	355/11512	0.482301	0.571985088	0.468524982
BP	GO:0007265	1/21	356/11512	0.4832754	0.572352346	0.46882581
BP	GO:0016311	1/21	358/11512	0.4852191	0.573864847	0.470064732
BP	GO:0042326	1/21	362/11512	0.4890854	0.577644098	0.473160396
BP	GO:1903706	1/21	365/11512	0.491967	0.580251521	0.475296191
BP	GO:0002683	1/21	367/11512	0.4938795	0.581710318	0.476491122
BP	GO:0045088	1/21	369/11512	0.4957851	0.583157062	0.47767618
BP	GO:0015711	1/21	370/11512	0.4967353	0.583477661	0.477938789
BP	GO:0046394	1/21	372/11512	0.4986307	0.58490604	0.479108805
BP	GO:0016053	1/21	373/11512	0.4995758	0.585217403	0.479363849
BP	GO:0006979	1/21	374/11512	0.5005193	0.585525934	0.479616573
BP	GO:0043434	1/21	378/11512	0.5042761	0.589120369	0.48256085
BP	GO:0001819	1/21	380/11512	0.5061444	0.589702736	0.483037879
BP	GO:0070838	1/21	380/11512	0.5061444	0.589702736	0.483037879
BP	GO:0003012	1/21	382/11512	0.508006	0.591071834	0.484159336
BP	GO:0062012	1/21	384/11512	0.5098609	0.59242947	0.485271404
BP	GO:0050708	1/21	386/11512	0.5117092	0.592976557	0.485719534
BP	GO:0072511	1/21	386/11512	0.5117092	0.592976557	0.485719534
BP	GO:0050900	1/21	389/11512	0.5144691	0.595373504	0.487682924
BP	GO:0007409	1/21	390/11512	0.5153858	0.595633748	0.487896095
BP	GO:0016049	1/21	400/11512	0.5244623	0.605311035	0.495822964
BP	GO:0048871	1/21	401/11512	0.525361	0.605536557	0.496007694
BP	GO:0002791	1/21	410/11512	0.5333768	0.613953742	0.502902387
BP	GO:0016055	1/21	412/11512	0.5351405	0.615161467	0.50389166
BP	GO:0198738	1/21	413/11512	0.5360199	0.615350877	0.504046809
BP	GO:0010975	1/21	414/11512	0.5368978	0.615537965	0.504200057
BP	GO:0071900	1/21	426/11512	0.5473097	0.626640527	0.513294399
BP	GO:0001501	1/21	430/11512	0.5507305	0.629719789	0.515816686
BP	GO:0050878	1/21	431/11512	0.5515819	0.629856781	0.5159289
BP	GO:0002521	1/21	433/11512	0.55328	0.630124432	0.516148138
BP	GO:0051493	1/21	433/11512	0.55328	0.630124432	0.516148138
BP	GO:0060627	1/21	434/11512	0.5541267	0.630255113	0.516255182
BP	GO:1903827	1/21	440/11512	0.5591752	0.635158125	0.520271342
BP	GO:0045936	1/21	446/11512	0.5641692	0.639240227	0.523615077
BP	GO:0007264	1/21	447/11512	0.5649963	0.639240227	0.523615077
BP	GO:0010563	1/21	447/11512	0.5649963	0.639240227	0.523615077
BP	GO:1901652	1/21	452/11512	0.5691093	0.643048716	0.52673469
BP	GO:0045860	1/21	454/11512	0.5707441	0.644050716	0.527555449
BP	GO:0051301	1/21	457/11512	0.5731853	0.645958804	0.529118404

BP	GO:0008015	1/21	466/11512	0.5804296	0.65241505	0.534406851
BP	GO:0031400	1/21	466/11512	0.5804296	0.65241505	0.534406851
BP	GO:0003013	1/21	476/11512	0.5883416	0.659586059	0.540280775
BP	GO:0048598	1/21	476/11512	0.5883416	0.659586059	0.540280775
BP	GO:0009617	1/21	478/11512	0.5899068	0.660480839	0.541013708
BP	GO:0010035	1/21	483/11512	0.5937952	0.663970942	0.543872524
BP	GO:0006820	1/21	484/11512	0.5945686	0.663973489	0.54387461
BP	GO:0048667	1/21	486/11512	0.5961113	0.663973878	0.543874929
BP	GO:0072657	1/21	486/11512	0.5961113	0.663973878	0.543874929
BP	GO:0033674	1/21	489/11512	0.5984148	0.665678498	0.545271219
BP	GO:1905114	1/21	499/11512	0.6060033	0.673250075	0.551473257
BP	GO:0001961	0/21	38/11512	1	1	0.819120973
BP	GO:0002218	0/21	259/11512	1	1	0.819120973
BP	GO:0002221	0/21	159/11512	1	1	0.819120973
BP	GO:0002224	0/21	119/11512	1	1	0.819120973
BP	GO:0002507	0/21	22/11512	1	1	0.819120973
BP	GO:0002643	0/21	14/11512	1	1	0.819120973
BP	GO:0002755	0/21	29/11512	1	1	0.819120973
BP	GO:0002756	0/21	31/11512	1	1	0.819120973
BP	GO:0002758	0/21	244/11512	1	1	0.819120973
BP	GO:0002793	0/21	243/11512	1	1	0.819120973
BP	GO:0002821	0/21	88/11512	1	1	0.819120973
BP	GO:0002824	0/21	84/11512	1	1	0.819120973
BP	GO:0002833	0/21	37/11512	1	1	0.819120973
BP	GO:0002836	0/21	10/11512	1	1	0.819120973
BP	GO:0002839	0/21	10/11512	1	1	0.819120973
BP	GO:0003170	0/21	52/11512	1	1	0.819120973
BP	GO:0003179	0/21	45/11512	1	1	0.819120973
BP	GO:0006909	0/21	234/11512	1	1	0.819120973
BP	GO:0007411	0/21	226/11512	1	1	0.819120973
BP	GO:0008037	0/21	116/11512	1	1	0.819120973
BP	GO:0008038	0/21	38/11512	1	1	0.819120973
BP	GO:0030100	0/21	225/11512	1	1	0.819120973
BP	GO:0031349	0/21	411/11512	1	1	0.819120973
BP	GO:0032613	0/21	45/11512	1	1	0.819120973
BP	GO:0032649	0/21	80/11512	1	1	0.819120973
BP	GO:0032653	0/21	42/11512	1	1	0.819120973
BP	GO:0032689	0/21	26/11512	1	1	0.819120973
BP	GO:0032693	0/21	14/11512	1	1	0.819120973
BP	GO:0032733	0/21	29/11512	1	1	0.819120973
BP	GO:0032945	0/21	66/11512	1	1	0.819120973
BP	GO:0033003	0/21	38/11512	1	1	0.819120973
BP	GO:0033004	0/21	11/11512	1	1	0.819120973
BP	GO:0034121	0/21	52/11512	1	1	0.819120973
BP	GO:0034122	0/21	28/11512	1	1	0.819120973
BP	GO:0035666	0/21	27/11512	1	1	0.819120973
BP	GO:0035710	0/21	73/11512	1	1	0.819120973
BP	GO:0036037	0/21	16/11512	1	1	0.819120973
BP	GO:0042130	0/21	52/11512	1	1	0.819120973
BP	GO:0043277	0/21	36/11512	1	1	0.819120973
BP	GO:0045089	0/21	308/11512	1	1	0.819120973

BP	GO:0045576	0/21	55/11512	1	1	0.819120973
BP	GO:0045806	0/21	45/11512	1	1	0.819120973
BP	GO:0045807	0/21	128/11512	1	1	0.819120973
BP	GO:0046007	0/21	10/11512	1	1	0.819120973
BP	GO:0046631	0/21	113/11512	1	1	0.819120973
BP	GO:0046633	0/21	26/11512	1	1	0.819120973
BP	GO:0046634	0/21	76/11512	1	1	0.819120973
BP	GO:0046636	0/21	31/11512	1	1	0.819120973
BP	GO:0046640	0/21	23/11512	1	1	0.819120973
BP	GO:0050672	0/21	66/11512	1	1	0.819120973
BP	GO:0050714	0/21	226/11512	1	1	0.819120973
BP	GO:0050715	0/21	113/11512	1	1	0.819120973
BP	GO:0050764	0/21	82/11512	1	1	0.819120973
BP	GO:0050765	0/21	17/11512	1	1	0.819120973
BP	GO:0050766	0/21	59/11512	1	1	0.819120973
BP	GO:0051047	0/21	369/11512	1	1	0.819120973
BP	GO:0051222	0/21	356/11512	1	1	0.819120973
BP	GO:0051259	0/21	434/11512	1	1	0.819120973
BP	GO:0051260	0/21	273/11512	1	1	0.819120973
BP	GO:0060538	0/21	130/11512	1	1	0.819120973
BP	GO:0060760	0/21	44/11512	1	1	0.819120973
BP	GO:0070227	0/21	56/11512	1	1	0.819120973
BP	GO:0070228	0/21	40/11512	1	1	0.819120973
BP	GO:0070230	0/21	12/11512	1	1	0.819120973
BP	GO:0070231	0/21	38/11512	1	1	0.819120973
BP	GO:0070232	0/21	24/11512	1	1	0.819120973
BP	GO:0070664	0/21	71/11512	1	1	0.819120973
BP	GO:0070670	0/21	31/11512	1	1	0.819120973
BP	GO:0071216	0/21	196/11512	1	1	0.819120973
BP	GO:0071219	0/21	177/11512	1	1	0.819120973
BP	GO:0071222	0/21	171/11512	1	1	0.819120973
BP	GO:0071353	0/21	29/11512	1	1	0.819120973
BP	GO:0071706	0/21	132/11512	1	1	0.819120973
BP	GO:0071887	0/21	88/11512	1	1	0.819120973
BP	GO:0090594	0/21	10/11512	1	1	0.819120973
BP	GO:0097485	0/21	227/11512	1	1	0.819120973
BP	GO:1901998	0/21	33/11512	1	1	0.819120973
BP	GO:1903532	0/21	344/11512	1	1	0.819120973
BP	GO:1903555	0/21	129/11512	1	1	0.819120973
BP	GO:1903556	0/21	52/11512	1	1	0.819120973
BP	GO:1904951	0/21	390/11512	1	1	0.819120973
BP	GO:2000106	0/21	67/11512	1	1	0.819120973
BP	GO:2000108	0/21	21/11512	1	1	0.819120973
BP	GO:2000514	0/21	48/11512	1	1	0.819120973
BP	GO:2000515	0/21	22/11512	1	1	0.819120973
BP	GO:2001185	0/21	10/11512	1	1	0.819120973
CC	GO:0043235	4/21	336/11816	0.0026201	0.18340475	0.16547797
CC	GO:0009897	3/21	281/11816	0.0128882	0.287150048	0.25908275
CC	GO:0031430	1/21	19/11816	0.033258	0.287150048	0.25908275
CC	GO:0031528	1/21	19/11816	0.033258	0.287150048	0.25908275
CC	GO:0032982	1/21	20/11816	0.0349789	0.287150048	0.25908275

CC	GO:0042101	1/21	21/11816	0.0366969	0.287150048	0.25908275
CC	GO:0098552	3/21	438/11816	0.0409853	0.287150048	0.25908275
CC	GO:0005865	1/21	25/11816	0.0435398	0.287150048	0.25908275
CC	GO:0036379	1/21	26/11816	0.0452432	0.287150048	0.25908275
CC	GO:0005912	3/21	473/11816	0.0496324	0.287150048	0.25908275
CC	GO:0009925	1/21	29/11816	0.0503364	0.287150048	0.25908275
CC	GO:0031672	1/21	29/11816	0.0503364	0.287150048	0.25908275
CC	GO:0070161	3/21	487/11816	0.0533279	0.287150048	0.25908275
CC	GO:0030667	2/21	237/11816	0.0655329	0.299699141	0.27040524
CC	GO:0060076	1/21	41/11816	0.0704512	0.299699141	0.27040524
CC	GO:0045178	1/21	42/11816	0.072109	0.299699141	0.27040524
CC	GO:0016324	2/21	257/11816	0.0754801	0.299699141	0.27040524
CC	GO:0035577	1/21	45/11816	0.0770655	0.299699141	0.27040524
CC	GO:0016328	1/21	49/11816	0.083635	0.304160355	0.274430395
CC	GO:0016459	1/21	51/11816	0.086903	0.304160355	0.274430395
CC	GO:0070821	1/21	61/11816	0.1030772	0.328318235	0.296226978
CC	GO:0045177	2/21	313/11816	0.1056463	0.328318235	0.296226978
CC	GO:0005902	1/21	64/11816	0.107876	0.328318235	0.296226978
CC	GO:0035579	1/21	76/11816	0.1268278	0.348121766	0.314094826
CC	GO:0005925	2/21	362/11816	0.1343269	0.348121766	0.314094826
CC	GO:0005924	2/21	365/11816	0.1361398	0.348121766	0.314094826
CC	GO:0030055	2/21	369/11816	0.1385662	0.348121766	0.314094826
CC	GO:0043202	1/21	84/11816	0.1392487	0.348121766	0.314094826
CC	GO:0031012	2/21	427/11816	0.1747779	0.412185635	0.371896814
CC	GO:0030018	1/21	110/11816	0.1784648	0.412185635	0.371896814
CC	GO:0044437	2/21	442/11816	0.1844062	0.412185635	0.371896814
CC	GO:0031674	1/21	119/11816	0.1916386	0.412185635	0.371896814
CC	GO:0005766	1/21	128/11816	0.2046111	0.412185635	0.371896814
CC	GO:0042582	1/21	128/11816	0.2046111	0.412185635	0.371896814
CC	GO:0042581	1/21	139/11816	0.2201972	0.412185635	0.371896814
CC	GO:0030426	1/21	142/11816	0.2243972	0.412185635	0.371896814
CC	GO:0070820	1/21	142/11816	0.2243972	0.412185635	0.371896814
CC	GO:0030427	1/21	146/11816	0.2299637	0.412185635	0.371896814
CC	GO:0005775	1/21	148/11816	0.2327327	0.412185635	0.371896814
CC	GO:0098802	1/21	156/11816	0.243714	0.412185635	0.371896814
CC	GO:0030658	1/21	160/11816	0.2491484	0.412185635	0.371896814
CC	GO:0030017	1/21	161/11816	0.2505012	0.412185635	0.371896814
CC	GO:0098858	1/21	163/11816	0.2531997	0.412185635	0.371896814
CC	GO:0044449	1/21	177/11816	0.2718323	0.421634464	0.380422073
CC	GO:0030016	1/21	179/11816	0.2744577	0.421634464	0.380422073
CC	GO:0016323	1/21	181/11816	0.2770741	0.421634464	0.380422073
CC	GO:0043292	1/21	188/11816	0.2861608	0.426196873	0.384538532
CC	GO:0150034	1/21	238/11816	0.3479732	0.500480558	0.451561406
CC	GO:0005938	1/21	240/11816	0.3503364	0.500480558	0.451561406
CC	GO:0005765	1/21	269/11816	0.3836998	0.526646739	0.47516999
CC	GO:0098852	1/21	269/11816	0.3836998	0.526646739	0.47516999
CC	GO:0031253	1/21	280/11816	0.3959227	0.532972887	0.480877793
CC	GO:0030133	1/21	306/11816	0.4239022	0.551468274	0.49756536
CC	GO:0005774	1/21	309/11816	0.42705	0.551468274	0.49756536
CC	GO:0033267	1/21	315/11816	0.4332965	0.551468274	0.49756536
CC	GO:0062023	1/21	342/11816	0.460612	0.575764976	0.519487196

CC	GO:0005911	1/21	367/11816	0.4847822	0.586222559	0.52892261
CC	GO:0099568	1/21	368/11816	0.4857273	0.586222559	0.52892261
CC	GO:0015629	1/21	403/11816	0.5177823	0.614317956	0.55427184
CC	GO:0043025	1/21	425/11816	0.5369473	0.62643849	0.56520766
CC	GO:0098797	1/21	469/11816	0.5731231	0.657682283	0.593397548
CC	GO:0044297	1/21	482/11816	0.5832855	0.658290327	0.59394616
CC	GO:0030424	1/21	494/11816	0.5924613	0.658290327	0.59394616
CC	GO:0005769	0/21	282/11816	1	1	0.902255639
CC	GO:0010008	0/21	374/11816	1	1	0.902255639
CC	GO:0031901	0/21	117/11816	1	1	0.902255639
CC	GO:0044291	0/21	65/11816	1	1	0.902255639
CC	GO:0044440	0/21	412/11816	1	1	0.902255639
CC	GO:0055037	0/21	140/11816	1	1	0.902255639
CC	GO:0055038	0/21	64/11816	1	1	0.902255639
MF	GO:0019838	3/19	122/11509	0.0009948	0.048744184	0.035602626
MF	GO:0004714	2/19	57/11509	0.0039041	0.09565064	0.069862981
MF	GO:0019199	2/19	72/11509	0.006161	0.100630379	0.073500169
MF	GO:0004713	2/19	124/11509	0.0174689	0.147149517	0.107477628
MF	GO:0015125	1/19	11/11509	0.0180183	0.147149517	0.107477628
MF	GO:0048407	1/19	11/11509	0.0180183	0.147149517	0.107477628
MF	GO:0005161	1/19	14/11509	0.0228788	0.152405103	0.111316294
MF	GO:0042288	1/19	18/11509	0.0293239	0.152405103	0.111316294
MF	GO:0051371	1/19	18/11509	0.0293239	0.152405103	0.111316294
MF	GO:0017134	1/19	20/11509	0.0325313	0.152405103	0.111316294
MF	GO:0043548	1/19	22/11509	0.0357288	0.152405103	0.111316294
MF	GO:0019865	1/19	23/11509	0.0373237	0.152405103	0.111316294
MF	GO:0004672	3/19	482/11509	0.0429493	0.152874848	0.111659395
MF	GO:0042287	1/19	27/11509	0.0436785	0.152874848	0.111659395
MF	GO:0051393	1/19	29/11509	0.046841	0.153013997	0.111761029
MF	GO:1901618	1/19	32/11509	0.0515662	0.153157582	0.111865903
MF	GO:0008028	1/19	33/11509	0.0531363	0.153157582	0.111865903
MF	GO:0042805	1/19	38/11509	0.06095	0.165919513	0.121187185
MF	GO:0008307	1/19	42/11509	0.067157	0.173194314	0.126500681
MF	GO:0003779	2/19	342/11509	0.1080988	0.264842153	0.193440026
MF	GO:1990782	1/19	81/11509	0.125672	0.293234576	0.214177778
MF	GO:0004896	1/19	87/11509	0.1343595	0.29848618	0.218013537
MF	GO:0005319	1/19	91/11509	0.1401058	0.29848618	0.218013537
MF	GO:0005342	1/19	107/11509	0.1627313	0.316221574	0.230967423
MF	GO:0046943	1/19	107/11509	0.1627313	0.316221574	0.230967423
MF	GO:0019955	1/19	115/11509	0.1738314	0.316221574	0.230967423
MF	GO:0070851	1/19	118/11509	0.1779579	0.316221574	0.230967423
MF	GO:0019903	1/19	120/11509	0.180698	0.316221574	0.230967423
MF	GO:0008201	1/19	137/11509	0.2036424	0.344085409	0.251319095
MF	GO:0008514	1/19	150/11509	0.2207759	0.355139177	0.259392739
MF	GO:0019902	1/19	153/11509	0.2246799	0.355139177	0.259392739
MF	GO:0051015	1/19	160/11509	0.2337173	0.357879555	0.261394304
MF	GO:0005516	1/19	170/11509	0.2464548	0.365948076	0.267287531
MF	GO:0005539	1/19	186/11509	0.2664186	0.376429949	0.274943464
MF	GO:0030246	1/19	188/11509	0.2688785	0.376429949	0.274943464
MF	GO:1901681	1/19	205/11509	0.2894748	0.394007404	0.287781992
MF	GO:0008509	1/19	239/11509	0.3290298	0.435742225	0.318264998

MF	GO:0004674	1/19	347/11509	0. 441294	0. 569037032	0. 415623181
MF	GO:0004930	1/19	363/11509	0. 4563278	0. 573334899	0. 418762332
MF	GO:0001786	0/19	42/11509	1	1	0. 730397422
MF	GO:0005126	0/19	242/11509	1	1	0. 730397422
MF	GO:0005543	0/19	316/11509	1	1	0. 730397422
MF	GO:0017124	0/19	103/11509	1	1	0. 730397422
MF	GO:0033218	0/19	298/11509	1	1	0. 730397422
MF	GO:0042169	0/19	31/11509	1	1	0. 730397422
MF	GO:0046625	0/19	17/11509	1	1	0. 730397422
MF	GO:0072341	0/19	68/11509	1	1	0. 730397422
MF	GO:0098631	0/19	45/11509	1	1	0. 730397422
MF	GO:0098632	0/19	38/11509	1	1	0. 730397422

geneID	Count
BTN3A1/CEACAM1/FCER1A/HHLA2/PIGR	5
CEACAM1/IL1R2	2
MYBPC1/PDGFRB	2
BTN3A1/CEACAM1/FCER1A/HHLA2/PIGR	5
FGFR2/MYBPC1/PDGFRB/SPEG	4
BTN3A1/HHLA2	2
BTN3A1/CEACAM1/HHLA2	3
LRIG2/PDGFRB	2
FGFR2/MYBPC1/PDGFRB	3
FGFR2/PDGFRB	2
FGFR2/MYBPC1	2
FGFR2/PDGFRB	2
FGFR2/PDGFRB	2
MYBPC1/PDGFRB	2
BTN3A1/CEACAM1/HHLA2	3
MYBPC1/PDGFRB	2
FGFR2/MYBPC1	2
CEACAM1/PDGFRB	2
CEACAM1/FGFR2/MCAM/PDGFRB	4
CEACAM1/IL1R2	2
MYBPC1/PDGFRB	2
FGFR2/MYBPC1	2
CEACAM1/LRIG2	2
CEACAM1/FGFR2/PDGFRB	3
CEACAM1/IL1R2	2
FGFR2/PDGFRB	2
CEACAM1/FGFR2/MCAM/PDGFRB	4
FGFR2/PDGFRB	2
CEACAM1/FGFR2/PDGFRB	3
MYBPC1/PDGFRB	2
FGFR2/PDGFRB	2
CEACAM1/IL1R2/LRIG2	3
MYBPC1/PDGFRB	2
CEACAM1/PIGR	2
CEACAM1/FGFR2	2
CEACAM1/PDGFRB	2
CEACAM1/FGFR2	2
FGFR2/MYBPC1/PDGFRB	3
MYBPC1	1
FGFR2	1
IL1R2	1
FGFR2	1
FGFR2	1
FGFR2	1
MCAM	1
PDGFRB	1
PDGFRB	1
CEACAM1	1
CEACAM1	1

BTN3A1/CEACAM1/HHLA2	3
FGFR2/MYBPC1/SPEG	3
MYBPC1	1
MYBPC1	1
CEACAM1	1
FGFR2	1
FGFR2	1
FGFR2	1
LRIG2	1
FGFR2/MYBPC1/PDGFRB	3
CEACAM1/PIGR	2
MYBPC1/PDGFRB	2
FGFR2/PDGFRB	2
CEACAM1	1
FGFR2	1
CEACAM1	1
FGFR2/PDGFRB	2
CEACAM1/PDGFRB	2
CEACAM1	1
MYBPC1	1
PDGFRB	1
FGFR2	1
FGFR2	1
PDGFRB	1
IL1R2	1
PDGFRB	1
PDGFRB	1
CEACAM1	1
MYBPC1/PDGFRB	2
CEACAM1	1
FGFR2	1
PDGFRB	1
PIGR	1
CEACAM1	1
MYBPC1	1
PDGFRB	1
PDGFRB	1
PDGFRB	1
FGFR2/PDGFRB	2
CEACAM1	1
FGFR2	1
PDGFRB	1
PDGFRB	1
CEACAM1	1
CEACAM1	1
CEACAM1	1

LRIG2	1
MYBPC1/PDGFRB	2
CEACAM1/LRIG2	2
FGFR2/PDGFRB	2
CEACAM1	1
MCAM	1
CEACAM1	1
FGFR2	1
FGFR2	1
CEACAM1	1
FGFR2/PDGFRB	2
FGFR2/PDGFRB	2
CEACAM1	1
PDGFRB	1
FGFR2	1
PDGFRB	1
MCAM	1
FGFR2/PDGFRB	2
BTN3A1/HHLA2	2
BTN3A1/CEACAM1/HHLA2	3
CEACAM1/PDGFRB	2
FGFR2	1
PDGFRB	1
HHLA2	1
CEACAM1	1
PDGFRB	1
PDGFRB	1
CEACAM1/PDGFRB	2
FGFR2	1
CEACAM1	1
LRIG2	1
MCAM	1
FGFR2	1
BTN3A1	1
MYBPC1/PDGFRB	2
CEACAM1	1
FGFR2	1
CEACAM1	1
LRIG2	1
LRIG2	1
FGFR2	1
FGFR2	1
PDGFRB	1
CEACAM1/IL1R2	2
FCER1A/PIGR	2
CEACAM1/IL1R2	2
FGFR2/PDGFRB	2
PIGR	1
PIGR	1
LRIG2	1
CEACAM1	1

PDGFRB	1
CEACAM1	1
FGFR2/PDGFRB	2
FGFR2/PDGFRB	2
FGFR2/PDGFRB	2
PDGFRB	1
CEACAM1	1
PIGR	1
FGFR2	1
PDGFRB	1
CEACAM1	1
FGFR2	1
FGFR2	1
PDGFRB	1
PDGFRB	1
PDGFRB	1
FGFR2	1
FGFR2	1
FGFR2	1
CEACAM1	1
BTN3A1/IL1R2	2
PIGR	1
FGFR2	1
PDGFRB	1
FGFR2	1
CEACAM1	1
PIGR	1
PDGFRB	1
PDGFRB	1
LRIG2	1
CEACAM1	1
FGFR2	1
BTN3A1/CEACAM1/HHLA2	3
CEACAM1/IL1R2	2
CEACAM1/HHLA2/PDGFRB	3
FGFR2/PDGFRB	2
PDGFRB	1
FGFR2	1
FGFR2/PDGFRB	2
FGFR2/MYBPC1/PDGFRB	3
CEACAM1	1
PDGFRB	1
PDGFRB	1
FGFR2	1
CEACAM1	1
FGFR2	1
PDGFRB	1
CEACAM1	1
CEACAM1	1
HHLA2	1

IL1R2	1
FGFR2	1
FGFR2	1
FGFR2	1
IL1R2	1
FGFR2	1
FGFR2	1
PDGFRB	1
CEACAM1	1
FGFR2/MYBPC1	2
CEACAM1/FGFR2	2
CEACAM1	1
FGFR2	1
PDGFRB	1
PDGFRB	1
PDGFRB	1
IL1R2	1
LRIG2	1
FGFR2/PDGFRB	2
FGFR2/PDGFRB	2
CEACAM1	1
PDGFRB	1
PDGFRB	1
CEACAM1	1
FGFR2	1
LRIG2	1
CEACAM1	1
FGFR2	1
FGFR2	1
MYBPC1/PDGFRB	2
IL1R2	1
CEACAM1	1
FGFR2	1
PDGFRB	1
PDGFRB	1
MYBPC1	1
MYBPC1	1
IL1R2	1
FGFR2	1
CEACAM1	1
CEACAM1	1
LRIG2	1
PDGFRB	1
CEACAM1/IL1R2	2
BTN3A1/HHLA2	2
CEACAM1	1
CEACAM1	1
FGFR2	1
PDGFRB	1
BTN3A1/HHLA2	2
PDGFRB	1

FGFR2	1
FGFR2	1
PIGR	1
FGFR2	1
FGFR2/PDGFRB	2
CEACAM1	1
PDGFRB	1
IL1R2	1
CEACAM1	1
PDGFRB	1
CEACAM1	1
FGFR2	1
FGFR2	1
LRIG2	1
CEACAM1	1
FGFR2	1
FGFR2	1
CEACAM1	1
FGFR2	1
FGFR2	1
CEACAM1	1
FGFR2	1
PDGFRB	1
CEACAM1	1
FGFR2	1
FGFR2/PDGFRB	2
CEACAM1/HHLA2	2
BTN3A1/HHLA2	2
FGFR2	1
PDGFRB	1
PDGFRB	1
MYBPC1	1
FGFR2	1
FGFR2	1
PDGFRB	1
FGFR2	1
FGFR2	1
CEACAM1/HHLA2	2
FGFR2	1
PDGFRB	1
CEACAM1	1
PIGR	1
PIGR	1
IL1R2	1
HHLA2	1
PDGFRB	1
CEACAM1	1
PDGFRB	1
IL1R2/LRIG2	2
CEACAM1	1
FGFR2	1

LRIG2	1
HHLA2	1
LRIG2	1
CEACAM1	1
FGFR2	1
FGFR2	1
PDGFRB	1
FGFR2	1
CEACAM1	1
CEACAM1	1
CEACAM1/FGFR2	2
FGFR2	1
IL1R2	1
CEACAM1	1
HHLA2/PDGFRB	2
FGFR2	1
LRIG2	1
PDGFRB	1
CEACAM1	1
PDGFRB	1
IL1R2	1
FGFR2	1
CEACAM1/HHLA2	2
FGFR2/PDGFRB	2
FGFR2/PDGFRB	2
PDGFRB	1
MYBPC1	1
PDGFRB	1
FGFR2	1
FGFR2	1
PDGFRB	1
CEACAM1	1
PDGFRB	1
IL1R2	1
FGFR2	1
PDGFRB	1
FGFR2	1
PDGFRB	1
FGFR2	1
FGFR2/PDGFRB	2
FGFR2	1
FGFR2/PDGFRB	2
PDGFRB	1
CEACAM1	1
PIGR	1
FGFR2	1
PDGFRB	1
CEACAM1	1

PDGFRB	1
CEACAM1	1
LRIG2	1
FGFR2/PDGFRB	2
FGFR2/PDGFRB	2
CEACAM1	1
LRIG2	1
FGFR2	1
FGFR2	1
FGFR2	1
CEACAM1	1
PDGFRB	1
FGFR2	1
FGFR2	1
CEACAM1	1
FGFR2	1
FGFR2	1
FGFR2	1
CEACAM1	1
CEACAM1/FGFR2	2
CEACAM1/PDGFRB	2
FGFR2	1
FGFR2	1
CEACAM1	1
PDGFRB	1
CEACAM1/HHLA2	2
FGFR2	1
PDGFRB	1
FGFR2	1
PDGFRB	1
CEACAM1	1
CEACAM1	1
PDGFRB	1
PDGFRB	1
FGFR2	1
FGFR2	1
CEACAM1	1
CEACAM1	1
PDGFRB	1
FGFR2	1
HHLA2	1
CEACAM1	1
CEACAM1/HHLA2	2
FGFR2	1
FGFR2	1
PDGFRB	1
PDGFRB	1
CEACAM1	1
BTN3A1/CEACAM1	2

CEACAM1	1
FGFR2	1
PDGFRB	1
FGFR2/PDGFRB	2
CEACAM1	1
FGFR2	1
FGFR2	1
FGFR2/PDGFRB	2
CEACAM1	1
PDGFRB	1
FGFR2	1
FGFR2	1
CEACAM1/IL1R2	2
CEACAM1	1
PDGFRB	1
PDGFRB	1
PIGR	1
BTN3A1	1
FGFR2	1
CEACAM1	1
CEACAM1	1
IL1R2	1
PDGFRB	1
CEACAM1	1
CEACAM1/FGFR2	2
CEACAM1	1
CEACAM1	1
FGFR2	1
CEACAM1	1
CEACAM1	1
FGFR2	1
PDGFRB	1
FGFR2	1
FGFR2	1
PIGR	1
IL1R2	1
CEACAM1	1
MYBPC1	1
IL1R2	1
IL1R2	1
CEACAM1/PIGR	2
CEACAM1	1
LRIG2	1

PDGFRB	1
FGFR2	1
MCAM	1
CEACAM1	1
FGFR2	1
PDGFRB	1
FGFR2	1
HHLA2	1
PIGR	1
CEACAM1/PIGR	2
CEACAM1/HHLA2	2
HHLA2	1
FGFR2	1
CEACAM1	1
FGFR2	1
LRIG2	1
PDGFRB	1
FCER1A	1
FGFR2	1
IL1R2	1
FGFR2/LRIG2	2
CEACAM1/PIGR	2
CEACAM1/PIGR	2
IL1R2	1
CEACAM1	1
CEACAM1	1
CEACAM1/PIGR	2
HHLA2	1
MCAM/PDGFRB	2
FGFR2	1
CEACAM1/FGFR2	2
FGFR2/PDGFRB	2
FGFR2	1
FGFR2/PDGFRB	2
MCAM/PDGFRB	2
PDGFRB	1
FGFR2	1
FGFR2/PDGFRB	2
CEACAM1	1
PDGFRB	1
FGFR2	1
PDGFRB	1

FGFR2	1
LRIG2/PIGR	2
CEACAM1	1
MYBPC1	1
PDGFRB	1
PDGFRB	1
CEACAM1	1
PDGFRB	1
FGFR2	1
FGFR2	1
PDGFRB	1
CEACAM1	1
MCAM/PDGFRB	2
CEACAM1/PIGR	2
CEACAM1	1
CEACAM1	1
PDGFRB	1
LRIG2	1
PIGR	1
FGFR2	1
LRIG2	1
CEACAM1	1
CEACAM1	1
PDGFRB	1
CEACAM1	1
FGFR2	1
PDGFRB	1
CEACAM1/PIGR	2
CEACAM1	1
BTN3A1/IL1R2	2
MCAM/PDGFRB	2
HHLA2	1
CEACAM1/PIGR	2
FGFR2	1
FGFR2	1
FGFR2	1
LRIG2	1
CEACAM1	1
CEACAM1	1
IL1R2	1
PDGFRB	1
FGFR2	1
PDGFRB	1
CEACAM1	1
PDGFRB	1
PDGFRB	1
PDGFRB	1
CEACAM1	1
CEACAM1	1
PDGFRB	1
IL1R2	1

FGFR2	1
BTN3A1/IL1R2	2
CEACAM1	1
IL1R2	1
CEACAM1	1
IL1R2	1
CEACAM1	1
FGFR2	1
FGFR2	1
FGFR2	1
CEACAM1	1
FGFR2	1
FGFR2	1
CEACAM1	1
PDGFRB	1
CEACAM1	1
LRIG2	1
IL1R2	1
PDGFRB	1
CEACAM1	1
PDGFRB	1
CEACAM1	1
PDGFRB	1
FGFR2	1
FGFR2	1
PDGFRB	1
FGFR2	1
IL1R2	1
CEACAM1	1
LRIG2	1
CEACAM1	1
FGFR2	1
CEACAM1	1
FGFR2	1
PSG9	1
HHLA2	1
HHLA2	1
HHLA2	1
FGFR2	1
FGFR2	1
PIGR	1
IL1R2	1
CEACAM1	1
PDGFRB	1
FGFR2	1

CEACAM1	1
HHLA2	1
PDGFRB	1
LRIG2	1
PDGFRB	1
HHLA2	1
PDGFRB	1
PDGFRB	1
CEACAM1	1
CEACAM1	1
FGFR2	1
FGFR2	1
CEACAM1	1
PDGFRB	1
PSG9	1
FGFR2	1
CEACAM1	1
PDGFRB	1
FGFR2	1
LRIG2	1
FGFR2	1
FGFR2	1
FGFR2	1
CEACAM1	1
PDGFRB	1
FGFR2	1
FGFR2	1
CEACAM1	1
IL1R2	1
CEACAM1	1
CEACAM1	1
HHLA2	1
FGFR2	1
PDGFRB	1
CEACAM1	1
PDGFRB	1
CEACAM1	1
FGFR2	1
HHLA2	1
CEACAM1	1
PIGR	1
PDGFRB	1
LRIG2	1
LRIG2	1
PDGFRB	1
FGFR2	1
CEACAM1	1

CEACAM1	1
CEACAM1	1
PDGFRB	1
CEACAM1	1
LRIG2	1
CEACAM1	1
CEACAM1	1
PDGFRB	1
PDGFRB	1
PDGFRB	1
FGFR2	1
FGFR2	1
HHLA2	1
IL1R2	1
PDGFRB	1
FGFR2	1
CEACAM1	1
CEACAM1	1
PDGFRB	1
LRIG2	1
FGFR2	1
FGFR2	1
CEACAM1	1
FGFR2	1
LRIG2	1
CEACAM1	1
PDGFRB	1
FGFR2	1
FGFR2	1
PDGFRB	1
CEACAM1	1
PDGFRB	1
CEACAM1	1
PDGFRB	1
MYBPC1	1
PDGFRB	1
FGFR2	1
PDGFRB	1
PDGFRB	1
PDGFRB	1
LRIG2	1
MYBPC1	1
FGFR2	1
IL1R2	1
PDGFRB	1
CEACAM1	1
CEACAM1	1

FGFR2	1
CEACAM1	1
PDGFRB	1
PDGFRB	1
CEACAM1	1
CEACAM1	1
CEACAM1	1
FGFR2	1
PIGR	1
PDGFRB	1
PDGFRB	1
HHLA2	1
FGFR2	1
PDGFRB	1
PDGFRB	1
CEACAM1	1
PDGFRB	1
CEACAM1	1
HHLA2	1
PDGFRB	1
MYBPC1	1
CEACAM1	1
IL1R2	1
PDGFRB	1
CEACAM1	1
FGFR2	1
CEACAM1	1
PIGR	1
IL1R2	1
FGFR2	1
FGFR2	1
LRIG2	1
PDGFRB	1
FGFR2	1
CEACAM1	1
CEACAM1	1
PDGFRB	1
CEACAM1	1
LRIG2	1
CEACAM1	1
PDGFRB	1
CEACAM1	1
CEACAM1	1
PDGFRB	1
FGFR2	1





CEACAM1	1
BTN3A1/HHLA2/MCAM	3
MYBPC1	1
MYBPC1	1
CEACAM1/MCAM/PDGFRB	3
CEACAM1	1
MYBPC1	1
CEACAM1/MCAM/PDGFRB	3
CEACAM1/PIGR	2
FGFR2	1
CEACAM1	1
CEACAM1/PDGFRB	2
PIGR	1
CEACAM1	1
MYBPC1	1
CEACAM1	1
CEACAM1/PDGFRB	2
CEACAM1	1
CEACAM1	1
MCAM/PDGFRB	2
MCAM/PDGFRB	2
MCAM/PDGFRB	2
PDGFRB	1
FGFR2/LRIG2	2
MYBPC1	1
PDGFRB/PIGR	2
MYBPC1	1
PIGR	1
PIGR	1
CEACAM1	1
LRIG2	1
CEACAM1	1
LRIG2	1
PDGFRB	1
CEACAM1	1
CEACAM1	1
MYBPC1	1
CEACAM1	1
MYBPC1	1
CEACAM1	1
MYBPC1	1
CEACAM1	1
MYBPC1	1
CEACAM1	1
LRIG2	1
FGFR2	1
PIGR	1
PIGR	1
CEACAM1	1
CEACAM1	1
PIGR	1
LRIG2	1
FGFR2	1

CEACAM1	1
FGFR2	1
MYBPC1	1
LRIG2	1
CEACAM1	1
LRIG2	1
LRIG2	1
	0
	0
	0
	0
	0
	0
	0
	0
FGFR2/IL1R2/PDGFRB	3
FGFR2/PDGFRB	2
FGFR2/PDGFRB	2
FGFR2/PDGFRB	2
CEACAM1	1
PDGFRB	1
PDGFRB	1
PILRA	1
MYBPC1	1
FGFR2	1
PDGFRB	1
FCER1A	1
FGFR2/PDGFRB/SPEG	3
PILRA	1
MYBPC1	1
CEACAM1	1
CEACAM1	1
MYBPC1	1
MYBPC1	1
CEACAM1/MYBPC1	2
CEACAM1	1
IL1R2	1
CEACAM1	1
CEACAM1	1
CEACAM1	1
IL1R2	1
PDGFRB	1
CEACAM1	1
FGFR2	1
CEACAM1	1
CEACAM1	1
MYBPC1	1
CEACAM1	1
FGFR2	1
SIGLEC8	1
FGFR2	1
CEACAM1	1

SPEG	1
PDGFRB	1
	0
	0
	0
	0
	0
	0
	0
	0
	0
	0
	0

**Description**

immune response-regulating cell surface receptor signaling pathway  
negative regulation of interleukin-1 production  
cardiac myofibril assembly  
immune response-regulating signaling pathway  
muscle cell differentiation  
activated T cell proliferation  
T cell receptor signaling pathway  
platelet-derived growth factor receptor signaling pathway  
cardiac muscle tissue development  
positive regulation of phospholipase activity  
cardiac muscle tissue morphogenesis  
positive regulation of lipase activity  
regulation of phospholipase activity  
myofibril assembly  
antigen receptor-mediated signaling pathway  
cardiac muscle cell development  
muscle tissue morphogenesis  
vasculogenesis  
angiogenesis  
regulation of interleukin-1 production  
cardiac cell development  
muscle organ morphogenesis  
negative regulation of response to wounding  
regulation of ERK1 and ERK2 cascade  
interleukin-1 production  
positive regulation of smooth muscle cell proliferation  
wound healing  
regulation of lipase activity  
ERK1 and ERK2 cascade  
cellular component assembly involved in morphogenesis  
response to retinoic acid  
negative regulation of response to external stimulus  
cardiac muscle cell differentiation  
epidermal growth factor receptor signaling pathway  
gland morphogenesis  
regulation of phosphatidylinositol 3-kinase signaling  
negative regulation of epithelial cell proliferation  
striated muscle tissue development  
myosin filament assembly  
neuronal stem cell division  
negative regulation of interleukin-1 secretion  
neuroblast division  
limb bud formation  
lateral sprouting from an epithelium  
prostate gland growth  
vascular wound healing  
glomerular mesangial cell proliferation  
fibroblast activation  
negative regulation of platelet aggregation  
positive regulation of vasculogenesis

immune response-activating cell surface receptor signaling pathway  
muscle organ development  
skeletal muscle thin filament assembly  
myosin filament organization  
negative regulation of homotypic cell-cell adhesion  
prostate glandular acinus development  
branching involved in labyrinthine layer morphogenesis  
epithelial cell differentiation involved in prostate gland development  
negative regulation of neuron projection regeneration  
muscle tissue development  
ERBB signaling pathway  
cardiocyte differentiation  
regulation of smooth muscle cell proliferation  
regulation of response to tumor cell  
regulation of immune response to tumor cell  
regulation of granulocyte differentiation  
negative regulation of vascular permeability  
negative regulation of leukocyte degranulation  
negative regulation of natural killer cell mediated cytotoxicity  
branching involved in prostate gland morphogenesis  
regulation of hepatocyte proliferation  
smooth muscle cell proliferation  
phosphatidylinositol 3-kinase signaling  
negative regulation of natural killer cell mediated immunity  
skeletal myofibril assembly  
platelet-derived growth factor receptor-beta signaling pathway  
morphogenesis of an epithelial bud  
otic vesicle development  
metanephric mesenchyme development  
negative regulation of cytokine production involved in inflammatory response  
coronary vasculature morphogenesis  
positive regulation of metanephros development  
regulation of vasculogenesis  
striated muscle cell development  
immune response to tumor cell  
hair follicle morphogenesis  
positive regulation of phosphoprotein phosphatase activity  
transcytosis  
negative regulation of fatty acid biosynthetic process  
cardiac muscle fiber development  
cell migration involved in heart development  
glomerular mesangium development  
metanephric glomerulus development  
positive regulation of protein kinase B signaling  
negative regulation of leukocyte mediated cytotoxicity  
embryonic digestive tract morphogenesis  
retina vasculature development in camera-type eye  
kidney mesenchyme development  
hepatocyte proliferation  
epithelial cell proliferation involved in liver morphogenesis  
regulation of platelet aggregation

positive regulation of protein localization to cell surface  
muscle cell development  
regulation of response to wounding  
inner ear development  
negative regulation of T cell mediated immunity  
glomerular filtration  
negative regulation of platelet activation  
somatic stem cell division  
branch elongation of an epithelium  
liver morphogenesis  
lung development  
organ growth  
response to tumor cell  
cellular response to platelet-derived growth factor stimulus  
epidermis morphogenesis  
positive regulation of calcium ion import  
renal filtration  
respiratory tube development  
T cell proliferation  
T cell activation  
phosphatidylinositol-mediated signaling  
regulation of osteoblast proliferation  
response to platelet-derived growth factor  
positive regulation of activated T cell proliferation  
negative regulation of T cell receptor signaling pathway  
response to hyperoxia  
cell proliferation involved in kidney development  
inositol lipid-mediated signaling  
cell proliferation in forebrain  
negative regulation of cell killing  
regulation of membrane protein ectodomain proteolysis  
angiogenesis involved in wound healing  
labyrinthine layer morphogenesis  
interferon-gamma secretion  
actomyosin structure organization  
bile acid and bile salt transport  
osteoblast proliferation  
regulation of homotypic cell-cell adhesion  
regulation of axon regeneration  
innervation  
branching involved in salivary gland morphogenesis  
morphogenesis of an epithelial fold  
metanephric nephron morphogenesis  
negative regulation of defense response  
Fc receptor signaling pathway  
negative regulation of secretion by cell  
ear development  
detection of chemical stimulus involved in sensory perception of bitter taste  
mucosal immune response  
regulation of platelet-derived growth factor receptor signaling pathway  
negative regulation of fatty acid metabolic process

regulation of metanephros development  
negative regulation of regulated secretory pathway  
respiratory system development  
muscle cell proliferation  
positive regulation of ERK1 and ERK2 cascade  
positive regulation of Rho protein signal transduction  
wound healing, spreading of cells  
detection of chemical stimulus involved in sensory perception of taste  
embryonic placenta morphogenesis  
glomerulus vasculature development  
epiboly involved in wound healing  
positive regulation of mesenchymal cell proliferation  
axis elongation  
positive regulation of collagen metabolic process  
positive regulation of collagen biosynthetic process  
response to increased oxygen levels  
regulation of smooth muscle cell differentiation  
positive regulation of cardiac muscle cell proliferation  
epithelial tube branching involved in lung morphogenesis  
prostate gland epithelium morphogenesis  
epiboly  
cytokine secretion  
organ or tissue specific immune response  
outflow tract septum morphogenesis  
positive regulation of phosphatase activity  
forebrain neuron development  
negative regulation of antigen receptor-mediated signaling pathway  
sensory perception of bitter taste  
renal system vasculature development  
kidney vasculature development  
regulation of neuron projection regeneration  
granulocyte differentiation  
prostate gland morphogenesis  
immune response-activating signal transduction  
negative regulation of secretion  
regulation of cell activation  
regulation of protein kinase B signaling  
metanephros morphogenesis  
specification of animal organ identity  
protein autophosphorylation  
heart development  
regulation of platelet activation  
aorta morphogenesis  
positive regulation of phosphatidylinositol 3-kinase activity  
mesodermal cell differentiation  
regulation of T cell mediated cytotoxicity  
stem cell division  
vascular endothelial growth factor signaling pathway  
regulation of endothelial cell differentiation  
negative regulation of exocytosis  
regulation of activated T cell proliferation

negative regulation of protein processing  
embryonic digestive tract development  
positive regulation of cardiac muscle tissue growth  
mammary gland duct morphogenesis  
negative regulation of protein maturation  
salivary gland morphogenesis  
regulation of mesenchymal cell proliferation  
regulation of collagen biosynthetic process  
negative regulation of animal organ morphogenesis  
heart morphogenesis  
regulation of animal organ morphogenesis  
regulation of vascular permeability  
lung epithelium development  
metanephric nephron development  
positive regulation of lipid kinase activity  
regulation of calcium ion import  
regulation of cytokine production involved in inflammatory response  
regulation of neuron migration  
protein kinase B signaling  
mesenchyme development  
negative regulation of lymphocyte mediated immunity  
response to fluid shear stress  
positive regulation of protein dephosphorylation  
regulation of natural killer cell mediated cytotoxicity  
lung alveolus development  
regulation of protein localization to cell surface  
regulation of natural killer cell mediated immunity  
salivary gland development  
positive regulation of heart growth  
striated muscle cell differentiation  
cytokine production involved in inflammatory response  
negative regulation of adaptive immune response based on somatic recombination of immune  
endochondral bone growth  
regulation of collagen metabolic process  
positive regulation of smooth muscle cell migration  
muscle filament sliding  
actin-myosin filament sliding  
regulation of interleukin-1 secretion  
ventricular septum morphogenesis  
blood vessel remodeling  
negative regulation of myeloid leukocyte differentiation  
membrane protein ectodomain proteolysis  
positive regulation of kidney development  
negative regulation of cytokine production  
lymphocyte proliferation  
negative regulation of response to biotic stimulus  
regulation of T cell receptor signaling pathway  
regulation of cardiac muscle cell proliferation  
coronary vasculature development  
mononuclear cell proliferation  
positive regulation of phospholipase C activity

embryonic cranial skeleton morphogenesis  
bone growth  
sensory perception of taste  
positive regulation of cardiac muscle tissue development  
kidney development  
negative regulation of adaptive immune response  
collagen biosynthetic process  
interleukin-1 secretion  
negative regulation of lipid biosynthetic process  
regulation of phospholipase C activity  
T cell mediated cytotoxicity  
mesenchymal cell proliferation  
forebrain neuron differentiation  
axon regeneration  
regulation of fatty acid biosynthetic process  
lung morphogenesis  
mammary gland morphogenesis  
morphogenesis of an epithelial sheet  
glandular epithelial cell differentiation  
exocrine system development  
regulation of leukocyte degranulation  
labyrinthine layer development  
positive regulation of phospholipid metabolic process  
negative regulation of leukocyte mediated immunity  
digestive tract morphogenesis  
renal system development  
regulation of leukocyte cell-cell adhesion  
leukocyte proliferation  
prostate gland development  
positive regulation of dephosphorylation  
regulation of phosphatidylinositol 3-kinase activity  
sarcomere organization  
positive regulation of organ growth  
ventricular cardiac muscle tissue morphogenesis  
positive regulation of mitotic nuclear division  
smooth muscle cell differentiation  
cardiac muscle cell proliferation  
regulation of T cell activation  
neuroblast proliferation  
cellular response to vascular endothelial growth factor stimulus  
natural killer cell mediated cytotoxicity  
receptor clustering  
retina homeostasis  
negative regulation of cytokine-mediated signaling pathway  
T cell costimulation  
aorta development  
negative regulation of innate immune response  
positive regulation of fibroblast proliferation  
negative regulation of proteolysis  
natural killer cell mediated immunity  
embryonic pattern specification

neuron projection regeneration  
lymphocyte costimulation  
membrane protein proteolysis  
negative regulation of blood coagulation  
animal organ formation  
regulation of morphogenesis of a branching structure  
regulation of kidney development  
forebrain generation of neurons  
negative regulation of coagulation  
negative regulation of hemostasis  
regulation of epithelial cell proliferation  
ventricular cardiac muscle tissue development  
negative regulation of response to cytokine stimulus  
platelet aggregation  
positive regulation of cell activation  
regulation of smoothened signaling pathway  
protein localization to cell surface  
positive regulation of Ras protein signal transduction  
regulation of antigen receptor-mediated signaling pathway  
regulation of lipid kinase activity  
negative regulation of cytokine secretion  
regulation of cardiac muscle tissue growth  
leukocyte cell-cell adhesion  
response to antibiotic  
urogenital system development  
glomerulus development  
muscle fiber development  
positive regulation of nuclear division  
cranial skeletal system development  
mesoderm formation  
regulation of smooth muscle cell migration  
regulation of sprouting angiogenesis  
positive regulation of DNA biosynthetic process  
production of molecular mediator involved in inflammatory response  
striated muscle cell proliferation  
positive regulation of small GTPase mediated signal transduction  
mesoderm morphogenesis  
artery morphogenesis  
regulation of heart growth  
ventricular septum development  
positive regulation of striated muscle tissue development  
positive regulation of muscle organ development  
response to acid chemical  
positive regulation of muscle tissue development  
positive regulation of cell cycle  
response to estrogen  
negative regulation of myeloid cell differentiation  
detection of chemical stimulus involved in sensory perception  
cellular response to retinoic acid  
nephron morphogenesis  
regulation of T cell mediated immunity

smooth muscle cell migration  
negative regulation of lipid metabolic process  
response to axon injury  
peptidyl-tyrosine phosphorylation  
peptidyl-tyrosine modification  
regulation of leukocyte mediated cytotoxicity  
nerve development  
cardiac ventricle morphogenesis  
cardiac septum morphogenesis  
mammary gland epithelium development  
hair follicle development  
regulation of tissue remodeling  
calcium ion import  
skin epidermis development  
midbrain development  
homotypic cell-cell adhesion  
positive regulation of animal organ morphogenesis  
central nervous system neuron development  
molting cycle process  
hair cycle process  
negative regulation of wound healing  
epithelial cell proliferation  
regulation of lipid metabolic process  
outflow tract morphogenesis  
regulation of cardiac muscle tissue development  
regulation of epidermal growth factor receptor signaling pathway  
regulation of phospholipid metabolic process  
regulation of cell-cell adhesion  
positive regulation of cell division  
regulation of fibroblast proliferation  
cardiac muscle tissue growth  
muscle cell migration  
regulation of fatty acid metabolic process  
regulation of blood coagulation  
fibroblast proliferation  
kidney morphogenesis  
post-embryonic development  
inner ear morphogenesis  
regulation of hemostasis  
regulation of coagulation  
metanephros development  
embryonic placenta development  
positive regulation of T cell proliferation  
regulation of ERBB signaling pathway  
regulation of lymphocyte activation  
embryonic skeletal system morphogenesis  
heart growth  
artery development  
positive regulation of phosphatidylinositol 3-kinase signaling  
negative regulation of leukocyte differentiation  
adaptive immune response

regulation of cell killing  
molting cycle  
hair cycle  
regulation of organ growth  
ureteric bud development  
positive regulation of reactive oxygen species metabolic process  
reproductive structure development  
negative regulation of small molecule metabolic process  
mesonephric epithelium development  
mesonephric tubule development  
reproductive system development  
T cell activation involved in immune response  
regulation of phosphoprotein phosphatase activity  
mesonephros development  
fibroblast growth factor receptor signaling pathway  
negative regulation of transport  
leukocyte mediated cytotoxicity  
aminoglycan biosynthetic process  
glycosaminoglycan biosynthetic process  
detection of chemical stimulus  
interferon-gamma production  
ear morphogenesis  
endothelial cell differentiation  
negative regulation of T cell activation  
interleukin-1-mediated signaling pathway  
regulation of DNA biosynthetic process  
integrin-mediated signaling pathway  
gland development  
T cell mediated immunity  
regulation of myeloid leukocyte differentiation  
smoothened signaling pathway  
receptor internalization  
sprouting angiogenesis  
cardiac septum development  
bone morphogenesis  
stem cell proliferation  
columnar/cuboidal epithelial cell differentiation  
limbic system development  
bone mineralization  
collagen metabolic process  
regulation of osteoblast differentiation  
formation of primary germ layer  
sensory perception of chemical stimulus  
regulation of protein processing  
negative regulation of leukocyte cell-cell adhesion  
actin-mediated cell contraction  
regulation of protein maturation  
negative regulation of protein secretion  
neutrophil degranulation  
homophilic cell adhesion via plasma membrane adhesion molecules  
negative regulation of protein catabolic process

positive regulation of calcium ion transport  
epithelial tube formation  
renal system process  
endothelium development  
mesoderm development  
regulation of protein dephosphorylation  
embryonic skeletal system development  
positive regulation of lymphocyte proliferation  
detection of stimulus involved in sensory perception  
neutrophil activation involved in immune response  
regulation of leukocyte activation  
positive regulation of mononuclear cell proliferation  
epithelial to mesenchymal transition  
negative regulation of immune effector process  
cardiac ventricle development  
sensory perception of sound  
regulation of Rho protein signal transduction  
Fc-epsilon receptor signaling pathway  
odontogenesis  
negative regulation of inflammatory response  
axon development  
neutrophil activation  
neutrophil mediated immunity  
negative regulation of peptide secretion  
regulation of response to biotic stimulus  
negative regulation of hemopoiesis  
granulocyte activation  
positive regulation of leukocyte proliferation  
positive regulation of cell migration  
cellular response to fibroblast growth factor stimulus  
cardiac chamber morphogenesis  
regulation of striated muscle tissue development  
response to ethanol  
tube formation  
digestive tract development  
regulation of muscle organ development  
morphogenesis of an epithelium  
sensory organ development  
regulation of muscle tissue development  
positive regulation of MAPK cascade  
positive regulation of cell motility  
retina development in camera-type eye  
morphogenesis of embryonic epithelium  
regulation of muscle cell differentiation  
neural precursor cell proliferation  
positive regulation of canonical Wnt signaling pathway  
response to toxic substance  
liver development  
male gonad development  
response to fibroblast growth factor  
nephron development

kidney epithelium development  
sensory perception  
regulation of adaptive immune response based on somatic recombination of immune receptor  
actin filament-based movement  
positive regulation of lipid metabolic process  
development of primary male sexual characteristics  
negative regulation of lymphocyte activation  
response to estradiol  
appendage morphogenesis  
limb morphogenesis  
positive regulation of chemotaxis  
hepatobiliary system development  
positive regulation of cellular component movement  
leukocyte degranulation  
regulation of lymphocyte mediated immunity  
regulation of epithelial cell differentiation  
response to hydrogen peroxide  
sensory perception of mechanical stimulus  
localization within membrane  
digestive system development  
neuron migration  
regulation of wound healing  
fatty acid biosynthetic process  
regulation of phosphatase activity  
monocarboxylic acid transport  
mammary gland development  
positive regulation of mitotic cell cycle  
myeloid cell activation involved in immune response  
negative regulation of immune response  
protein secretion  
positive regulation of locomotion  
regulation of T cell proliferation  
myeloid leukocyte mediated immunity  
branching morphogenesis of an epithelial tube  
regulation of cell division  
placenta development  
negative regulation of neuron projection development  
regulation of regulated secretory pathway  
cell killing  
regulation of cytokine-mediated signaling pathway  
glycosaminoglycan metabolic process  
biomineral tissue development  
phosphatidylinositol metabolic process  
regulation of adaptive immune response  
regulation of mitotic nuclear division  
hematopoietic progenitor cell differentiation  
aminoglycan metabolic process  
regulation of endothelial cell migration  
platelet activation  
male sex differentiation  
negative regulation of protein transport

central nervous system neuron differentiation  
peptide secretion  
negative regulation of cell-cell adhesion  
regulation of response to cytokine stimulus  
negative regulation of leukocyte activation  
negative regulation of establishment of protein localization  
lymphocyte activation involved in immune response  
appendage development  
limb development  
positive regulation of Wnt signaling pathway  
cardiac chamber development  
regulation of cellular ketone metabolic process  
positive regulation of developmental growth  
gastrulation  
tissue remodeling  
regulation of nuclear division  
vascular process in circulatory system  
negative regulation of cell projection organization  
cellular response to interleukin-1  
regulation of dephosphorylation  
regulation of lipid biosynthetic process  
regulation of reactive oxygen species metabolic process  
receptor metabolic process  
positive regulation of vasculature development  
Rho protein signal transduction  
regulation of ossification  
positive regulation of epithelial cell proliferation  
DNA biosynthetic process  
morphogenesis of a branching epithelium  
regulation of cytokine secretion  
negative regulation of cell activation  
regeneration  
myeloid leukocyte differentiation  
morphogenesis of a branching structure  
regulation of leukocyte mediated immunity  
mesenchymal cell differentiation  
female pregnancy  
regulation of lymphocyte proliferation  
positive regulation of T cell activation  
regulation of mononuclear cell proliferation  
bone development  
osteoblast differentiation  
tissue homeostasis  
response to interleukin-1  
regulation of myeloid cell differentiation  
cellular response to insulin stimulus  
endothelial cell migration  
negative regulation of protein kinase activity  
regulation of exocytosis  
gonad development  
cellular response to acid chemical

cell-cell adhesion via plasma-membrane adhesion molecules  
regulation of leukocyte proliferation  
development of primary sexual characteristics  
negative regulation of neuron differentiation  
regulation of chemotaxis  
positive regulation of leukocyte cell-cell adhesion  
positive regulation of DNA metabolic process  
regulation of Ras protein signal transduction  
regulation of epithelial cell migration  
organic hydroxy compound transport  
skeletal system morphogenesis  
developmental growth involved in morphogenesis  
negative regulation of kinase activity  
response to reactive oxygen species  
multi-multicellular organism process  
cellular response to transforming growth factor beta stimulus  
cellular ketone metabolic process  
regulation of calcium ion transport  
sensory organ morphogenesis  
negative regulation of cellular catabolic process  
response to alcohol  
cell fate commitment  
response to transforming growth factor beta  
negative regulation of transferase activity  
mitotic nuclear division  
positive regulation of growth  
stem cell differentiation  
receptor-mediated endocytosis  
protein processing  
regulation of leukocyte differentiation  
lymphocyte mediated immunity  
positive regulation of cell-cell adhesion  
regulation of canonical Wnt signaling pathway  
positive regulation of MAP kinase activity  
adaptive immune response based on somatic recombination of immune receptors built from individual genes  
sex differentiation  
positive regulation of ion transport  
reactive oxygen species metabolic process  
connective tissue development  
positive regulation of cell cycle process  
response to insulin  
embryonic organ morphogenesis  
positive regulation of lymphocyte activation  
negative regulation of cell adhesion  
detection of stimulus  
glycerophospholipid metabolic process  
negative regulation of neurogenesis  
negative regulation of catabolic process  
protein dephosphorylation  
skin development  
epithelial cell migration

epithelium migration  
regulation of angiogenesis  
cell chemotaxis  
tissue migration  
negative regulation of nervous system development  
organic acid transport  
carboxylic acid transport  
positive regulation of response to external stimulus  
camera-type eye development  
regulation of small GTPase mediated signal transduction  
canonical Wnt signaling pathway  
epithelial tube morphogenesis  
positive regulation of leukocyte activation  
protein maturation  
regulation of actin cytoskeleton organization  
regionalization  
cellular response to peptide hormone stimulus  
lipid transport  
aging  
negative regulation of cell development  
response to lipopolysaccharide  
regulation of Wnt signaling pathway  
regulation of vasculature development  
regulation of developmental growth  
positive regulation of cellular protein localization  
monocarboxylic acid biosynthetic process  
positive regulation of protein serine/threonine kinase activity  
epidermis development  
response to molecule of bacterial origin  
regulation of MAP kinase activity  
fatty acid metabolic process  
blood coagulation  
coagulation  
hemostasis  
eye development  
lipid localization  
visual system development  
nuclear division  
muscle contraction  
glycerolipid metabolic process  
in utero embryonic development  
regulation of metal ion transport  
regulation of actin filament-based process  
sensory system development  
regulation of protein catabolic process  
actin filament organization  
forebrain development  
regulation of inflammatory response  
phospholipid metabolic process  
myeloid cell differentiation  
negative regulation of protein phosphorylation

ossification  
cellular response to peptide  
organelle fission  
regulation of DNA metabolic process  
ameboidal-type cell migration  
regulation of immune effector process  
regulation of cell growth  
pattern specification process  
anatomical structure homeostasis  
response to oxygen levels  
calcium ion transport  
positive regulation of cell adhesion  
embryonic organ development  
Ras protein signal transduction  
dephosphorylation  
negative regulation of phosphorylation  
regulation of hemopoiesis  
negative regulation of immune system process  
regulation of innate immune response  
organic anion transport  
carboxylic acid biosynthetic process  
organic acid biosynthetic process  
response to oxidative stress  
response to peptide hormone  
positive regulation of cytokine production  
divalent metal ion transport  
muscle system process  
regulation of small molecule metabolic process  
regulation of protein secretion  
divalent inorganic cation transport  
leukocyte migration  
axonogenesis  
cell growth  
multicellular organismal homeostasis  
regulation of peptide secretion  
Wnt signaling pathway  
cell-cell signaling by wnt  
regulation of neuron projection development  
regulation of protein serine/threonine kinase activity  
skeletal system development  
regulation of body fluid levels  
leukocyte differentiation  
regulation of cytoskeleton organization  
regulation of vesicle-mediated transport  
regulation of cellular protein localization  
negative regulation of phosphate metabolic process  
small GTPase mediated signal transduction  
negative regulation of phosphorus metabolic process  
response to peptide  
positive regulation of protein kinase activity  
cell division

blood circulation  
negative regulation of protein modification process  
circulatory system process  
embryonic morphogenesis  
response to bacterium  
response to inorganic substance  
anion transport  
cell morphogenesis involved in neuron differentiation  
protein localization to membrane  
positive regulation of kinase activity  
cell surface receptor signaling pathway involved in cell-cell signaling  
positive regulation of cytokine-mediated signaling pathway  
activation of innate immune response  
pattern recognition receptor signaling pathway  
toll-like receptor signaling pathway  
tolerance induction  
regulation of tolerance induction  
MyD88-dependent toll-like receptor signaling pathway  
MyD88-independent toll-like receptor signaling pathway  
innate immune response-activating signal transduction  
positive regulation of peptide secretion  
positive regulation of adaptive immune response  
positive regulation of adaptive immune response based on somatic recombination of immune  
positive regulation of response to biotic stimulus  
positive regulation of response to tumor cell  
positive regulation of immune response to tumor cell  
heart valve development  
heart valve morphogenesis  
phagocytosis  
axon guidance  
cell recognition  
neuron recognition  
regulation of endocytosis  
positive regulation of defense response  
interleukin-10 production  
regulation of interferon-gamma production  
regulation of interleukin-10 production  
negative regulation of interferon-gamma production  
negative regulation of interleukin-10 production  
positive regulation of interleukin-10 production  
negative regulation of mononuclear cell proliferation  
regulation of mast cell activation  
negative regulation of mast cell activation  
regulation of toll-like receptor signaling pathway  
negative regulation of toll-like receptor signaling pathway  
TRIF-dependent toll-like receptor signaling pathway  
CD4-positive, alpha-beta T cell activation  
CD8-positive, alpha-beta T cell activation  
negative regulation of T cell proliferation  
apoptotic cell clearance  
positive regulation of innate immune response

mast cell activation  
negative regulation of endocytosis  
positive regulation of endocytosis  
negative regulation of activated T cell proliferation  
alpha-beta T cell activation  
alpha-beta T cell proliferation  
regulation of alpha-beta T cell activation  
negative regulation of alpha-beta T cell activation  
regulation of alpha-beta T cell proliferation  
negative regulation of lymphocyte proliferation  
positive regulation of protein secretion  
positive regulation of cytokine secretion  
regulation of phagocytosis  
negative regulation of phagocytosis  
positive regulation of phagocytosis  
positive regulation of secretion  
positive regulation of protein transport  
protein complex oligomerization  
protein homooligomerization  
skeletal muscle organ development  
positive regulation of response to cytokine stimulus  
lymphocyte apoptotic process  
regulation of lymphocyte apoptotic process  
positive regulation of lymphocyte apoptotic process  
T cell apoptotic process  
regulation of T cell apoptotic process  
negative regulation of leukocyte proliferation  
response to interleukin-4  
cellular response to biotic stimulus  
cellular response to molecule of bacterial origin  
cellular response to lipopolysaccharide  
cellular response to interleukin-4  
tumor necrosis factor superfamily cytokine production  
leukocyte apoptotic process  
inflammatory response to wounding  
neuron projection guidance  
toxin transport  
positive regulation of secretion by cell  
regulation of tumor necrosis factor superfamily cytokine production  
negative regulation of tumor necrosis factor superfamily cytokine production  
positive regulation of establishment of protein localization  
regulation of leukocyte apoptotic process  
positive regulation of leukocyte apoptotic process  
regulation of CD4-positive, alpha-beta T cell activation  
negative regulation of CD4-positive, alpha-beta T cell activation  
regulation of CD8-positive, alpha-beta T cell activation  
receptor complex  
external side of plasma membrane  
M band  
microvillus membrane  
myosin filament

T cell receptor complex  
side of membrane  
striated muscle thin filament  
myofilament  
adherens junction  
basal plasma membrane  
A band  
anchoring junction  
secretory granule membrane  
excitatory synapse  
basal part of cell  
apical plasma membrane  
azurophil granule membrane  
lateral plasma membrane  
myosin complex  
tertiary granule membrane  
apical part of cell  
microvillus  
specific granule membrane  
focal adhesion  
cell-substrate adherens junction  
cell-substrate junction  
lysosomal lumen  
extracellular matrix  
Z disc  
vacuolar part  
I band  
primary lysosome  
azurophil granule  
specific granule  
growth cone  
tertiary granule  
site of polarized growth  
vacuolar lumen  
plasma membrane receptor complex  
transport vesicle membrane  
sarcomere  
actin-based cell projection  
contractile fiber part  
myofibril  
basolateral plasma membrane  
contractile fiber  
distal axon  
cell cortex  
lysosomal membrane  
lytic vacuole membrane  
cell projection membrane  
transport vesicle  
vacuolar membrane  
axon part  
collagen-containing extracellular matrix

cell-cell junction  
cytoplasmic region  
actin cytoskeleton  
neuronal cell body  
plasma membrane protein complex  
cell body  
axon  
early endosome  
endosome membrane  
early endosome membrane  
cell-cell contact zone  
endosomal part  
recycling endosome  
recycling endosome membrane  
growth factor binding  
transmembrane receptor protein tyrosine kinase activity  
transmembrane receptor protein kinase activity  
protein tyrosine kinase activity  
bile acid transmembrane transporter activity  
platelet-derived growth factor binding  
platelet-derived growth factor receptor binding  
MHC class I protein binding  
muscle alpha-actinin binding  
fibroblast growth factor binding  
phosphatidylinositol 3-kinase binding  
immunoglobulin binding  
protein kinase activity  
MHC protein binding  
alpha-actinin binding  
organic hydroxy compound transmembrane transporter activity  
monocarboxylic acid transmembrane transporter activity  
actinin binding  
structural constituent of muscle  
actin binding  
protein tyrosine kinase binding  
cytokine receptor activity  
lipid transporter activity  
organic acid transmembrane transporter activity  
carboxylic acid transmembrane transporter activity  
cytokine binding  
growth factor receptor binding  
protein phosphatase binding  
heparin binding  
organic anion transmembrane transporter activity  
phosphatase binding  
actin filament binding  
calmodulin binding  
glycosaminoglycan binding  
carbohydrate binding  
sulfur compound binding  
anion transmembrane transporter activity

protein serine/threonine kinase activity  
G protein-coupled receptor activity  
phosphatidylserine binding  
cytokine receptor binding  
phospholipid binding  
SH3 domain binding  
amide binding  
SH2 domain binding  
sphingolipid binding  
modified amino acid binding  
cell adhesion mediator activity  
cell-cell adhesion mediator activity

ID	Description	GeneRatio
hsa05215	Prostate cancer	3/8
hsa05230	Central carbon metabolism in cancer	2/8
hsa01521	EGFR tyrosine kinase inhibitor resistance	2/8
hsa04072	Phospholipase D signaling pathway	2/8
hsa04015	Rap1 signaling pathway	2/8
hsa04810	Regulation of actin cytoskeleton	2/8
hsa04014	Ras signaling pathway	2/8
hsa04020	Calcium signaling pathway	2/8
hsa05310	Asthma	1/8
hsa04010	MAPK signaling pathway	2/8
hsa04151	PI3K-Akt signaling pathway	2/8
hsa04672	Intestinal immune network for IgA production	1/8
hsa04664	Fc epsilon RI signaling pathway	1/8
hsa05218	Melanoma	1/8
hsa05214	Glioma	1/8
hsa04540	Gap junction	1/8
hsa05235	PD-L1 expression and PD-1 checkpoint pathway in cancer	1/8
hsa05231	Choline metabolism in cancer	1/8
hsa04640	Hematopoietic cell lineage	1/8
hsa05146	Amoebiasis	1/8
hsa04071	Sphingolipid signaling pathway	1/8
hsa05418	Fluid shear stress and atherosclerosis	1/8
hsa04550	Signaling pathways regulating pluripotency of stem cells	1/8
hsa04514	Cell adhesion molecules	1/8
hsa05226	Gastric cancer	1/8
hsa04630	JAK-STAT signaling pathway	1/8
hsa04360	Axon guidance	1/8
hsa05202	Transcriptional misregulation in cancer	1/8
hsa04510	Focal adhesion	1/8
hsa05166	Human T-cell leukemia virus 1 infection	1/8
hsa04144	Endocytosis	1/8
hsa04060	Cytokine-cytokine receptor interaction	1/8
hsa05206	MicroRNAs in cancer	1/8
hsa05165	Human papillomavirus infection	1/8
hsa05168	Herpes simplex virus 1 infection	1/8

BgRatio	pvalue	p.adjust	qvalue	geneID	Count
97/8087	8. 97E-05	0. 003139206	0. 002171481	FGFR2/IL1R2/PDGFRB	3
70/8087	0. 00199965	0. 0296304	0. 020496216	FGFR2/PDGFRB	2
79/8087	0. 00253975	0. 0296304	0. 020496216	FGFR2/PDGFRB	2
148/8087	0. 00866502	0. 075818895	0. 052446153	FCER1A/PDGFRB	2
210/8087	0. 01694969	0. 095475968	0. 066043527	FGFR2/PDGFRB	2
218/8087	0. 01819627	0. 095475968	0. 066043527	FGFR2/PDGFRB	2
232/8087	0. 02047094	0. 095475968	0. 066043527	FGFR2/PDGFRB	2
240/8087	0. 02182308	0. 095475968	0. 066043527	FGFR2/PDGFRB	2
31/8087	0. 03027113	0. 111659607	0. 077238224	FCER1A	1
294/8087	0. 03190274	0. 111659607	0. 077238224	FGFR2/PDGFRB	2
354/8087	0. 04491371	0. 138475692	0. 095787697	FGFR2/PDGFRB	2
49/8087	0. 04747738	0. 138475692	0. 095787697	PIGR	1
68/8087	0. 06534915	0. 167671311	0. 115983162	FCER1A	1
72/8087	0. 06907402	0. 167671311	0. 115983162	PDGFRB	1
75/8087	0. 07185913	0. 167671311	0. 115983162	PDGFRB	1
88/8087	0. 0838439	0. 169048133	0. 116935551	PDGFRB	1
89/8087	0. 08476017	0. 169048133	0. 116935551	CD274	1
98/8087	0. 09297059	0. 169048133	0. 116935551	PDGFRB	1
99/8087	0. 09387887	0. 169048133	0. 116935551	IL1R2	1
102/8087	0. 09659893	0. 169048133	0. 116935551	IL1R2	1
119/8087	0. 11187808	0. 186463473	0. 128982252	FCER1A	1
139/8087	0. 12956367	0. 193606454	0. 133923262	IL1R2	1
143/8087	0. 13306357	0. 193606454	0. 133923262	FGFR2	1
149/8087	0. 13829032	0. 193606454	0. 133923262	CD274	1
149/8087	0. 13829032	0. 193606454	0. 133923262	FGFR2	1
162/8087	0. 14952047	0. 201277555	0. 139229587	PDGFRB	1
182/8087	0. 16654759	0. 215895021	0. 149340917	LRIG2	1
192/8087	0. 17494873	0. 218685909	0. 151271456	IL1R2	1
201/8087	0. 1824463	0. 220193814	0. 152314518	PDGFRB	1
219/8087	0. 19726281	0. 230139942	0. 159194547	IL1R2	1
251/8087	0. 22302387	0. 251801141	0. 174178233	FGFR2	1
295/8087	0. 25726303	0. 281381438	0. 194639792	IL1R2	1
310/8087	0. 26862978	0. 284910376	0. 197080862	PDGFRB	1
331/8087	0. 28428743	0. 292648823	0. 202433772	PDGFRB	1
498/8087	0. 39871809	0. 398718085	0. 275804991	PILRA	1