KNOWLEDGE DRIVEN BINNING AND PHEWAS ANALYSIS IN MARSHFIELD PERSONALIZED MEDICINE RESEARCH PROJECT USING BIOBIN

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KNOWLEDGE DRIVEN BINNING AND PHEWAS ANALYSIS IN MARSHFIELD PERSONALIZED MEDICINE RESEARCH PROJECT USING BIOBIN*

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Next-generation sequencing technology has presented an opportunity for rare variant discovery and association of these variants with disease. To address the challenges of rare variant analysis, multiple statistical methods have been developed for combining rare variants to increase statistical power for detecting associations. BioBin is an automated tool that expands on collapsing/binning methods by performing multi-level variant aggregation with a flexible, biologically informed binning strategy using an internal biorepository, the Library of Knowledge (LOKI). The databases within LOKI provide variant details, regional annotations and pathway interactions which can be used to generate bins of biologically-related variants, thereby increasing the power of any subsequent statistical test. In this study, we expand the framework of BioBin to incorporate statistical tests, including a dispersion-based test, SKAT, thereby providing the option of performing a unified collapsing and statistical rare variant analysis in one tool. Extensive simulation studies performed on gene-coding regions showed a Bin-KAT analysis to have greater power than BioBin-regression in all simulated conditions, including variants influencing the phenotype in the same direction, a scenario where burden tests often retain greater power. The use of Madsen-Browning variant weighting increased power in the burden analysis to that equitable with Bin-KAT; but overall Bin-KAT retained equivalent or higher power under all conditions. Bin-KAT was applied to a study of 82 pharmacogenes sequenced in the Marshfield Personalized Medicine Research Project (PMRP). We looked for association of these genes with 9 different phenotypes extracted from the electronic health record. This study demonstrates that Bin-KAT is a powerful tool for the identification of genes harboring low frequency variants for complex phenotypes.

1. Introduction

Examining the genetic influence of low frequency or rare variation to complex disease susceptibility may elucidate additional trait variability and disease risk which has largely remained unexplained by traditional GWAS approaches[29]. In recent years, studies on multifactorial diseases including Alzheimer's disease and prostate cancer have provided compelling evidence that rare variants are associated with complex traits and should be further examined[9, 16]. Advances in sequencing technologies and decreases in sequencing cost have provided an opportunity for rare variant discovery. However, due to the frequency of these variants, there is often low statistical power for detecting association with a phenotype, and therefore, a necessity for prohibitively large sample sizes. Collapsing or binning methods are commonly used to aggregate variants into a single genetic variable for subsequent statistical testing, reducing the

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degrees of freedom in the analysis and improving power[23]. BioBin[33, 34] is an automated bioinformatics tool initially developed for the multi-level collapsing of rare variants into user-designated biological features such as genes, pathways, evolutionary conserved regions (ECRs), protein families, and regulatory regions. BioBin follows a binning approach driven by prior biological knowledge by using an internal biorepository, the Library of Knowledge Integration (LOKI)[40]. LOKI combines biological information from over a dozen public databases providing variant details, regional annotations and pathway interactions. The flexible knowledge-driven binning design of BioBin allows the user to test multiple hypotheses within one unified analysis.

Rare variant association analysis of binned variants is often performed using burden or dispersion tests. Burden methods test the cumulative effect of variants within a bin and are easily applied to case-control studies as they assess the frequency of variant counts between these phenotypic groups[24]. Burden tests assume that all variants influence the trait in the same direction and magnitude of effect, and will suffer a loss of power if a mixture of protective and risk variants is present. Standard burden tests include generalized linear model regression analyses and the weighted sum statistic(WSS)[28]. Instead of testing the cumulative effect of variants within a region, dispersion or nonburden methods will test the distribution of these variants in the cases and controls thereby maintaining statistical power in the presence of a mixture of variants. The SKAT[46] package is a dispersion test that has gained widespread use as it allows for easy covariate adjustment, analyzes both dichotomous and quantitative phenotypes, and applies multiple variant weighting options. SKAT is a score-based variance component test that uses a multiple regression kernel-based approach to assess variant distribution and test for association. Both standard burden tests and the SKAT dispersion method have been well assessed in rare variant analysis.

While various tools have been specifically developed to facilitate rare variant association analysis, many methods focus either on the creation of a relevant set of variants or on the statistical analysis of already collapsed variants. This may often lead to file conversion issues for specific tools, as well as more complicated and longer analysis time. Herein we expand the framework of BioBin by integrating select statistical tests, regression and SKAT, as well as capabilities for multiple phenotype analysis (or Phenome-wide Association Studies (PheWAS)), thereby providing a comprehensive, unified bioinformatics tool for the biological binning and association analysis of rare variants. We have evaluated the commonly used regression burden analysis and SKAT in the context of BioBin with data simulations based on individuals of European descent from 1000 Genomes Project Phase I. We have also applied a BioBin-SKAT, or Bin-KAT, test to analyze nine complex human phenotypes from the Marshfield-PMRP project[31], part of the eMERGE network[14]. Our analyses highlight the utility of BioBin as a fast, comprehensive and versatile tool for the biological binning and analysis of low frequency variants in sequence data for multiple complex phenotypes and PheWAS.

2. Methods

2.1. BioBin

2.1.1.Overview of BioBin

BioBin is a unified command line bioinformatics tool written in C++ that utilizes the LOKI database for biologically inspired binning of variants, and also provides a platform for the association analysis of rare variant bins. The framework of a BioBin analysis is to determine biological features upon which data will be binned, such as genes, pathways or intergenic regions, execute bin generation using LOKI, and apply statistical association analysis to each bin. BioBin follows an allele frequency threshold binning approach using the non-major allele frequency (NMAF), defined as 1 minus the frequency of the most common allele. As NMAF and MAF are interchangeable for biallelic markers, MAF will be used in this work. BioBin allows variants below a user-specified MAF in the case or the control group to be binned thereby facilitating the aggregation of both potential risk and protective variants. BioBin was originally developed solely for the biologically informed binning of rare variants in an automated manner. To facilitate more efficient statistical analysis, we have incorporated an extensible testing infrastructure, implementing select burden and dispersion-based tests, namely regression, wilcoxon and SKAT[46] into BioBin. These are commonly used statistical tests in rare variant association analysis, and their direct implementation into BioBin streamlines the analysis, saves time, and also avoids any potential file conversion issues. Also, if an alternate statistical test is desired, BioBin may still be utilized strictly for its biologically inspired variant collapsing function. We have also integrated multiple phenotype capabilities allowing the user to efficiently perform a binned rare variant PheWAS[35, 41, 42]. BioBin analyzes each phenotype separately and uses parallel processing to increase the speed of a PheWAS analysis through a user-specified number of processors. BioBin is open source and the code is freely available at https://ritchielab.psu.edu. It is also available on demand from the authors. All supplemental files for this manuscript are available at https://ritchielab.psu.edu/publications/supplementary-data/psb-2016/biobin-on-multiple-phenotype.

2.1.2. *Library of Knowledge Integration (LOKI)*

BioBin collapses variants into biological features by consulting the Library of Knowledge Integration (LOKI), an internal repository containing diverse knowledge from multiple sources including NCBI dbSNP and gene Entrez[38], Kyoto Encyclopedia of Genes and Genomes (KEGG)[18], Gene Ontology (GO)[11], and Pharmacogenomics Knowledge Base (PharmGKB)[32]. LOKI integrates information from these external databases into a single local repository containing knowledge from the downloaded raw data in each database. The main data types used within LOKI are position, region, group, and source. Position refers to the chromosome and base-pair position of single variants, and region represents biological features containing a start and stop position including genes and copy number variants[33]. Sources are the external databases compiled in LOKI, while groups represent various groupings of biological features such as protein interactions, protein families and pathways. While LOKI is not distributed within the BioBin code due to size constraints, tools are provided within the source distribution allowing a user to compile and perform a local installation of LOKI by downloading data directly from the external sources. The data sources within LOKI can be individually updated as necessary in order to provide the most up-to-date information.

2.2. Simulations

Simulation testing was performed in order to evaluate regression (a standard burden test) and SKAT (a dispersion test) within the framework of a BioBin variant collapsing analysis. All tests were performed using SeqSIMLA2[4] to simulate sequence data as it allowed for the simulation of common burden and dispersion test assumptions. Randomly selected protein-coding variants with a MAF<5% in individuals of European descent from the 1000 Genomes Project Phase I[8] dataset were used as the basis for our simulations. This dataset was used to obtain a distribution of allele frequencies across the whole exome for each non-monomorphic single nucleotide variant site in the represented individuals of European descent (CEU, TSI, FIN, GBR, and IBS). This allele frequency distribution was then used to create the input for SeqSIMLA2. All simulations were performed with 100 variants as we calculated this to be an approximate average number of variants expected in a median sized 24,000bp gene[12]. For this calculation, we used known gene regions in the UCSC Human Genome Browser[19] to define the total gene region length and the 1000 Genomes Project to estimate the number of SNPs identified in these gene regions.

Simulation tests and specific parameters are shown in Table 1. Our simulations focused on two main tests: altering the odds ratio (OR) and altering the proportion of risk variants, with numerous parameters tested in each of these categories. Multiple testing parameters separated by commas in Table 1 correspond to independent simulations. The proportion of causal variants represents the percentage of disease sites of the total 100 variants being simulated. Likewise, the proportion of risk variants provides the number of risk variants of these causal sites. For instance, in our altering OR test category, when simulating 40% causal variants, we had 40 disease sites, and either 40-risk variants (when testing a 100% proportion of risk variants) or 20-risk variants and 20-protective variants (when testing a 50% proportion of risk variants). The specified OR corresponds to that of the individual causal variants. Type I error was estimated with 1,000 simulated null datasets using an OR of 1. Significance was assessed using $\alpha=0.05$.

Table1. Simulation tests and Parameters

Test Parameter	Altering OR	Altering Proportion of Risk Variants
Number of Simulations	1000	1000
Sample Size	1000 cases and 1000 controls	1000 cases and 1000 controls
Proportion of Causal Variants (n=100)	40%, 10%	40%
Disease Prevalence	5%	5%, 50%
Odds Ratio (OR)	1.5, 2.0, 3.0	3.0
Proportion of Risk Variants	50%, 100%	25%, 40%, 50%, 60%, 75%, 100%
Variant Weighting	No Weighting, Madsen and Browning	No Weighting, Madsen and Browning

2.3. Application of Bin-KAT to natural dataset

A Bin-KAT test was used to analyze type II diabetes (TIID) and eight diagnosis indicators in 740 de-identified European American subjects from the Marshfield Clinic Personalized Medicine

Research Project (PMRP) sequenced in the electronic Medical Records and Genomics (eMERGE) Network[15], as part of the eMERGE-PGX study[43]. Subjects were sequenced using PGRNseq[43], a next-generation sequencing platform designed for the targeted capture of selected pharmacogenes[43]. Case control status for TIID was determined using Mount Sinai's diabetes algorithm[20] from the Diabetes HTN CKD algorithm[37]. The eight diagnosis indicators analyzed are asthma, benign prostatic hyperplasia (BPH), cataracts, diverticulosis, gastroesophageal reflux disease (GERD), hypertension, hypothyroidism, and uterine fibrosis. For each diagnosis indicator, a subject was considered a case if diagnosed with one of the listed ICD-9 codes in Table 2 on two or more dates. Controls were defined as non-cases who did not meet the criteria of ICD-9 diagnosis on two or more dates.

Table 2. Analyzed Phenotypes

Phenotype	Diagnosis	Cases	Controls
TIID	Diabetes HTN CKD algorithm	99	594
Asthma	ICD-9 codes: Between '493.00' and '493.92'	90	650
(BPH)	ICD-9 codes: '600', '600.0', '600.00', '600.01', '600.09', '600.2', '600.20', '600.21', '600.9', '600.90', '600.91'	122	250
Cataracts	ICD-9 codes: '366.10', '366.12', '366.14', '366.15', '366.16', '366.17', '366.9'	202	538
Diverticulosis	ICD-9 codes: '562.00', '562.01', '562.02', '562.03', '562.10', '562.11', '562.12', '562.13'	134	606
GERD	ICD-9 codes: '530.81','530.11'	204	536
Hypertension	ICD-9 codes: Between '401.00' and '401.99'	374	366
Hypothyroidism	ICD-9 codes: '244', '244.8', '244.9', '245', '245.2', '245.8', '245.9'	98	642
Uterine Fibroids	ICD-9 codes: '218.0', '218.1', '218.2', '218.9', '654.10', '654.11', '654.12', '654.13', '654.14'	58	313

To highlight the multiple variant collapsing functions within BioBin, we binned variants having a MAF less than 0.05 by three features: gene, biological pathway and SNPEff[5] functional predictions with a minimum bin size of 5 variants. Gene binning analysis was performed on the 82 targeted pharmacogenes that passed QC. SNPEff functional predictions were used as a secondary collapsing strategy following gene binning. Variants annotated as having intergenic and intragenic effects by SNPEff were excluded from the analysis. Biological pathway variant binning was achieved using all pathway sources currently in the LOKI biorepository[40]. Overall Madsen and Browning[28] weighting was used to weigh binned variants inversely proportional to their MAF. SKAT was used to test for association between binned variants and each phenotype while adjusting for sex, year of birth, and median BMI.

3. Results

3.1. Simulations

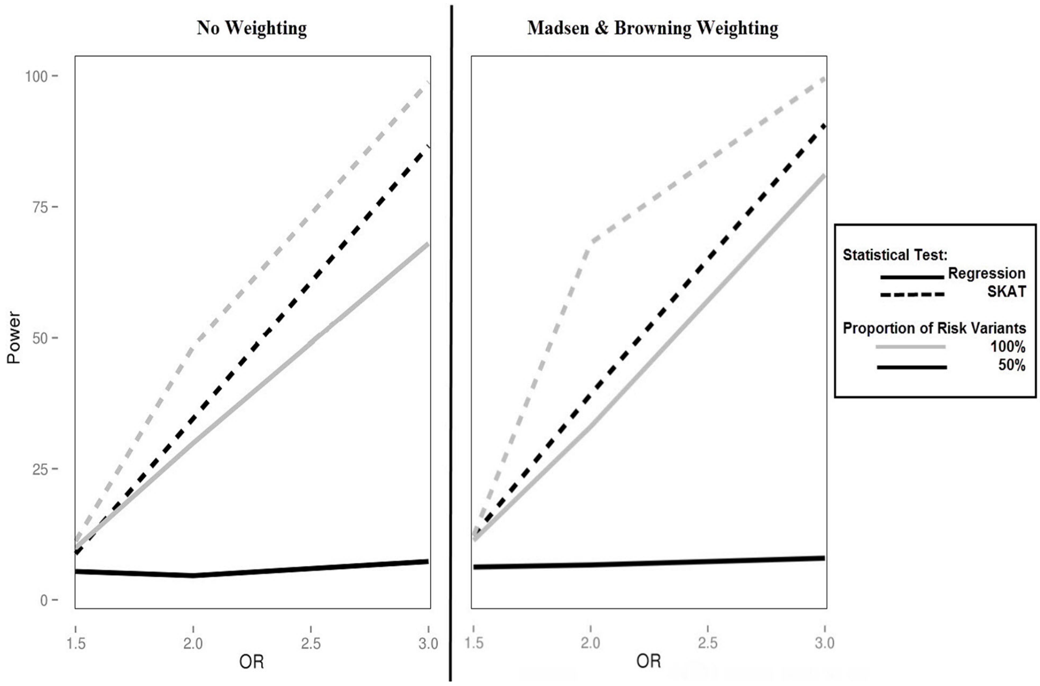
We evaluated regression and SKAT within a BioBin coupled collapsing analysis using data simulations of 100 variants based on the allele frequencies of European subjects from the 1000 Genomes Project. All simulated conditions are shown in Table 1 and aim to test the assumptions of burden and dispersion methods. Table 3 displays that Type I error was well controlled in the analyses and was not being sacrificed in the regression or SKAT analysis.

Table 3. Type I Error Results, standard error is in parentheses.

Variant Weighting	SKAT Type I Error Rate	Regression Type I Error Rate
None	0.045 (±0.011)	0.061(±0.011)
Madsen-Browning	0.037(±0.005)	0.039(±0)

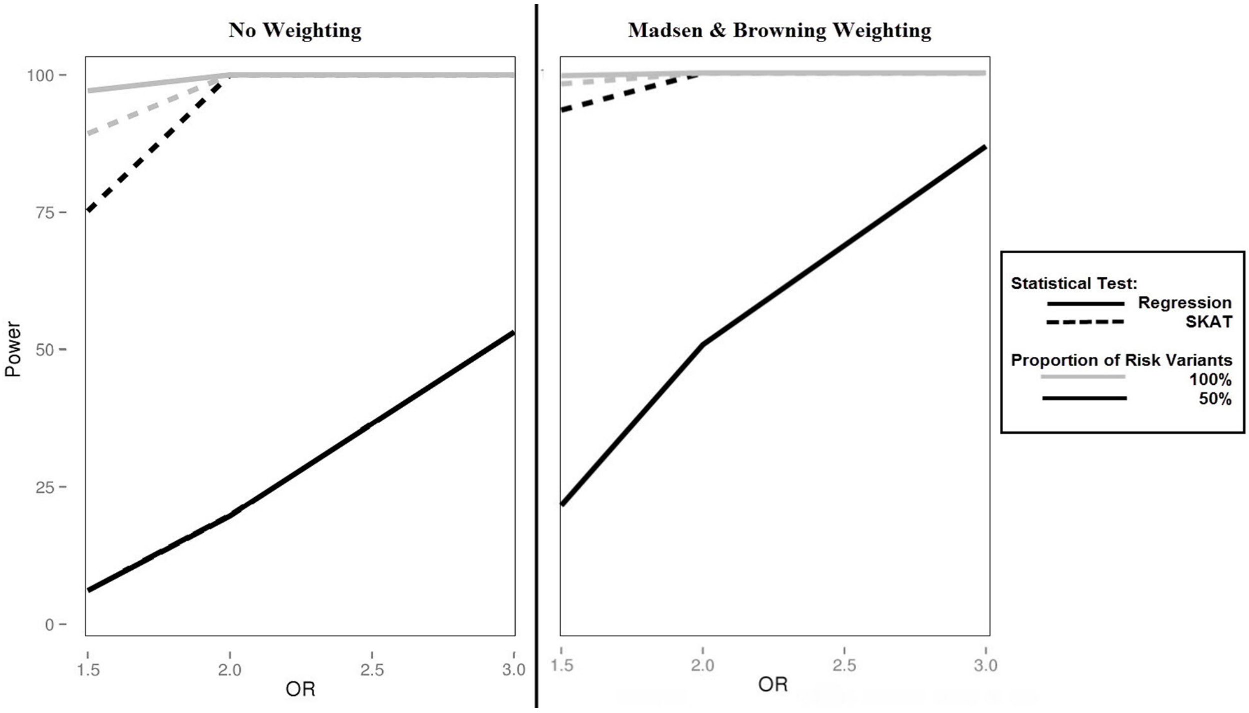
A key limitation of burden tests is loss of statistical power in the presence of a mixture of variant effects. We simulated the direction of effect by testing 100% risk variants and 50% risk, 50% protective variants. We evaluated the impact of differing directions of effect on statistical power in a Bin-KAT and BioBin-regression analysis over a varying OR range from 1.5 to 3.0. These results are shown with 10% and 40% causal variants in Figure 1 and 2, respectively. Both figures highlight the influence of variant weighting by displaying results with and without Madsen and Browning weighting.

Figure 1. Power plot of Bin-KAT and BioBin-regression analyses with a causal variant proportion of 10%. SKAT results are represented by a dashed line; regression results have a solid line. Simulations of 100% risk variants are in grey while 50% risk variants are black.



To further explore the impact of a mixture of variant effects on statistical power, we simulated data altering the proportion of risk variants over a wide range, from 25% to 100%, as seen with a disease prevalence of 5% in Figure 3. We increased this disease prevalence to 50% and present these results in Supplementary Figure 1. While a disease prevalence of 50% is high, it allowed us to create a balance in the case to control ratio and thereby symmetry in the results with comparable statistical power between 25%-75%, and 40%-60%, and a significant loss of power at 50%. This is not seen with a lower disease prevalence of 5% (Figure 3) as we are oversampling our population, so that symmetry is likely shifted.

Figure 2. Power plot of Bin-KAT and BioBin-regression analyses with a causal variant proportion of 40%. SKAT results are represented by a dashed line; regression results have a solid line. Simulations of 100% risk variants are in grey while 50% risk variants are black.



3.2 Application of Bin-KAT to natural dataset

As Bin-KAT consistently maintained greater power than a BioBin-regression, we applied this method coupled with variant weighting to simultaneously analyze 9 phenotypes in subjects of European descent from the Marshfield cohort of eMERGE-PGX project. These subjects were target sequenced for 82 pharmacogenes. We found numerous association results with p-values less than 0.05 in our gene, pathway, and SNPEff functional prediction analysis. Due to the hypothesis generating nature of this method we present all results with a p-value less than 0.05 or 0.01. As sequencing was performed on specific, targeted genes, the statistical tests are highly correlated, and therefore do not meet the independence assumptions of Bonferroni correction, which would prove too stringent in our analysis[7]. In addition, this study is exploratory in nature and all findings should be replicated in independent datasets in the future.

A full list of the results may be found in Supplementary Tables 1 and 2. Table 4 shows the number of results per phenotype and binned biological feature below a p-value cutoff of 0.05 for genes and SNPEff annotations, and an additional 0.01 cutoff for pathway analysis. We found significant associations with binned variants in 59 of the 82 targeted pharmacogenes. Figure 4 shows a Phenogram plot of all significant results collapsed by gene and SNPEff functional prediction displayed by chromosomal location of the gene. Details on the specific annotated SNPEff effect and impact can be found in Supplementary Table 1.

Figure 3. Power plot of a Bin-KAT and BioBin-regression analysis performed when altering the proportion of risk variants between 25% and 100% with a disease prevalence of 5%. SKAT results are represented by a dashed line; regression results have a solid line.

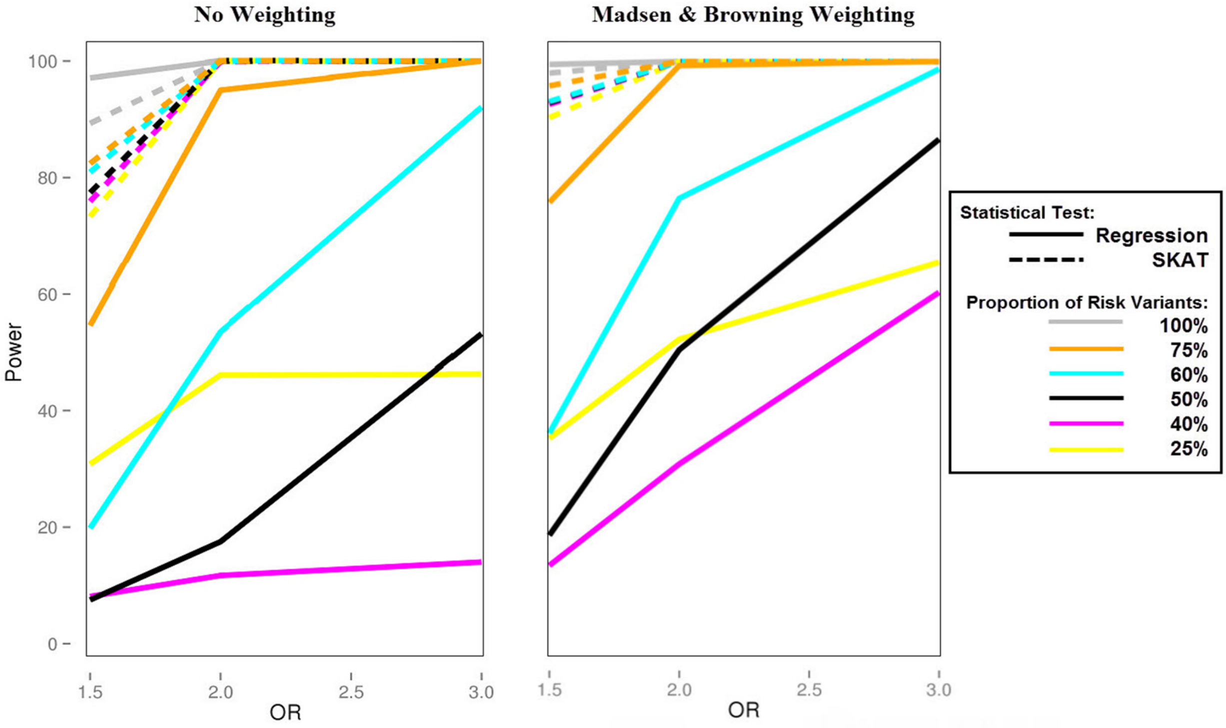


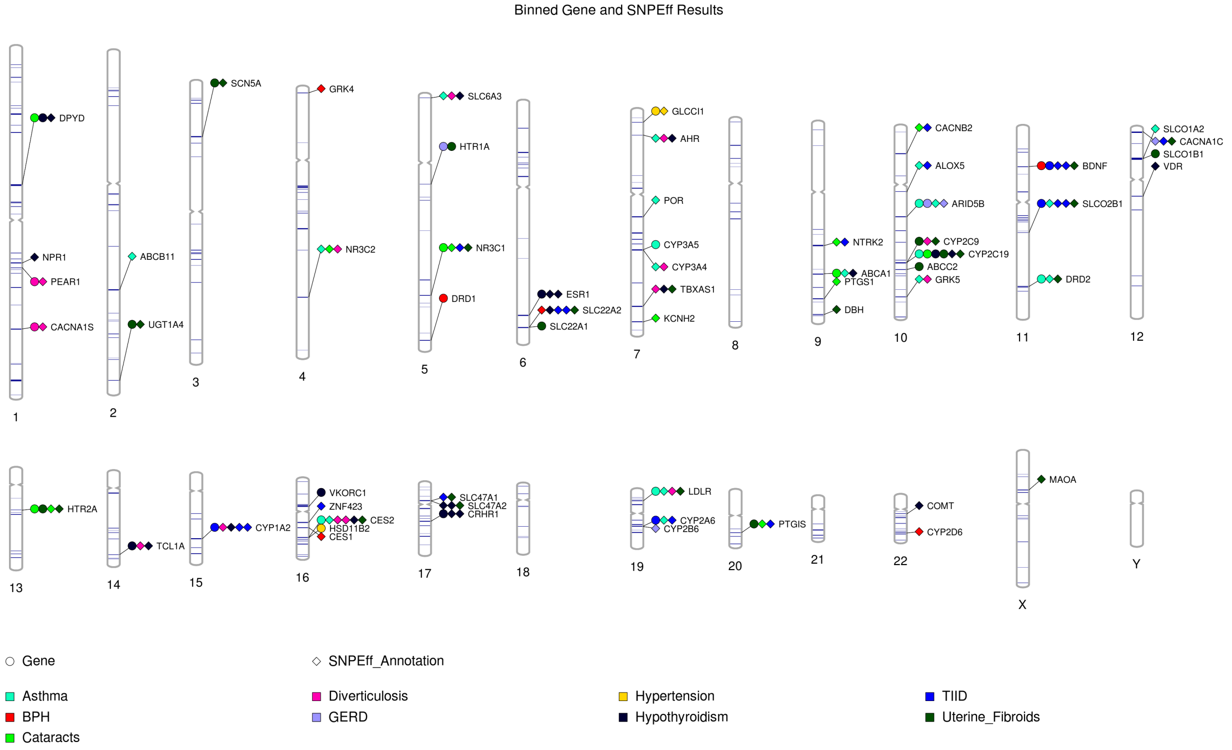
Table 4. Number of association results per phenotype and biological feature at the specified p value cutoff. Total number of bins in each biological feature is noted in parentheses.

Phenotype	Gene (p-value < 0.05)	Pathway (p-value<0.05)	Pathway (p-value<0.01)	SNPEff annotation (p-value <0.05)
Type II Diabetes	4 (82)	233 (8911)	13	17 (458)
Cataracts	5 (82)	777 (8964)	17	8 (458)
Hypothyroidism	6 (82)	324 (8991)	6	19 (458)
Hypertension	2 (82)	234 (8964)	62	1 (458)
Diverticulosis	2 (82)	248 (8964)	148	14 (458)
Asthma	6 (82)	297 (8984)	135	16 (458)
GERD	2 (82)	177 (8964)	19	3 (458)
BPH	2 (82)	102 (8964)	18	4 (458)
Uterine Fibroids	10 (82)	390 (8991)	102	18 (458)

4. Discussion

In this work, we sought to expand the framework of BioBin by integrating statistical tests to provide a tool for the automated, biologically-driven binning and association analysis of rare variants. The choice of binning algorithm is often research specific, and BioBin supports this by providing variant collapsing on multiple biological levels, as well as supporting user-customized analysis. BioBin also includes multiple variant weighting schemes outside of those within a SKAT analysis, including minimum and maximum variant weighting, as well as weighting based on

Figure 4. Phenogram plot of significant association results (p-value<0.05) in a binned gene and SNPEff functional prediction Bin-KAT analysis. The biological features are designated with different shapes, and each phenotype is represented by a different color. The target capture of the PGRNseq platform is shown by blue horizontal bands across the chromosome. The specific SNPEff effect can be found in Supplementary Table 1.



allele frequencies only within our phenotypic controls. Further, BioBin supports polyallelic variant sites and will incorporate all allelic information from these sites, a characteristic that is not supported by all tools. While multiple studies have performed exhaustive comparisons of burden and dispersion methods[2,6,10], we specifically chose to focus on regression and SKAT. Regression is a commonly used burden test, and several popular rare variant methods use a regression framework[1, 26, 27, 36]. SKAT was chosen due to its vast popularity as a dispersion method, its ease of covariate adjustment, and application to binary or quantitative phenotypes. Regression and SKAT have previously been compared in rare variant analysis[2, 10, 22] and here, are evaluated within the context of a biologically inspired binning method.

Simulation testing shows a Bin-KAT analysis maintains greater overall statistical power than BioBin-Regression. We found SKAT to outperform regression even in conditions where a burden analysis is assumed to have greater power than a dispersion test, such as variants influencing the phenotype in the same direction, as is presented in Figure 1 with 10% causal variants. In the 40% causal variant simulations (Figure 2), regression maintains higher power over SKAT in both weighted and unweighted tests. This suggests that the power of regression may be affected by the proportion of causal variants having the same direction of effect. However, when we encounter a mixture of both risk and protective variants, regression suffers a significant loss of power. In fact, SKAT maintains high power regardless of the proportion of risk variants simulated, and is held at 100% from an OR 2.0-3.0 (Figure 3). Our results also highlight that applying Madsen and Browning variant weighting to the binning analysis increases power.

We performed a Bin-KAT test with Madsen and Browning weighting to analyze 9 different phenotypes from Marshfield-PGX subjects who were target sequenced for specific pharmacogenes. We, and others, hypothesize that pharmacogenes related to drug response may also be associated with the diseases for which the drugs are used to treat. Using Bin-KAT, a series of significant associations were found. In the gene-binning analysis, an association between *BDNF* and type II diabetes (p-val 0.000437) was identified. Literature indicates that low levels of *BDNF* may be involved in type II diabetes pathogenesis, providing a potential explanation for the clustering of dementia, depression and type II diabetes[13, 21]. *BDNF* may also play a role in blood glucose metabolism and insulin resistance, a characteristic of type II diabetes[21, 30]. A number of significant results in the pathway-binning analysis performed using asthma patients included leukotriene pathways. Leukotrienes are inflammatory chemicals that can act as lipid mediators and have been well established in the pathobiology of asthma[3, 17, 44]. Leukotriene-B4 is being further investigated for its regulatory role in the development of asthma [17].

The results of this study show indications of potential pleiotropy where gene-binned variants are associated with more than one phenotype. We see this with *CYP2C19*, which is significantly associated with asthma, cataracts, hypothyroidism, and uterine fibroids. *CYP2C19* has a highly polymorphic sequence, accounting for its variability in drug metabolism as it acts on up to 10% of clinical drugs[25]. In lung tissue, cytochrome P450 enzymes may be affected by air pollutants, and the CYP2C19*2 genotype has been implicated as a risk factor for asthma[47]. Also, linkage analysis on families with endometriosis, a disorder that may be correlated with uterine fibroids[45], indicates a potential role of *CYP2C19* in endometriosis risk[39]. Association results with *CYP2C19* present exciting connections that warrant further exploration. We have looked at the co-occurrence of these four phenotypes and the correlation is fairly low. Future work will aim to evaluate *CYP2C19* and medication usage.

Bin-KAT serves as a powerful and versatile method for the biological binning and analysis of rare variants in sequence data. This approach was successful in the identifying novel and well-studied genes and pathways harboring low frequency variants in a multiple complex phenotype analysis. Studying the influence of low frequency variants has the potential to identify underlying risk factors, and uncover complex genotype-phenotype associations in multifactorial diseases.

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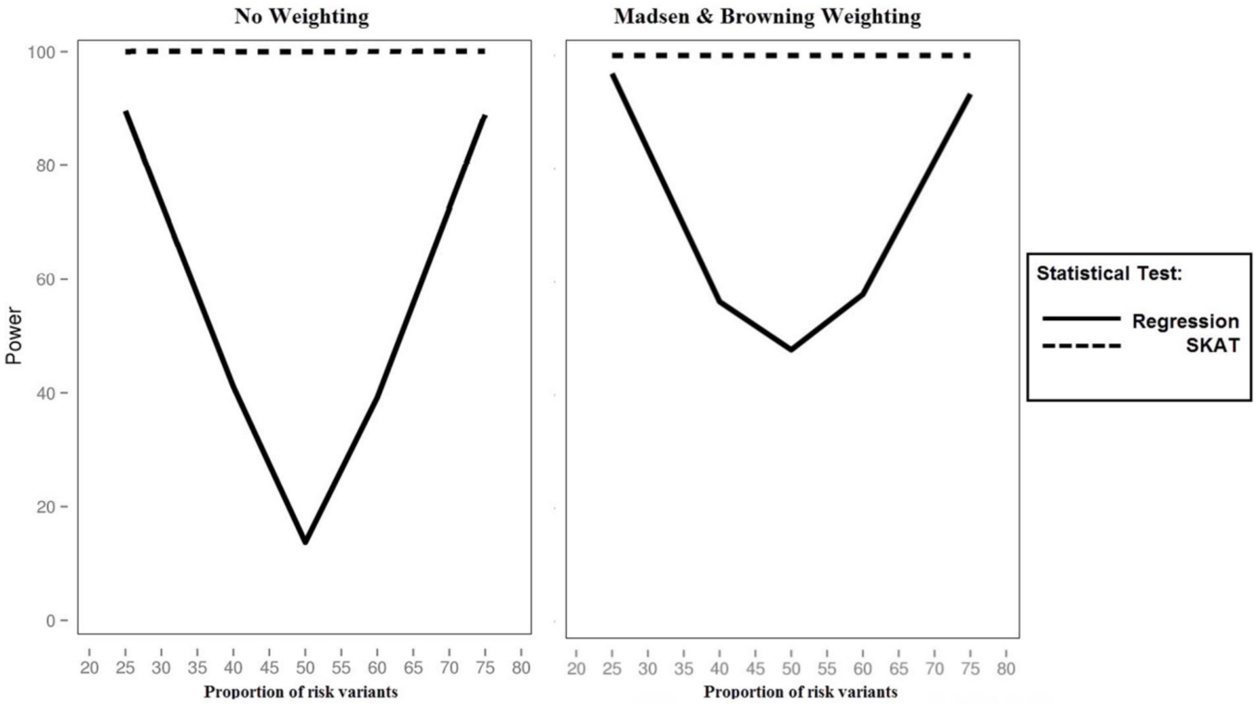
Supplementary Figure 1. Power plot of a BioBin-SKAT and BioBin-regression analysis performed when altering the proportion of risk variants between 25% and 100% with a disease prevalence of 50%. SKAT results are represented by a dashed line; regression results have a solid line.



Supplementary Table 1

Chr	Gene	p-value	Binned_variants	Phenotype	Biological_Feature	Note
11	*DRD2*	0.001179727	35	Asthma	Gene	
16	*CES2*	0.010970381	40	Asthma	Gene	
19	*LDLR*	0.023074213	43	Asthma	Gene	
10	*ARID5B*	0.025870289	44	Asthma	Gene	
10	*CYP2C19*	0.040866325	30	Asthma	Gene	
7	*CYP3A5*	0.042479211	42	Asthma	Gene	
5	*DRD1*	0.033968407	58	BPH	Gene	
11	*BDNF*	0.038833425	159	BPH	Gene	
13	*HTR2A*	0.010330326	32	Cataracts	Gene	
5	*NR3C1*	0.027598606	44	Cataracts	Gene	
10	*CYP2C19*	0.036277824	30	Cataracts	Gene	
1	*DPYD*	0.039427962	16	Cataracts	Gene	
9	*ABCA1*	0.044537277	71	Cataracts	Gene	
1	*CACNA1S*	0.020284554	51	Diverticulosis	Gene	
1	*PEAR1*	0.028351634	50	Diverticulosis	Gene	
5	*HTR1A*	0.046794883	12	GERD	Gene	
10	*ARID5B*	0.04819509	44	GERD	Gene	
16	*HSD11B2*	0.0189713	13	Hypertension	Gene	
7	*GLCCI1*	0.032181082	33	Hypertension	Gene	
17	*CRHR1*	0.000259278	17	Hypothyroidism	Gene	
1	*DPYD*	0.004257397	16	Hypothyroidism	Gene	
16	*VKORC1*	0.021326534	16	Hypothyroidism	Gene	
14	*TCL1A*	0.030896426	24	Hypothyroidism	Gene	
10	*CYP2C19*	0.03386573	33	Hypothyroidism	Gene	
6	*ESR1*	0.038379725	74	Hypothyroidism	Gene	
11	*BDNF*	0.000436774	52	Type II Diabetes	Gene	
19	*CYP2A6*	0.012372677	28	Type II Diabetes	Gene	
11	*SLCO2B1*	0.019923123	93	Type II Diabetes	Gene	
15	*CYP1A2*	0.049973505	26	Type II Diabetes	Gene	
10	*CYP2C19*	0.004225134	33	Uterine Fibroids	Gene	
10	*CYP2C9*	0.007992446	22	Uterine Fibroids	Gene	
2	*UGT1A4*	0.009799857	58	Uterine Fibroids	Gene	
20	*PTGIS*	0.014972429	23	Uterine Fibroids	Gene	
6	*SLC22A1*	0.021172076	28	Uterine Fibroids	Gene	
10	*ABCC2*	0.024574614	50	Uterine Fibroids	Gene	
13	*HTR2A*	0.031245627	34	Uterine Fibroids	Gene	
5	*HTR1A*	0.035444674	12	Uterine Fibroids	Gene	
12	*SLCO1B1*	0.037177345	14	Uterine Fibroids	Gene	
3	*SCN5A*	0.037279917	60	Uterine Fibroids	Gene	
10	*ARID5B*	0.001755935	25	ASTHMA	SNPEff_Annotation	UTR_3_PRIME_MODIFIER
19	*LDLR*	0.010478566	18	ASTHMA	SNPEff_Annotation	NON_SYNONYMOUS_CODING_MODERATE
4	*NR3C2*	0.01085317	7	ASTHMA	SNPEff_Annotation	unk
10	*GRK5*	0.011766182	9	ASTHMA	SNPEff_Annotation	NON_SYNONYMOUS_CODING_MODERATE
7	*CYP3A4*	0.012038997	6	ASTHMA	SNPEff_Annotation	DOWNSTREAM_MODIFIER
9	*ABCA1*	0.018221739	25	ASTHMA	SNPEff_Annotation	NON_SYNONYMOUS_CODING_MODERATE

2	*ABCB11*	0.021104772	12	ASTHMA	SNPEff_ Annotation	SYNONYMOUS_ CODING_LOW
12	*SLCO1A2*	0.027377813	8	ASTHMA	SNPEff_ Annotation	NON_SYNONYMOUS_ CODING_MODERATE
16	*CES2*	0.027993208	11	ASTHMA	SNPEff_ Annotation	UTR_3_ PRIME_MODIFIER
19	*CYP2A6*	0.029548969	12	ASTHMA	SNPEff_ Annotation	NON_SYNONYMOUS_ CODING_MODERATE
11	*SLCO2B1*	0.036529913	9	ASTHMA	SNPEff_ Annotation	DOWNSTREAM_ MODIFIER
7	*POR*	0.039319253	18	ASTHMA	SNPEff_ Annotation	NON_SYNONYMOUS_ CODING_MODERATE
7	*AHR*	0.04315453	13	ASTHMA	SNPEff_ Annotation	UTR_3_ PRIME_MODIFIER
5	*SLC6A3*	0.043604982	11	ASTHMA	SNPEff_ Annotation	SYNONYMOUS_ CODING_LOW
10	*ALOX5*	0.044745316	10	ASTHMA	SNPEff_ Annotation	NON_SYNONYMOUS_ CODING_MODERATE
11	*DRD2*	0.045325023	11	ASTHMA	SNPEff_ Annotation	unk
22	*CYP2D6*	0.025116534	11	BPH	SNPEff_ Annotation	NON_SYNONYMOUS_ CODING_MODERATE
16	*CES1*	0.031960697	9	BPH	SNPEff_ Annotation	NON_SYNONYMOUS_ CODING_MODERATE
6	*SLC22A2*	0.038772161	10	BPH	SNPEff_ Annotation	unk
4	*GRK4*	0.049865559	16	BPH	SNPEff_ Annotation	unk
13	*HTR2A*	0.000198635	6	Cataracts	SNPEff_ Annotation	SYNONYMOUS_ CODING_LOW
10	*CACNB2*	0.008360411	5	Cataracts	SNPEff_ Annotation	DOWNSTREAM_ MODIFIER
20	*PTGIS*	0.019950914	11	Cataracts	SNPEff_ Annotation	UTR_3_PRIME_ MODIFIER
7	*KCNH2*	0.021404617	6	Cataracts	SNPEff_ Annotation	SYNONYMOUS_ CODING_LOW
5	*NR3C1*	0.024958136	13	Cataracts	SNPEff_ Annotation	DOWNSTREAM_ MODIFIER
9	*PTGS1*	0.030600589	24	Cataracts	SNPEff_ Annotation	UTR_3_ PRIME_MODIFIER
4	*NR3C2*	0.033061258	6	Cataracts	SNPEff_ Annotation	NON_SYNONYMOUS_ CODING_MODERATE
9	*NTRK2*	0.048490121	14	Cataracts	SNPEff_ Annotation	DOWNSTREAM_ MODIFIER
15	*CYP1A2*	0.012328458	8	Diverticulosis	SNPEff_ Annotation	NON_SYNONYMOUS_ CODING_MODERATE
14	*TCL1A*	0.014062167	9	Diverticulosis	SNPEff_ Annotation	unk
16	*CES2*	0.019868355	6	Diverticulosis	SNPEff_ Annotation	SYNONYMOUS_ CODING_LOW
4	*NR3C2*	0.025332602	6	Diverticulosis	SNPEff_ Annotation	NON_SYNONYMOUS_ CODING_MODERATE
19	*LDLR*	0.027152085	11	Diverticulosis	SNPEff_ Annotation	DOWNSTREAM_ MODIFIER

7	*CYP3A4*	0.029999188	7	Diverticulosis	SNPEff_Annotation	NON_SYNONYMOUS_CODING_MODERATE
1	*PEAR1*	0.030777266	13	Diverticulosis	SNPEff_Annotation	UTR_3_PRIME_MODIFIER
5	*SLC6A3*	0.032172077	8	Diverticulosis	SNPEff_Annotation	unk
7	*AHR*	0.032549079	7	Diverticulosis	SNPEff_Annotation	unk
10	*CYP2C9*	0.038275773	5	Diverticulosis	SNPEff_Annotation	NON_SYNONYMOUS_CODING_MODERATE
7	*TBXAS1*	0.041546504	30	Diverticulosis	SNPEff_Annotation	unk
10	*GRK5*	0.042818405	9	Diverticulosis	SNPEff_Annotation	NON_SYNONYMOUS_CODING_MODERATE
1	*CACNA1S*	0.044733305	18	Diverticulosis	SNPEff_Annotation	SYNONYMOUS_CODING_LOW
16	*CES2*	0.048695098	8	Diverticulosis	SNPEff_Annotation	NON_SYNONYMOUS_CODING_MODERATE
12	*CACNA1C*	0.024027275	19	GERD	SNPEff_Annotation	SYNONYMOUS_CODING_LOW
10	*ARID5B*	0.041590807	25	GERD	SNPEff_Annotation	UTR_3_PRIME_MODIFIER
19	*CYP2B6*	0.047463803	5	GERD	SNPEff_Annotation	SYNONYMOUS_CODING_LOW
7	*GLCCI1*	0.003235229	11	Hypertension	SNPEff_Annotation	unk
6	*SLC22A2*	0.000128038	7	Hypothyroidism	SNPEff_Annotation	NON_SYNONYMOUS_CODING_MODERATE
17	*CRHR1*	0.000323349	7	Hypothyroidism	SNPEff_Annotation	UTR_3_PRIME_MODIFIER
1	*DPYD*	0.000364321	7	Hypothyroidism	SNPEff_Annotation	unk
10	*CYP2C19*	0.001784709	8	Hypothyroidism	SNPEff_Annotation	SYNONYMOUS_CODING_LOW
12	*VDR*	0.004426486	13	Hypothyroidism	SNPEff_Annotation	DOWNSTREAM_MODIFIER
17	*SLC47A2*	0.00716923	6	Hypothyroidism	SNPEff_Annotation	NON_SYNONYMOUS_CODING_MODERATE
14	*TCL1A*	0.012234609	10	Hypothyroidism	SNPEff_Annotation	UTR_3_PRIME_MODIFIER
1	*NPR1*	0.015094886	5	Hypothyroidism	SNPEff_Annotation	UTR_3_PRIME_MODIFIER
5	*SLC6A3*	0.017532987	11	Hypothyroidism	SNPEff_Annotation	SYNONYMOUS_CODING_LOW
7	*AHR*	0.018685128	9	Hypothyroidism	SNPEff_Annotation	NON_SYNONYMOUS_CODING_MODERATE
17	*SLC47A2*	0.024156956	9	Hypothyroidism	SNPEff_Annotation	UPSTREAM_MODIFIER
17	*CRHR1*	0.025450264	5	Hypothyroidism	SNPEff_Annotation	NON_SYNONYMOUS_CODING_MODERATE
6	*ESR1*	0.026856792	30	Hypothyroidism	SNPEff_Annotation	UTR_3_PRIME_MODIFIER
7	*TBXAS1*	0.032735052	30	Hypothyroidism	SNPEff_Annotation	unk

9	*ABCA1*	0.032997832	25	Hypothyroidism	SNPEff_Annotation	NON_SYNONYMOUS_CODING_MODERATE
22	*COMT*	0.0344895	26	Hypothyroidism	SNPEff_Annotation	unk
16	*CES2*	0.034945829	7	Hypothyroidism	SNPEff_Annotation	unk
6	*ESR1*	0.043833196	10	Hypothyroidism	SNPEff_Annotation	NON_SYNONYMOUS_CODING_MODERATE
15	*CYP1A2*	0.044017175	6	Hypothyroidism	SNPEff_Annotation	SYNONYMOUS_CODING_LOW
11	*BDNF*	0.003787583	26	Type II Diabetes	SNPEff_Annotation	unk
16	*ZNF423*	0.005577542	19	Type II Diabetes	SNPEff_Annotation	NON_SYNONYMOUS_CODING_MODERATE
11	*SLCO2B1*	0.007949934	9	Type II Diabetes	SNPEff_Annotation	DOWNSTREAM_MODIFIER
11	*SLCO2B1*	0.010474391	16	Type II Diabetes	SNPEff_Annotation	UTR_3_PRIME_MODIFIER
11	*BDNF*	0.012872105	21	Type II Diabetes	SNPEff_Annotation	UTR_3_PRIME_MODIFIER
12	*CACNA1C*	0.013648638	39	Type II Diabetes	SNPEff_Annotation	DOWNSTREAM_MODIFIER
9	*NTRK2*	0.019015237	7	Type II Diabetes	SNPEff_Annotation	SYNONYMOUS_CODING_LOW
17	*SLC47A1*	0.020840979	8	Type II Diabetes	SNPEff_Annotation	NON_SYNONYMOUS_CODING_MODERATE
15	*CYP1A2*	0.02378342	8	Type II Diabetes	SNPEff_Annotation	NON_SYNONYMOUS_CODING_MODERATE
6	*SLC22A2*	0.024021181	5	Type II Diabetes	SNPEff_Annotation	SPLICE_SITE_REGION_LOW
5	*NR3C1*	0.024946113	13	Type II Diabetes	SNPEff_Annotation	DOWNSTREAM_MODIFIER
10	*ALOX5*	0.026613266	7	Type II Diabetes	SNPEff_Annotation	UTR_3_PRIME_MODIFIER
19	*CYP2A6*	0.038160526	7	Type II Diabetes	SNPEff_Annotation	SYNONYMOUS_CODING_LOW
20	*PTGIS*	0.038690427	5	Type II Diabetes	SNPEff_Annotation	NON_SYNONYMOUS_CODING_MODERATE
6	*SLC22A2*	0.04265011	8	Type II Diabetes	SNPEff_Annotation	SYNONYMOUS_CODING_LOW
10	*CACNB2*	0.043087625	23	Type II Diabetes	SNPEff_Annotation	unk
15	*CYP1A2*	0.044687188	7	Type II Diabetes	SNPEff_Annotation	unk
10	*CYP2C19*	0.000161732	11	Uterine Fibroids	SNPEff_Annotation	unk
2	*UGT1A4*	0.001646409	38	Uterine Fibroids	SNPEff_Annotation	unk
17	*SLC47A2*	0.010052284	6	Uterine Fibroids	SNPEff_Annotation	SYNONYMOUS_CODING_LOW
9	*DBH*	0.011661478	14	Uterine Fibroids	SNPEff_Annotation	UTR_3_PRIME_MODIFIER
11	*SLCO2B1*	0.016486164	12	Uterine Fibroids	SNPEff_Annotation	NON_SYNONYMOUS_CODING_MODERATE

16	*CES2*	0.021966783	6	Uterine Fibroids	SNPEff_ Annotation	SYNONYMOUS_ CODING_LOW
3	*SCN5A*	0.028153856	17	Uterine Fibroids	SNPEff_ Annotation	SYNONYMOUS_ CODING_LOW
11	*BDNF*	0.028219488	21	Uterine Fibroids	SNPEff_ Annotation	UTR_3_ PRIME_MODIFIER
10	*CYP2C9*	0.030688042	6	Uterine Fibroids	SNPEff_ Annotation	NON_SYNONYMOUS_ CODING_MODERATE
7	*TBXAS1*	0.031793844	18	Uterine Fibroids	SNPEff_ Annotation	NON_SYNONYMOUS_ CODING_MODERATE
19	*LDLR*	0.031897119	10	Uterine Fibroids	SNPEff_ Annotation	DOWNSTREAM_ MODIFIER
13	*HTR2A*	0.037920869	11	Uterine Fibroids	SNPEff_ Annotation	UTR_3_ PRIME_MODIFIER
5	*NR3C1*	0.038854493	14	Uterine Fibroids	SNPEff_ Annotation	UPSTREAM_ MODIFIER
12	*CACNA1C*	0.040187026	19	Uterine Fibroids	SNPEff_ Annotation	SYNONYMOUS_ CODING_LOW
11	*DRD2*	0.04188187	12	Uterine Fibroids	SNPEff_ Annotation	unk
X	*MAOA*	0.04641349	6	Uterine Fibroids	SNPEff_ Annotation	UPSTREAM_ MODIFIER
17	*SLC47A1*	0.047281965	12	Uterine Fibroids	SNPEff_ Annotation	unk
6	*SLC22A2*	0.04982027	8	Uterine Fibroids	SNPEff_ Annotation	SYNONYMOUS_ CODING_LOW

Supplementary Table 2

Pathway_Name	**p-value**	**Binned_ variants**	**Phenotype**
biogrid:biogrid:738779	0.001708	8	Asthma
biogrid:biogrid:876356	0.001708	8	Asthma
biogrid:biogrid:891911	0.001708	8	Asthma
biogrid:biogrid:892247	0.001708	8	Asthma
biogrid:biogrid:892248	0.001708	8	Asthma
biogrid:biogrid:892249	0.001708	8	Asthma
biogrid:biogrid:892250	0.001708	8	Asthma
go:mitochondrial_outer_membrane	0.001761	31	Asthma
go:positive_regulation_of_icosanoid_secretion	0.001913	23	Asthma
biogrid:biogrid:1034692	0.002211	43	Asthma
biogrid:biogrid:275739	0.002211	43	Asthma
biogrid:biogrid:275916	0.002211	43	Asthma
biogrid:biogrid:276456	0.002211	43	Asthma
biogrid:biogrid:278281	0.002211	43	Asthma
biogrid:biogrid:288228	0.002211	43	Asthma
biogrid:biogrid:288450	0.002211	43	Asthma
biogrid:biogrid:302980	0.002211	43	Asthma
biogrid:biogrid:303431	0.002211	43	Asthma
biogrid:biogrid:303435	0.002211	43	Asthma
biogrid:biogrid:303442	0.002211	43	Asthma
biogrid:biogrid:316220	0.002211	43	Asthma
biogrid:biogrid:555676	0.002211	43	Asthma
biogrid:biogrid:559028	0.002211	43	Asthma
biogrid:biogrid:559029	0.002211	43	Asthma
biogrid:biogrid:683115	0.002211	43	Asthma
biogrid:biogrid:823021	0.002211	43	Asthma
biogrid:biogrid:823022	0.002211	43	Asthma
biogrid:biogrid:823023	0.002211	43	Asthma
biogrid:biogrid:823024	0.002211	43	Asthma
biogrid:biogrid:824719	0.002211	43	Asthma
biogrid:biogrid:830061	0.002211	43	Asthma
biogrid:biogrid:893887	0.002211	43	Asthma
go:apical_part_of_cell	0.002211	43	Asthma
go:clathrin-coated_endocytic_ vesicle_membrane	0.002211	43	Asthma
go:clathrin_heavy_chain_binding	0.002211	43	Asthma
go:coated_pit	0.002211	43	Asthma
go:endocytosis	0.002211	43	Asthma
go:glycoprotein_binding	0.002211	43	Asthma
go:intestinal_cholesterol_absorption	0.002211	43	Asthma
go:low-density_lipoprotein_particle_clearance	0.002211	43	Asthma
go:low-density_lipoprotein_receptor_activity	0.002211	43	Asthma
go:phospholipid_transport	0.002211	43	Asthma

go:positive_regulation_of_triglyceride_biosynthetic_process	0.002211	43	Asthma
go:regulation_of_phosphatidylcholine_catabolic_process	0.002211	43	Asthma
go:very-low-density_lipoprotein_particle_receptor_activity	0.002211	43	Asthma
mint:mint:MINT-4301346	0.002211	43	Asthma
mint:mint:MINT-6177086	0.002211	43	Asthma
mint:mint:MINT-6177157	0.002211	43	Asthma
mint:mint:MINT-6177193	0.002211	43	Asthma
mint:mint:MINT-6804492	0.002211	43	Asthma
pfam:Coagulation_Factor_Xa_inhibitory_site	0.002211	43	Asthma
pfam:Low-density_lipoprotein_receptor_repeat_class_B	0.002211	43	Asthma
reactome:REACT_6934	0.002211	43	Asthma
pfam:Low-density_lipoprotein_receptor_domain_class_A	0.00238	46	Asthma
go:leukotriene-B4_20-monooxygenase_activity	0.002402	35	Asthma
go:leukotriene_B4_catabolic_process	0.002402	35	Asthma
go:long-chain_fatty_acid_metabolic_process	0.002402	35	Asthma
go:pressure_natriuresis	0.002402	35	Asthma
biogrid:biogrid:809629	0.003091	13	Asthma
biogrid:biogrid:824781	0.003091	13	Asthma
mint:mint:MINT-64803	0.003091	13	Asthma
pfam:TMPIT-like_protein	0.003091	13	Asthma
pfam:Flavin_containing_amine_oxidoreductase	0.004292	37	Asthma
reactome:REACT_263961	0.005464	60	Asthma
reactome:REACT_264155	0.005798	61	Asthma
reactome:REACT_264165	0.005798	61	Asthma
biogrid:biogrid:593191	0.006124	5	Asthma
biogrid:biogrid:854909	0.006124	5	Asthma
biogrid:biogrid:854910	0.006124	5	Asthma
biogrid:biogrid:876664	0.006124	5	Asthma
go:aromatic_compound_catabolic_process	0.006754	11	Asthma
pfam:Arylesterase	0.006754	11	Asthma
kegg:Glycosaminoglycan_biosynthesis_-_chondroitin_sulfate_dermatan_sulfate	0.007027	47	Asthma
go:arylesterase_activity	0.007059	9	Asthma
go:carboxylic_acid_catabolic_process	0.007059	9	Asthma
go:response_to_external_stimulus	0.007059	9	Asthma
biogrid:biogrid:631840	0.007124	6	Asthma
biogrid:biogrid:746198	0.007124	6	Asthma

biogrid:biogrid:752222	0.007124	6	Asthma
biogrid:biogrid:753156	0.007124	6	Asthma
go:methionine_adenosyltransferase_activity	0.007124	6	Asthma
go:sulfur_amino_acid_metabolic_process	0.007124	6	Asthma
kegg:Biosynthesis_of_amino_acids	0.007124	6	Asthma
kegg:Cysteine_and_methionine_metabolism	0.007124	6	Asthma
pfam:S-adenosylmethionine_synthetase__central_domain	0.007124	6	Asthma
pfam:S-adenosylmethionine_synthetase__C-terminal_domain	0.007124	6	Asthma
pfam:S-adenosylmethionine_synthetase__N-terminal_domain	0.007124	6	Asthma
reactome:REACT_115639	0.007124	6	Asthma
reactome:REACT_268063	0.007124	6	Asthma
go:late_endosome	0.008464	67	Asthma
go:chondroitin_sulfate_biosynthetic_process	0.008477	52	Asthma
go:chondroitin_sulfate_metabolic_process	0.008477	52	Asthma
reactome:REACT_120989	0.008477	52	Asthma
reactome:REACT_121206	0.008477	52	Asthma
go:primary_amine_oxidase_activity	0.009225	26	Asthma
pfam:KRAB_box	0.009313	2	Asthma
go:positive_regulation_of_defense_response_to_virus_by_host	0.009969	18	Asthma
go:carbohydrate_metabolic_process	0.009975	107	Asthma
go:early_endosome	0.010744	63	Asthma
go:dopamine_catabolic_process	0.010757	21	Asthma
kegg:Glycine__serine_and_threonine_metabolism	0.010757	21	Asthma
reactome:REACT_1875	0.010757	21	Asthma
reactome:REACT_416	0.010757	21	Asthma
go:glycosaminoglycan_metabolic_process	0.010882	76	Asthma
reactome:REACT_121315	0.010882	76	Asthma
go:cholesterol_import	0.010889	50	Asthma
go:cholesterol_transport	0.010889	50	Asthma
reactome:REACT_474	0.011215	95	Asthma
go:endosome_membrane	0.012883	110	Asthma
go:Golgi_membrane	0.013517	94	Asthma
biogrid:biogrid:603664	0.013533	9	Asthma
biogrid:biogrid:833278	0.013533	9	Asthma
biogrid:biogrid:892338	0.013533	9	Asthma
biogrid:biogrid:892339	0.013533	9	Asthma
biogrid:biogrid:940095	0.013533	9	Asthma
biogrid:biogrid:940811	0.013533	9	Asthma
go:androgen_binding	0.013533	9	Asthma

go:retinal_dehydrogenase_activity	0.013533	9	Asthma
mint:mint:MINT-68416	0.013533	9	Asthma
go:cellular_biogenic_amine_metabolic_process	0.013704	27	Asthma
go:chondroitin_4-sulfotransferase_activity	0.013804	24	Asthma
go:basolateral_plasma_membrane	0.01385	217	Asthma
biogrid:biogrid:1050783	0.014295	44	Asthma
biogrid:biogrid:614154	0.014295	44	Asthma
biogrid:biogrid:631317	0.014295	44	Asthma
biogrid:biogrid:663159	0.014295	44	Asthma
biogrid:biogrid:678119	0.014295	44	Asthma
biogrid:biogrid:690467	0.014295	44	Asthma
biogrid:biogrid:734878	0.014295	44	Asthma
biogrid:biogrid:863106	0.014295	44	Asthma
biogrid:biogrid:871845	0.014295	44	Asthma
biogrid:biogrid:871934	0.014295	44	Asthma
go:adipose_tissue_development	0.014295	44	Asthma
go:liver_development	0.014295	44	Asthma
go:RNA_polymerase_II_ transcription_regulatory_region_sequence-specific_DNA_binding_transcription_ factor_activity_involved_in_ negative_regulation_of_transcription	0.014295	44	Asthma
pfam:ARID/BRIGHT_DNA_binding_domain	0.014295	44	Asthma
go:receptor-mediated_endocytosis	0.014994	127	Asthma
go:alkane_1-monooxygenase_activity	0.015011	52	Asthma
pfam:Sulfotransferase_family	0.015261	53	Asthma
go:renal_water_homeostasis	0.015466	41	Asthma
go:sodium_ion_homeostasis	0.015466	41	Asthma
go:bone_mineralization	0.015709	10	Asthma
go:calcidiol_1-monooxygenase_activity	0.015709	10	Asthma
go:calcium_ion_homeostasis	0.015709	10	Asthma
go:G1_to_G0_transition	0.015709	10	Asthma
go:negative_regulation_of_ calcidiol_1-monooxygenase_activity	0.015709	10	Asthma
go:positive_regulation_of_vitamin_D _receptor_signaling_pathway	0.015709	10	Asthma
go:regulation_of_bone_mineralization	0.015709	10	Asthma
go:response_to_interferon-gamma	0.015709	10	Asthma
reactome:REACT_268633	0.015709	10	Asthma
kegg:Toxoplasmosis	0.016376	83	Asthma
kegg:Endocytosis	0.016789	185	Asthma
go:phototransduction__visible_light	0.017578	52	Asthma
reactome:REACT_160125	0.017578	52	Asthma
reactome:REACT_24968	0.017578	52	Asthma
reactome:REACT_6841	0.017578	52	Asthma
go:response_to_lipopolysaccharide	0.017965	11	Asthma
biogrid:biogrid:892337	0.018645	11	Asthma

go:neurotransmitter_secretion	0.018675	56	Asthma
biogrid:biogrid:442570	0.019383	19	Asthma
biogrid:biogrid:626632	0.019383	19	Asthma
biogrid:biogrid:632516	0.019383	19	Asthma
reactome:REACT_267863	0.019383	19	Asthma
kegg:Phenylalanine_metabolism	0.020718	30	Asthma
go:cellular_component	0.020863	47	Asthma
go:N-acetylgalactosamine_ 4-O-sulfotransferase_activity	0.021181	36	Asthma
pfam:Sulfotransferase_domain	0.02137	117	Asthma
reactome:REACT_15391	0.021838	21	Asthma
reactome:REACT_15532	0.021838	21	Asthma
go:response_to_vitamin_D	0.022543	22	Asthma
kegg:Arginine_and_proline_metabolism	0.023717	36	Asthma
go:positive_regulation_of_GTPase_activity	0.025308	28	Asthma
pfam:Leucine_Rich_repeat	0.027473	2	Asthma
go:cellular_detoxification_of_nitrogen_compound	0.027941	12	Asthma
go:nitrobenzene_metabolic_process	0.027941	12	Asthma
go:sulfotransferase_activity	0.028305	105	Asthma
biogrid:biogrid:631794	0.028472	18	Asthma
biogrid:biogrid:854524	0.028472	18	Asthma
biogrid:biogrid:854913	0.028472	18	Asthma
biogrid:biogrid:876663	0.028472	18	Asthma
go:alpha-tocopherol_ omega-hydroxylase_activity	0.028472	18	Asthma
go:arachidonic_acid_ omega-hydroxylase_activity	0.028472	18	Asthma
go:negative_regulation_of_icosanoid_secretion	0.028472	18	Asthma
go:tocotrienol_omega-hydroxylase_activity	0.028472	18	Asthma
go:calcium_ion_binding	0.030419	18	Asthma
go:glutathione_binding	0.033099	15	Asthma
kegg:Ovarian_steroidogenesis	0.033722	128	Asthma
kegg:Tryptophan_metabolism	0.035616	90	Asthma
kegg:Hepatitis_C	0.036627	131	Asthma
go:negative_regulation_of_ blood_coagulation	0.036764	30	Asthma
go:very_long-chain_fatty_acid_ metabolic_process	0.036764	30	Asthma
go:vitamin_E_metabolic_process	0.036764	30	Asthma
go:vitamin_K_biosynthetic_process	0.036764	30	Asthma
go:GTPase_activator_activity	0.037665	17	Asthma
biogrid:biogrid:1051043	0.038105	5	Asthma
biogrid:biogrid:632173	0.038105	5	Asthma
biogrid:biogrid:728115	0.038105	5	Asthma
go:aryldialkylphosphatase_activity	0.038105	5	Asthma
go:negative_regulation_of_ plasma_lipoprotein_particle_oxidation	0.038105	5	Asthma

go:organophosphate_catabolic_process	0.038105	5	Asthma
go:phosphatidylcholine_metabolic_process	0.038105	5	Asthma
go:positive_regulation_ of_binding	0.038105	5	Asthma
go:positive_regulation_ of_cholesterol_efflux	0.038105	5	Asthma
go:positive_regulation_ of_transporter_activity	0.038105	5	Asthma
go:3'-phosphoadenosine_5'- phosphosulfate_metabolic_process	0.041281	74	Asthma
reactome:REACT_6913	0.041281	74	Asthma
biogrid:biogrid:1051446	0.0457	7	Asthma
biogrid:biogrid:1052013	0.0457	7	Asthma
biogrid:biogrid:1052957	0.0457	7	Asthma
biogrid:biogrid:243052	0.0457	7	Asthma
biogrid:biogrid:566053	0.0457	7	Asthma
biogrid:biogrid:601512	0.0457	7	Asthma
biogrid:biogrid:604765	0.0457	7	Asthma
biogrid:biogrid:815981	0.0457	7	Asthma
biogrid:biogrid:876133	0.0457	7	Asthma
biogrid:biogrid:951342	0.0457	7	Asthma
go:establishment_of_blood-nerve_barrier	0.0457	7	Asthma
mint:mint:MINT-8167646	0.0457	7	Asthma
mint:mint:MINT-8270473	0.0457	7	Asthma
biogrid:biogrid:316292	0.045789	5	Asthma
biogrid:biogrid:618508	0.045789	5	Asthma
go:regulation_of_skeletal_muscle_ contraction_by_regulation_of_release _of_sequestered_calcium_ion	0.045789	5	Asthma
go:relaxation_of_cardiac_muscle	0.045789	5	Asthma
kegg:Histidine_metabolism	0.046912	50	Asthma
go:drug_transport	0.047726	48	Asthma
go:lysosome	0.049056	119	Asthma
biogrid:biogrid:424435	0.049432	16	Asthma
biogrid:biogrid:534905	0.049432	16	Asthma
biogrid:biogrid:534906	0.049432	16	Asthma
biogrid:biogrid:534907	0.049432	16	Asthma
biogrid:biogrid:534908	0.049432	16	Asthma
biogrid:biogrid:534909	0.049432	16	Asthma
biogrid:biogrid:534910	0.049432	16	Asthma
biogrid:biogrid:534912	0.049432	16	Asthma
biogrid:biogrid:534914	0.049432	16	Asthma
biogrid:biogrid:534915	0.049432	16	Asthma
biogrid:biogrid:622570	0.049432	16	Asthma
go:histone_demethylase_activity_ (H3-dimethyl-K4_specific)	0.049432	16	Asthma

go:histone_demethylase_activity_(H3-monomethyl-K4_specific)	0.049432	16	Asthma
go:histone_H3-K4_demethylation	0.049432	16	Asthma
go:regulation_of_DNA_methylation	0.049432	16	Asthma
go:regulation_of_gene_expression_by_genetic_imprinting	0.049432	16	Asthma
pfam:CW-type_Zinc_Finger	0.049432	16	Asthma
go:Golgi_apparatus	0.049499	196	Asthma
go:purine_nucleoside_transmembrane_transport	0.002107	9	BPH
go:purine_nucleoside_transmembrane_transporter_activity	0.002107	9	BPH
go:adult_walking_behavior	0.005025	63	BPH
go:cerebral_cortex_GABAergic_interneuron_migration	0.005025	63	BPH
go:phospholipase_C-activating_dopamine_receptor_signaling_pathway	0.005025	63	BPH
go:positive_regulation_of_cytosolic_calcium_ion_concentration_involved_in_phospholipase_C-activating_G-protein_coupled_signaling_pathway	0.005025	63	BPH
go:prepulse_inhibition	0.005025	63	BPH
go:regulation_of_dopamine_uptake_involved_in_synaptic_transmission	0.005025	63	BPH
go:synapse_assembly	0.005025	63	BPH
go:visual_learning	0.005025	63	BPH
reactome:REACT_16968	0.005025	63	BPH
pfam:7_transmembrane_receptor_(rhodopsin_family)	0.005078	130	BPH
reactome:REACT_16983	0.005078	130	BPH
reactome:REACT_14828	0.005244	131	BPH
kegg:Neuroactive_ligand-receptor_interaction	0.007176	193	BPH
kegg:Gap_junction	0.007326	169	BPH
go:positive_regulation_of_cAMP_biosynthetic_process	0.008451	110	BPH
reactome:REACT_21340	0.008988	151	BPH
reactome:REACT_19184	0.011032	178	BPH
go:dopamine_metabolic_process	0.012001	65	BPH
kegg:Parkinson's_disease	0.012453	111	BPH
reactome:REACT_14797	0.012593	239	BPH
go:response_to_drug	0.012802	241	BPH
biogrid:biogrid:278849	0.013059	28	BPH
biogrid:biogrid:280299	0.013059	28	BPH
biogrid:biogrid:306166	0.013059	28	BPH
biogrid:biogrid:306168	0.013059	28	BPH
biogrid:biogrid:306169	0.013059	28	BPH
biogrid:biogrid:478404	0.013059	28	BPH
biogrid:biogrid:948551	0.013059	28	BPH
biogrid:biogrid:948552	0.013059	28	BPH

go:adenylate_cyclase-activating_dopamine_receptor_signaling_pathway	0.013059	28	BPH
go:adenylate_cyclase-activating_G-protein_coupled_receptor_signaling_pathway	0.013059	28	BPH
go:cellular_response_to_catecholamine_stimulus	0.013059	28	BPH
go:dopamine_binding	0.013059	28	BPH
go:dopamine_neurotransmitter_receptor_activity	0.013059	28	BPH
go:dopamine_neurotransmitter_receptor_activity__coupled_via_Gs	0.013059	28	BPH
go:G-protein_coupled_amine_receptor_activity	0.013059	28	BPH
go:G-protein_coupled_receptor_signaling_pathway_coupled_to_cyclic_nucleotide_second_messenger	0.013059	28	BPH
go:mating_behavior	0.013059	28	BPH
go:positive_regulation_of_potassium_ion_transport	0.013059	28	BPH
go:positive_regulation_of_release_of_sequestered_calcium_ion_into_cytosol	0.013059	28	BPH
go:positive_regulation_of_synaptic_transmission__glutamatergic	0.013059	28	BPH
go:sensory_perception_of_chemical_stimulus	0.013059	28	BPH
go:synaptic_transmission__dopaminergic	0.013059	28	BPH
go:transmission_of_nerve_impulse	0.013059	28	BPH
kegg:Cocaine_addiction	0.018626	184	BPH
reactome:REACT_19327	0.019372	75	BPH
go:positive_regulation_of_cell_migration	0.020225	90	BPH
biogrid:biogrid:279619	0.022972	15	BPH
mint:mint:MINT-8170022	0.022972	15	BPH
go:detection_of_chemical_stimulus	0.025534	11	BPH
biogrid:biogrid:610034	0.026912	13	BPH
go:positive_regulation_of_adenylate_cyclase_activity_involved_in_G-protein_coupled_receptor_signaling_pathway	0.030651	51	BPH
go:epithelial_cell_differentiation	0.030986	50	BPH
kegg:Morphine_addiction	0.032207	87	BPH
go:calcium_ion_binding	0.034158	18	BPH
biogrid:biogrid:1037052	0.036619	8	BPH
biogrid:biogrid:593342	0.036619	8	BPH
biogrid:biogrid:893338	0.036619	8	BPH
biogrid:biogrid:893425	0.036619	8	BPH
go:cerebroside-sulfatase_activity	0.036619	8	BPH
go:glycosphingolipid_metabolic_process	0.036619	8	BPH
go:lysosomal_lumen	0.036619	8	BPH
go:sphingolipid_metabolic_process	0.036619	8	BPH
go:sulfuric_ester_hydrolase_activity	0.036619	8	BPH
mint:mint:MINT-8165171	0.036619	8	BPH

pfam:C-terminal_region_of_aryl-sulfatase	0.036619	8	BPH
pfam:Sulfatase	0.036619	8	BPH
reactome:REACT_116105	0.036619	8	BPH
reactome:REACT_121036	0.036619	8	BPH
reactome:REACT_19323	0.036619	8	BPH
go:anion_transmembrane_transport	0.042603	105	BPH
biogrid:biogrid:245524	0.044772	9	BPH
biogrid:biogrid:593047	0.044772	9	BPH
biogrid:biogrid:593048	0.044772	9	BPH
biogrid:biogrid:838614	0.044772	9	BPH
biogrid:biogrid:892674	0.044772	9	BPH
biogrid:biogrid:893016	0.044772	9	BPH
biogrid:biogrid:893590	0.044772	9	BPH
biogrid:biogrid:893591	0.044772	9	BPH
biogrid:biogrid:893592	0.044772	9	BPH
biogrid:biogrid:893593	0.044772	9	BPH
biogrid:biogrid:893594	0.044772	9	BPH
biogrid:biogrid:894523	0.044772	9	BPH
biogrid:biogrid:894524	0.044772	9	BPH
biogrid:biogrid:894525	0.044772	9	BPH
biogrid:biogrid:914396	0.044772	9	BPH
go:neuron-neuron_synaptic_transmission	0.04764	37	BPH
kegg:Non-alcoholic_fatty_liver_disease_(NAFLD)	0.04989	24	BPH
go:glucocorticoid_biosynthetic_process	0.00395	39	Cataracts
reactome:REACT_13812	0.005215	130	Cataracts
go:water-soluble_vitamin_metabolic_process	0.005691	76	Cataracts
biogrid:biogrid:259322	0.005956	32	Cataracts
biogrid:biogrid:282008	0.005956	32	Cataracts
biogrid:biogrid:677630	0.005956	32	Cataracts
biogrid:biogrid:868463	0.005956	32	Cataracts
go:1-(4-iodo-2_5-dimethoxyphenyl) propan-2-amine_binding	0.005956	32	Cataracts
go:phosphatidylinositol_3-kinase_signaling	0.005956	32	Cataracts
go:positive_regulation_of_ phosphatidylinositol_biosynthetic_process	0.005956	32	Cataracts
go:serotonin_binding	0.005956	32	Cataracts
mint:mint:MINT-73187	0.005956	32	Cataracts
reactome:REACT_268601	0.006617	18	Cataracts
kegg:Inflammatory_ mediator_regulation_of_TRP_channels	0.007016	41	Cataracts
reactome:REACT_11193	0.007164	87	Cataracts
reactome:REACT_11238	0.007164	87	Cataracts
go:vitamin_metabolic_process	0.008387	136	Cataracts
biogrid:biogrid:1032071	0.010076	28	Cataracts
biogrid:biogrid:594211	0.010076	28	Cataracts
biogrid:biogrid:594329	0.010076	28	Cataracts
biogrid:biogrid:608938	0.010076	28	Cataracts

biogrid:biogrid:747641	0.010076	28	Cataracts
biogrid:biogrid:747977	0.010076	28	Cataracts
biogrid:biogrid:748071	0.010076	28	Cataracts
biogrid:biogrid:748631	0.010076	28	Cataracts
biogrid:biogrid:748888	0.010076	28	Cataracts
biogrid:biogrid:748997	0.010076	28	Cataracts
biogrid:biogrid:749776	0.010076	28	Cataracts
biogrid:biogrid:749982	0.010076	28	Cataracts
biogrid:biogrid:750070	0.010076	28	Cataracts
biogrid:biogrid:750094	0.010076	28	Cataracts
biogrid:biogrid:750520	0.010076	28	Cataracts
biogrid:biogrid:750522	0.010076	28	Cataracts
biogrid:biogrid:751337	0.010076	28	Cataracts
biogrid:biogrid:751699	0.010076	28	Cataracts
biogrid:biogrid:751939	0.010076	28	Cataracts
biogrid:biogrid:752521	0.010076	28	Cataracts
biogrid:biogrid:752714	0.010076	28	Cataracts
biogrid:biogrid:752737	0.010076	28	Cataracts
biogrid:biogrid:752864	0.010076	28	Cataracts
biogrid:biogrid:752925	0.010076	28	Cataracts
biogrid:biogrid:753211	0.010076	28	Cataracts
biogrid:biogrid:753362	0.010076	28	Cataracts
biogrid:biogrid:753563	0.010076	28	Cataracts
biogrid:biogrid:754559	0.010076	28	Cataracts
biogrid:biogrid:893428	0.010076	28	Cataracts
biogrid:biogrid:893948	0.010076	28	Cataracts
biogrid:biogrid:893949	0.010076	28	Cataracts
go:cobalamin_metabolic_process	0.010076	28	Cataracts
kegg:Sphingolipid_signaling_pathway	0.010076	28	Cataracts
reactome:REACT_163862	0.010076	28	Cataracts
reactome:REACT_11036	0.012439	32	Cataracts
go:glucose_homeostasis	0.012599	24	Cataracts
go:mitochondrial_inner_membrane	0.013925	57	Cataracts
biogrid:biogrid:874910	0.014103	69	Cataracts
go:prostaglandin_biosynthetic_process	0.014103	69	Cataracts
biogrid:biogrid:906563	0.014312	31	Cataracts
biogrid:biogrid:906721	0.014312	31	Cataracts
biogrid:biogrid:914827	0.014312	31	Cataracts
pfam:Protein_Family_FAM117	0.014312	31	Cataracts
biogrid:biogrid:601292	0.014372	22	Cataracts
biogrid:biogrid:601525	0.014372	22	Cataracts
biogrid:biogrid:603326	0.014372	22	Cataracts
biogrid:biogrid:913903	0.014372	22	Cataracts
mint:mint:MINT-8252901	0.014372	22	Cataracts
mint:mint:MINT-8252934	0.014372	22	Cataracts
mint:mint:MINT-8254921	0.014372	22	Cataracts
pfam:RUN_domain	0.014372	22	Cataracts

go:ATPase_activity	0.015706	37	Cataracts
go:aldosterone_biosynthetic_process	0.01599	24	Cataracts
go:cellular_response_to_potassium_ion	0.01599	24	Cataracts
go:cortisol_biosynthetic_process	0.01599	24	Cataracts
go:steroid_11-beta-monooxygenase_activity	0.01599	24	Cataracts
go:DNA_damage_response__signal_transduction_by_p53_class_mediator_resulting_in_cell_cycle_arrest	0.016852	25	Cataracts
go:extrinsic_component_of_membrane	0.016852	25	Cataracts
reactome:REACT_263897	0.016852	25	Cataracts
reactome:REACT_264071	0.016852	25	Cataracts
reactome:REACT_264075	0.016852	25	Cataracts
reactome:REACT_264164	0.016852	25	Cataracts
reactome:REACT_264487	0.016852	25	Cataracts
go:C21-steroid_hormone_biosynthetic_process	0.017853	32	Cataracts
reactome:REACT_11057	0.017892	89	Cataracts
reactome:REACT_unknown_1773	0.017892	89	Cataracts
reactome:REACT_268786	0.017895	3	Cataracts
pfam:Trypsin	0.018258	27	Cataracts
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go:regulation_of_blood_pressure	0.02902	184	Cataracts
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biogrid:biogrid:1029172	0.002389	17	Diverticulosis
biogrid:biogrid:1029173	0.002389	17	Diverticulosis
biogrid:biogrid:1032930	0.002389	17	Diverticulosis
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biogrid:biogrid:1101067	0.002389	17	Diverticulosis
biogrid:biogrid:1101068	0.002389	17	Diverticulosis
biogrid:biogrid:252707	0.002389	17	Diverticulosis
biogrid:biogrid:252827	0.002389	17	Diverticulosis
biogrid:biogrid:253164	0.002389	17	Diverticulosis
biogrid:biogrid:253168	0.002389	17	Diverticulosis
biogrid:biogrid:256014	0.002389	17	Diverticulosis
biogrid:biogrid:256015	0.002389	17	Diverticulosis
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biogrid:biogrid:282083	0.002389	17	Diverticulosis

biogrid:biogrid:300357	0.002389	17	Diverticulosis
biogrid:biogrid:314470	0.002389	17	Diverticulosis
biogrid:biogrid:314472	0.002389	17	Diverticulosis
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biogrid:biogrid:480177	0.002389	17	Diverticulosis
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biogrid:biogrid:876609	0.002389	17	Diverticulosis
biogrid:biogrid:892880	0.002389	17	Diverticulosis
go:DNA_damage_response_signal_transduction_by_p53_class_mediator_resulting_in_transcription_of_p21_class_mediator	0.002389	17	Diverticulosis
go:erythrocyte_differentiation	0.002389	17	Diverticulosis
go:eye_development	0.002389	17	Diverticulosis
go:intrinsic_apoptotic_signaling_pathway	0.002389	17	Diverticulosis
go:intrinsic_apoptotic_signaling_pathway_in_response_to_DNA_damage_by_p53_class_mediator	0.002389	17	Diverticulosis
go:negative_regulation_of_BMP_signaling_pathway	0.002389	17	Diverticulosis
go:nuclear_body	0.002389	17	Diverticulosis
go:peptidyl-threonine_phosphorylation	0.002389	17	Diverticulosis
go:PML_body	0.002389	17	Diverticulosis
go:PML_body_organization	0.002389	17	Diverticulosis
go:positive_regulation_of_JNK_cascade	0.002389	17	Diverticulosis
go:positive_regulation_of_protein_binding	0.002389	17	Diverticulosis
go:positive_regulation_of_transforming_growth_factor_beta_receptor_signaling_pathway	0.002389	17	Diverticulosis
go:RNA_polymerase_II_activating_transcription_factor_binding	0.002389	17	Diverticulosis
go:RNA_polymerase_II_transcription_coactivator_activity	0.002389	17	Diverticulosis
go:SMAD_binding	0.002389	17	Diverticulosis
go:SMAD_protein_signal_transduction	0.002389	17	Diverticulosis
go:transcription_corepressor_activity	0.002389	17	Diverticulosis
go:virion_binding	0.002389	17	Diverticulosis
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mint:mint:MINT-2982487	0.002389	17	Diverticulosis
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mint:mint:MINT-8085171	0.002389	17	Diverticulosis
mint:mint:MINT-8085226	0.002389	17	Diverticulosis
mint:mint:MINT-8085240	0.002389	17	Diverticulosis
mint:mint:MINT-8085254	0.002389	17	Diverticulosis
mint:mint:MINT-8088896	0.002389	17	Diverticulosis
go:protein_serine/threonine_kinase_activity	0.006728	47	Diverticulosis
go:urate_transport	0.00907	10	Diverticulosis
go:regulation_of_cell_cycle	0.00976	42	Diverticulosis
go:protein_complex	0.010817	122	Diverticulosis
biogrid:biogrid:255859	0.010938	107	Diverticulosis
biogrid:biogrid:268182	0.010938	107	Diverticulosis
biogrid:biogrid:268183	0.010938	107	Diverticulosis
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biogrid:biogrid:834434	0.010938	107	Diverticulosis
biogrid:biogrid:844342	0.010938	107	Diverticulosis
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biogrid:biogrid:888720	0.010938	107	Diverticulosis
biogrid:biogrid:905886	0.010938	107	Diverticulosis
go:calcium_channel_complex	0.010938	107	Diverticulosis
go:calcium-induced_calcium_release_activity	0.010938	107	Diverticulosis
go:calcium-mediated_signaling	0.010938	107	Diverticulosis
go:calcium-mediated_signaling_using_intracellular_calcium_source	0.010938	107	Diverticulosis
go:cardiac_muscle_hypertrophy	0.010938	107	Diverticulosis
go:cellular_response_to_epinephrine_stimulus	0.010938	107	Diverticulosis
go:detection_of_calcium_ion	0.010938	107	Diverticulosis
go:embryonic_heart_tube_morphogenesis	0.010938	107	Diverticulosis
go:establishment_of_protein_localization_to_endoplasmic_reticulum	0.010938	107	Diverticulosis
go:intracellular_ligand-gated_calcium_channel_activity	0.010938	107	Diverticulosis
go:left_ventricular_cardiac_muscle_tissue_morphogenesis	0.010938	107	Diverticulosis
go:positive_regulation_of_calcium-transporting_ATPase_activity	0.010938	107	Diverticulosis
go:positive_regulation_of_heart_rate	0.010938	107	Diverticulosis
go:positive_regulation_of_sequestering_of_calcium_ion	0.010938	107	Diverticulosis
go:positive_regulation_of_the_force_of_heart_contraction	0.010938	107	Diverticulosis
go:protein_kinase_A_catalytic_subunit_binding	0.010938	107	Diverticulosis
go:protein_kinase_A_regulatory_subunit_binding	0.010938	107	Diverticulosis
go:Purkinje_myocyte_to_ventricular_cardiac_muscle_cell_signaling	0.010938	107	Diverticulosis
go:regulation_of_atrial_cardiac_muscle_cell_action_potential	0.010938	107	Diverticulosis

go:regulation_of_AV_node_cell_action_potential	0.010938	107	Diverticulosis
go:regulation_of_cardiac_muscle_contraction	0.010938	107	Diverticulosis
go:regulation_of_cardiac_muscle_contraction_by_calcium_ion_signaling	0.010938	107	Diverticulosis
go:regulation_of_SA_node_cell_action_potential	0.010938	107	Diverticulosis
go:regulation_of_ventricular_cardiac_muscle_cell_action_potential	0.010938	107	Diverticulosis
go:response_to_muscle_activity	0.010938	107	Diverticulosis
go:response_to_muscle_stretch	0.010938	107	Diverticulosis
go:sarcoplasmic_reticulum_calcium_ion_transport	0.010938	107	Diverticulosis
go:suramin_binding	0.010938	107	Diverticulosis
go:type_B_pancreatic_cell_apoptotic_process	0.010938	107	Diverticulosis
mint:mint:MINT-19747	0.010938	107	Diverticulosis
mint:mint:MINT-19826	0.010938	107	Diverticulosis
mint:mint:MINT-19871	0.010938	107	Diverticulosis
mint:mint:MINT-61836	0.010938	107	Diverticulosis
go:response_to_redox_state	0.011069	108	Diverticulosis
kegg:Pancreatic_secretion	0.011351	109	Diverticulosis
biogrid:biogrid:825627	0.012248	112	Diverticulosis
go:modulation_by_virus_of_host_morphology_or_physiology	0.031025	32	Diverticulosis
reactome:REACT_118713	0.031025	32	Diverticulosis
go:cellular_ketone_metabolic_process	0.034151	36	Diverticulosis
biogrid:biogrid:1047106	0.034778	6	Diverticulosis
biogrid:biogrid:618791	0.034778	6	Diverticulosis
biogrid:biogrid:688619	0.034778	6	Diverticulosis
mint:mint:MINT-8164383	0.034778	6	Diverticulosis
reactome:REACT_12627	0.036128	440	Diverticulosis
pfam:SCAN_domain	0.037147	69	Diverticulosis
reactome:REACT_71	0.03914	458	Diverticulosis
pfam:Protein_kinase_domain	0.04173	83	Diverticulosis
biogrid:biogrid:300829	0.041955	8	Diverticulosis
biogrid:biogrid:300831	0.041955	8	Diverticulosis
biogrid:biogrid:692361	0.041955	8	Diverticulosis
go:basic_amino_acid_transmembrane_transporter_activity	0.041955	8	Diverticulosis
go:basic_amino_acid_transport	0.041955	8	Diverticulosis
go:L-alpha-amino_acid_transmembrane_transport	0.041955	8	Diverticulosis
go:L-amino_acid_transport	0.041955	8	Diverticulosis
go:protein_complex_assembly	0.041955	8	Diverticulosis
go:regulation_of_arginine_metabolic_process	0.041955	8	Diverticulosis
go:cardiac_muscle_contraction	0.042233	194	Diverticulosis

go:ventricular_cardiac_ muscle_cell_action_potential	0.042233	194	Diverticulosis
go:ion_channel_binding	0.046266	185	Diverticulosis
go:oxidoreductase_activity__acting_on_ paired_donors__with_incorporation_or_reduction _of_molecular_oxygen__NAD(P)H_as_one_donor_ and_incorporation_of_one_atom_of_oxygen	0.004952	110	GERD
go:cholesterol_catabolic_process	0.005962	8	GERD
go:cellular_response_to_cholesterol	0.006451	7	GERD
go:cellular_response_to_glucose_stimulus	0.006451	7	GERD
go:cholesterol_7-alpha-monooxygenase_activity	0.006451	7	GERD
go:regulation_of_bile_acid_biosynthetic_process	0.006451	7	GERD
kegg:Primary_bile_acid_biosynthesis	0.006644	28	GERD
biogrid:biogrid:281849	0.009569	12	GERD
biogrid:biogrid:281850	0.009569	12	GERD
biogrid:biogrid:281851	0.009569	12	GERD
biogrid:biogrid:281852	0.009569	12	GERD
biogrid:biogrid:281853	0.009569	12	GERD
biogrid:biogrid:680220	0.009569	12	GERD
biogrid:biogrid:718762	0.009569	12	GERD
go:adenylate_cyclase-inhibiting_serotonin_ receptor_signaling_pathway	0.009569	12	GERD
go:behavioral_fear_response	0.009569	12	GERD
go:exploration_behavior	0.009569	12	GERD
go:regulation_of_dopamine_metabolic_process	0.009569	12	GERD
go:regulation_of_serotonin_secretion	0.009569	12	GERD
biogrid:biogrid:893312	0.012892	5	GERD
biogrid:biogrid:305777	0.014023	81	GERD
biogrid:biogrid:833264	0.014023	81	GERD
go:positive_regulation_of_vascular_endothelial _growth_factor_production	0.014741	17	GERD
biogrid:biogrid:1035644	0.0151	8	GERD
biogrid:biogrid:1052632	0.0151	8	GERD
biogrid:biogrid:1053640	0.0151	8	GERD
biogrid:biogrid:277855	0.0151	8	GERD
biogrid:biogrid:277856	0.0151	8	GERD
biogrid:biogrid:505169	0.0151	8	GERD
biogrid:biogrid:561201	0.0151	8	GERD
biogrid:biogrid:561202	0.0151	8	GERD
biogrid:biogrid:621623	0.0151	8	GERD
biogrid:biogrid:685231	0.0151	8	GERD
biogrid:biogrid:749216	0.0151	8	GERD
biogrid:biogrid:750154	0.0151	8	GERD
biogrid:biogrid:752692	0.0151	8	GERD
biogrid:biogrid:752945	0.0151	8	GERD
biogrid:biogrid:753673	0.0151	8	GERD
biogrid:biogrid:826871	0.0151	8	GERD

biogrid:biogrid:836990	0.0151	8	GERD
biogrid:biogrid:876160	0.0151	8	GERD
biogrid:biogrid:914967	0.0151	8	GERD
biogrid:biogrid:914968	0.0151	8	GERD
biogrid:biogrid:940036	0.0151	8	GERD
biogrid:biogrid:940514	0.0151	8	GERD
go:regulation_of_cellular_amino_acid_metabolic_process	0.0151	8	GERD
go:synaptic_transmission__cholinergic	0.0151	8	GERD
mint:mint:MINT-6616019	0.0151	8	GERD
mint:mint:MINT-6616047	0.0151	8	GERD
mint:mint:MINT-6616064	0.0151	8	GERD
pfam:Flavodoxin-like_fold	0.0151	8	GERD
reactome:REACT_13565	0.0151	8	GERD
reactome:REACT_19231	0.017784	47	GERD
go:nitric_oxide_biosynthetic_process	0.017824	21	GERD
biogrid:biogrid:245524	0.019995	9	GERD
biogrid:biogrid:593047	0.019995	9	GERD
biogrid:biogrid:593048	0.019995	9	GERD
biogrid:biogrid:838614	0.019995	9	GERD
biogrid:biogrid:892674	0.019995	9	GERD
biogrid:biogrid:893016	0.019995	9	GERD
biogrid:biogrid:893590	0.019995	9	GERD
biogrid:biogrid:893591	0.019995	9	GERD
biogrid:biogrid:893592	0.019995	9	GERD
biogrid:biogrid:893593	0.019995	9	GERD
biogrid:biogrid:893594	0.019995	9	GERD
biogrid:biogrid:894523	0.019995	9	GERD
biogrid:biogrid:894524	0.019995	9	GERD
biogrid:biogrid:894525	0.019995	9	GERD
biogrid:biogrid:914396	0.019995	9	GERD
biogrid:biogrid:833268	0.021359	106	GERD
biogrid:biogrid:879407	0.021359	106	GERD
go:negative_regulation_of_blood_coagulation	0.02635	30	GERD
go:very_long-chain_fatty_acid_metabolic_process	0.02635	30	GERD
go:vitamin_E_metabolic_process	0.02635	30	GERD
go:vitamin_K_biosynthetic_process	0.02635	30	GERD
biogrid:biogrid:252662	0.030932	33	GERD
go:biological_process	0.03159	68	GERD
go:alkane_1-monooxygenase_activity	0.037451	52	GERD
go:leukotriene-B4_20-monooxygenase_activity	0.04123	35	GERD
go:leukotriene_B4_catabolic_process	0.04123	35	GERD
go:long-chain_fatty_acid_metabolic_process	0.04123	35	GERD
go:pressure_natriuresis	0.04123	35	GERD
biogrid:biogrid:631794	0.042788	18	GERD

biogrid:biogrid:854524	0.042788	18	GERD
biogrid:biogrid:854913	0.042788	18	GERD
biogrid:biogrid:876663	0.042788	18	GERD
go:alpha-tocopherol_ omega-hydroxylase_activity	0.042788	18	GERD
go:arachidonic_acid_omega-hydroxylase_activity	0.042788	18	GERD
go:negative_regulation_of_ icosanoid_secretion	0.042788	18	GERD
go:tocotrienol_omega-hydroxylase_activity	0.042788	18	GERD
pfam:PAS_domain	0.044148	31	GERD
pfam:PAS_domain	0.044148	31	GERD
biogrid:biogrid:478465	0.044438	10	GERD
biogrid:biogrid:478466	0.044438	10	GERD
go:menaquinone_catabolic_process	0.045141	29	GERD
go:phylloquinone_catabolic_process	0.045141	29	GERD
go:vitamin_K_catabolic_process	0.045141	29	GERD
go:serotonin_metabolic_process	0.045328	14	GERD
biogrid:biogrid:320253	0.047635	34	GERD
biogrid:biogrid:320254	0.047635	34	GERD
biogrid:biogrid:831163	0.047635	34	GERD
biogrid:biogrid:838616	0.047635	34	GERD
biogrid:biogrid:893597	0.047635	34	GERD
biogrid:biogrid:914324	0.047635	34	GERD
biogrid:biogrid:914325	0.047635	34	GERD
biogrid:biogrid:914327	0.047635	34	GERD
go:testosterone_6-beta-hydroxylase_activity	0.047635	34	GERD
go:vitamin_D3_25-hydroxylase_activity	0.047635	34	GERD
kegg:Ubiquinone_and_other_ terpenoid-quinone_biosynthesis	0.048636	24	GERD
kegg:RNA_degradation	0.001493	14	Hypertension
biogrid:biogrid:1032065	0.001515	13	Hypertension
biogrid:biogrid:1049143	0.001515	13	Hypertension
biogrid:biogrid:424420	0.001515	13	Hypertension
biogrid:biogrid:590649	0.001515	13	Hypertension
biogrid:biogrid:621770	0.001515	13	Hypertension
biogrid:biogrid:823610	0.001515	13	Hypertension
biogrid:biogrid:823611	0.001515	13	Hypertension
biogrid:biogrid:823612	0.001515	13	Hypertension
biogrid:biogrid:823631	0.001515	13	Hypertension
biogrid:biogrid:823632	0.001515	13	Hypertension
biogrid:biogrid:823633	0.001515	13	Hypertension
biogrid:biogrid:834207	0.001515	13	Hypertension
biogrid:biogrid:905463	0.001515	13	Hypertension
biogrid:biogrid:905464	0.001515	13	Hypertension
biogrid:biogrid:905691	0.001515	13	Hypertension
biogrid:biogrid:905699	0.001515	13	Hypertension

biogrid:biogrid:905706	0.001515	13	Hypertension
biogrid:biogrid:941601	0.001515	13	Hypertension
biogrid:biogrid:941604	0.001515	13	Hypertension
biogrid:biogrid:941605	0.001515	13	Hypertension
biogrid:biogrid:949190	0.001515	13	Hypertension
biogrid:biogrid:949191	0.001515	13	Hypertension
biogrid:biogrid:949192	0.001515	13	Hypertension
go:cytoplasmic_mRNA_processing_body	0.001515	13	Hypertension
go:deadenylation-dependent_decapping_of_nuclear-transcribed_mRNA	0.001515	13	Hypertension
go:deadenylation-independent_decapping_of_nuclear-transcribed_mRNA	0.001515	13	Hypertension
go:enzyme_regulator_activity	0.001515	13	Hypertension
go:exonucleolytic_nuclear-transcribed_mRNA_catabolic_process_involved_in_deadenylation-dependent_decay	0.001515	13	Hypertension
go:mRNA_binding	0.001515	13	Hypertension
go:nuclear-transcribed_mRNA_catabolic_process_deadenylation-dependent_decay	0.001515	13	Hypertension
go:regulation_of_catalytic_activity	0.001515	13	Hypertension
go:RNA_7-methylguanosine_cap_binding	0.001515	13	Hypertension
mint:mint:MINT-61962	0.001515	13	Hypertension
mint:mint:MINT-8169356	0.001515	13	Hypertension
pfam:Dcp1-like_decapping_family	0.001515	13	Hypertension
reactome:REACT_20518	0.001515	13	Hypertension
reactome:REACT_20639	0.001515	13	Hypertension
biogrid:biogrid:1032054	0.003591	24	Hypertension
biogrid:biogrid:559871	0.003591	24	Hypertension
biogrid:biogrid:609388	0.003591	24	Hypertension
biogrid:biogrid:857472	0.003591	24	Hypertension
biogrid:biogrid:887062	0.003591	24	Hypertension
biogrid:biogrid:887063	0.003591	24	Hypertension
biogrid:biogrid:887064	0.003591	24	Hypertension
biogrid:biogrid:887065	0.003591	24	Hypertension
biogrid:biogrid:887066	0.003591	24	Hypertension
biogrid:biogrid:903799	0.003591	24	Hypertension
biogrid:biogrid:903801	0.003591	24	Hypertension
go:15-hydroxyprostaglandin_dehydrogenase_(NAD+)_activity	0.003591	24	Hypertension
go:platelet_dense_granule_membrane	0.003591	24	Hypertension
go:platelet_activation	0.006878	37	Hypertension
reactome:REACT_798	0.006878	37	Hypertension
go:blood_coagulation	0.009588	99	Hypertension
biogrid:biogrid:481827	0.010764	13	Hypertension
biogrid:biogrid:481828	0.010764	13	Hypertension
biogrid:biogrid:481831	0.010764	13	Hypertension
biogrid:biogrid:483771	0.010764	13	Hypertension

biogrid:biogrid:483772	0.010764	13	Hypertension
biogrid:biogrid:906563	0.012609	33	Hypertension
biogrid:biogrid:906721	0.012609	33	Hypertension
biogrid:biogrid:914827	0.012609	33	Hypertension
pfam:Protein_Family_FAM117	0.012609	33	Hypertension
go:platelet_degranulation	0.013652	36	Hypertension
reactome:REACT_1280	0.013652	36	Hypertension
reactome:REACT_318	0.013652	36	Hypertension
reactome:REACT_unknown_1765	0.013652	36	Hypertension
kegg:Rheumatoid_arthritis	0.013957	6	Hypertension
go:cellular_iron_ion_homeostasis	0.017339	41	Hypertension
biogrid:biogrid:561037	0.017431	5	Hypertension
biogrid:biogrid:673509	0.017431	5	Hypertension
biogrid:biogrid:720484	0.017431	5	Hypertension
biogrid:biogrid:737342	0.017431	5	Hypertension
biogrid:biogrid:749128	0.017431	5	Hypertension
biogrid:biogrid:809380	0.017431	5	Hypertension
biogrid:biogrid:934535	0.017431	5	Hypertension
biogrid:biogrid:934662	0.017431	5	Hypertension
biogrid:biogrid:934789	0.017431	5	Hypertension
biogrid:biogrid:950375	0.017431	5	Hypertension
go:cilium_assembly	0.017431	5	Hypertension
go:insulin_receptor_signaling_pathway	0.017431	5	Hypertension
go:IRE1-mediated_unfolded_protein_response	0.017431	5	Hypertension
go:phagocytic_vesicle_membrane	0.017431	5	Hypertension
go:transferrin_transport	0.017431	5	Hypertension
go:vacuolar_proton-transporting_V-type_ATPase_complex	0.017431	5	Hypertension
kegg:Collecting_duct_acid_secretion	0.017431	5	Hypertension
kegg:Synaptic_vesicle_cycle	0.017431	5	Hypertension
kegg:Vibrio_cholerae_infection	0.017431	5	Hypertension
mint:mint:MINT-2865933	0.017431	5	Hypertension
pfam:ATP_synthase_(C/AC39)_subunit	0.017431	5	Hypertension
reactome:REACT_1109	0.017431	5	Hypertension
reactome:REACT_18273	0.017431	5	Hypertension
reactome:REACT_18368	0.017431	5	Hypertension
reactome:REACT_25283	0.017431	5	Hypertension
reactome:REACT_498	0.017431	5	Hypertension
reactome:REACT_25060	0.018011	38	Hypertension
reactome:REACT_604	0.01841	54	Hypertension
pfam:short_chain_dehydrogenase	0.019619	24	Hypertension
go:endoplasmic_reticulum_unfolded_protein_response	0.021006	8	Hypertension
reactome:REACT_18356	0.021006	8	Hypertension
go:flavonoid_metabolic_process	0.021573	12	Hypertension
go:interaction_with_host	0.023009	6	Hypertension
go:phagosome_maturation	0.023009	6	Hypertension

kegg:Phagosome	0.023009	6	Hypertension
reactome:REACT_121237	0.023009	6	Hypertension
reactome:REACT_121256	0.023009	6	Hypertension
kegg:Aldosterone-regulated_sodium_reabsorption	0.024033	63	Hypertension
go:lysosomal_membrane	0.025308	13	Hypertension
biogrid:biogrid:29155	0.025812	19	Hypertension
biogrid:biogrid:846459	0.025812	19	Hypertension
biogrid:biogrid:870284	0.025812	19	Hypertension
biogrid:biogrid:870286	0.025812	19	Hypertension
go:G-protein_coupled_peptide_receptor_activity	0.025812	19	Hypertension
go:guanylate_cyclase_activity	0.025812	19	Hypertension
go:hormone_binding	0.025812	19	Hypertension
go:natriuretic_peptide_receptor_activity	0.025812	19	Hypertension
mint:mint:MINT-61913	0.025812	19	Hypertension
pfam:Adenylate_and_Guanylate_cyclase_catalytic_domain	0.025812	19	Hypertension
pfam:Receptor_family_ligand_binding_region	0.025812	19	Hypertension
kegg:Oxidative_phosphorylation	0.026979	8	Hypertension
netpath:IL6	0.02866	66	Hypertension
kegg:Tuberculosis	0.029646	58	Hypertension
reactome:REACT_355497	0.031731	10	Hypertension
biogrid:biogrid:623483	0.032982	5	Hypertension
biogrid:biogrid:746649	0.032982	5	Hypertension
biogrid:biogrid:747194	0.032982	5	Hypertension
biogrid:biogrid:747274	0.032982	5	Hypertension
biogrid:biogrid:747357	0.032982	5	Hypertension
biogrid:biogrid:748545	0.032982	5	Hypertension
biogrid:biogrid:748632	0.032982	5	Hypertension
biogrid:biogrid:748795	0.032982	5	Hypertension
biogrid:biogrid:748948	0.032982	5	Hypertension
biogrid:biogrid:749025	0.032982	5	Hypertension
biogrid:biogrid:749134	0.032982	5	Hypertension
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biogrid:biogrid:749334	0.032982	5	Hypertension
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biogrid:biogrid:749823	0.032982	5	Hypertension
biogrid:biogrid:749825	0.032982	5	Hypertension
biogrid:biogrid:749906	0.032982	5	Hypertension
biogrid:biogrid:750557	0.032982	5	Hypertension
biogrid:biogrid:750653	0.032982	5	Hypertension
biogrid:biogrid:750825	0.032982	5	Hypertension
biogrid:biogrid:751150	0.032982	5	Hypertension
biogrid:biogrid:751156	0.032982	5	Hypertension
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biogrid:biogrid:751235	0.032982	5	Hypertension
biogrid:biogrid:751252	0.032982	5	Hypertension
biogrid:biogrid:751253	0.032982	5	Hypertension
biogrid:biogrid:751341	0.032982	5	Hypertension
biogrid:biogrid:751433	0.032982	5	Hypertension
biogrid:biogrid:751985	0.032982	5	Hypertension
biogrid:biogrid:752019	0.032982	5	Hypertension
biogrid:biogrid:752151	0.032982	5	Hypertension
biogrid:biogrid:752158	0.032982	5	Hypertension
biogrid:biogrid:753111	0.032982	5	Hypertension
biogrid:biogrid:754428	0.032982	5	Hypertension
biogrid:biogrid:870285	0.036213	28	Hypertension
go:cGMP_biosynthetic_process	0.036213	28	Hypertension
go:negative_regulation_of_angiogenesis	0.036213	28	Hypertension
go:positive_regulation_of_renal _sodium_excretion	0.036213	28	Hypertension
go:positive_regulation_of_urine_volume	0.036213	28	Hypertension
go:receptor_guanylyl_cyclase_ signaling_pathway	0.036213	28	Hypertension
go:regulation_of_vascular_permeability	0.036213	28	Hypertension
go:oxidoreductase_activity__acting_on _paired_donors__with_incorporation_ or_reduction_of_molecular_oxygen__ NAD(P)H_as_one_donor__and_ incorporation_ of_one_atom_of_oxygen	0.038554	109	Hypertension
go:negative_regulation_of_cell_growth	0.040279	46	Hypertension
biogrid:biogrid:1066834	0.043188	71	Hypertension
biogrid:biogrid:1066845	0.043188	71	Hypertension
biogrid:biogrid:1066925	0.043188	71	Hypertension
biogrid:biogrid:559900	0.043188	71	Hypertension
biogrid:biogrid:601377	0.043188	71	Hypertension
biogrid:biogrid:607870	0.043188	71	Hypertension
biogrid:biogrid:643883	0.043188	71	Hypertension
biogrid:biogrid:733895	0.043188	71	Hypertension
biogrid:biogrid:831166	0.043188	71	Hypertension
biogrid:biogrid:831168	0.043188	71	Hypertension
biogrid:biogrid:831170	0.043188	71	Hypertension
biogrid:biogrid:894043	0.043188	71	Hypertension
go:cellular_organofluorine_ metabolic_process	0.043188	71	Hypertension
go:NADPH-hemoprotein_ reductase_activity	0.043188	71	Hypertension
go:positive_regulation_of_ monooxygenase_activity	0.043188	71	Hypertension
mint:mint:MINT-51099	0.043188	71	Hypertension
mint:mint:MINT-63487	0.043188	71	Hypertension

mint:mint:MINT-8267830	0.043188	71	Hypertension
pfam:FAD_binding_domain	0.043188	71	Hypertension
pfam:Flavodoxin	0.043188	71	Hypertension
pfam:Oxidoreductase_NAD-binding_domain	0.043188	71	Hypertension
biogrid:biogrid:906563	0.007463	31	Hypothyroidism
biogrid:biogrid:906721	0.007463	31	Hypothyroidism
biogrid:biogrid:914827	0.007463	31	Hypothyroidism
pfam:Protein_Family_FAM117	0.007463	31	Hypothyroidism
biogrid:biogrid:625721	0.00968	7	Hypothyroidism
go:polysaccharide_metabolic_process	0.00968	7	Hypothyroidism
go:vitamin_K_metabolic_process	0.010101	25	Hypothyroidism
biogrid:biogrid:817635	0.011745	29	Hypothyroidism
reactome:REACT_268491	0.013796	21	Hypothyroidism
go:response_to_ethanol	0.015122	7	Hypothyroidism
biogrid:biogrid:809629	0.017185	13	Hypothyroidism
biogrid:biogrid:824781	0.017185	13	Hypothyroidism
mint:mint:MINT-64803	0.017185	13	Hypothyroidism
pfam:TMPIT-like_protein	0.017185	13	Hypothyroidism
pfam:gag-polyprotein_putative_aspartyl_protease	0.021038	5	Hypothyroidism
pfam:Retrotransposon_gag_protein	0.021038	5	Hypothyroidism
biogrid:biogrid:1037996	0.023394	16	Hypothyroidism
biogrid:biogrid:609620	0.023394	16	Hypothyroidism
biogrid:biogrid:750253	0.023394	16	Hypothyroidism
biogrid:biogrid:951317	0.023394	16	Hypothyroidism
go:dihydropyrimidine_dehydrogenase_(NADP+)_activity	0.023394	16	Hypothyroidism
go:purine_nucleobase_catabolic_process	0.023394	16	Hypothyroidism
go:pyrimidine_nucleobase_catabolic_process	0.023394	16	Hypothyroidism
go:pyrimidine_nucleoside_catabolic_process	0.023394	16	Hypothyroidism
go:thymidine_catabolic_process	0.023394	16	Hypothyroidism
go:thymine_catabolic_process	0.023394	16	Hypothyroidism
go:uracil_catabolic_process	0.023394	16	Hypothyroidism
kegg:Pantothenate_and_CoA_biosynthesis	0.023394	16	Hypothyroidism
pfam:4Fe-4S_dicluster_domain	0.023394	16	Hypothyroidism
pfam:Dihydroorotate_dehydrogenase	0.023394	16	Hypothyroidism
pfam:Dihydroprymidine_dehydrogenase_domain_II__4Fe-4S_cluster	0.023394	16	Hypothyroidism
pfam:NAD(P)-binding_Rossmann-like_domain	0.023394	16	Hypothyroidism
reactome:REACT_1023	0.023394	16	Hypothyroidism
reactome:REACT_13523	0.023632	43	Hypothyroidism
biogrid:biogrid:1031712	0.024386	8	Hypothyroidism
biogrid:biogrid:1038889	0.024386	8	Hypothyroidism
biogrid:biogrid:1038890	0.024386	8	Hypothyroidism

biogrid:biogrid:1038891	0.024386	8	Hypothyroidism
biogrid:biogrid:1038892	0.024386	8	Hypothyroidism
biogrid:biogrid:1038893	0.024386	8	Hypothyroidism
biogrid:biogrid:1038894	0.024386	8	Hypothyroidism
biogrid:biogrid:1057721	0.024386	8	Hypothyroidism
biogrid:biogrid:244393	0.024386	8	Hypothyroidism
biogrid:biogrid:261584	0.024386	8	Hypothyroidism
biogrid:biogrid:270387	0.024386	8	Hypothyroidism
biogrid:biogrid:271126	0.024386	8	Hypothyroidism
biogrid:biogrid:314883	0.024386	8	Hypothyroidism
biogrid:biogrid:558455	0.024386	8	Hypothyroidism
biogrid:biogrid:618504	0.024386	8	Hypothyroidism
biogrid:biogrid:632150	0.024386	8	Hypothyroidism
biogrid:biogrid:667734	0.024386	8	Hypothyroidism
biogrid:biogrid:678173	0.024386	8	Hypothyroidism
biogrid:biogrid:687098	0.024386	8	Hypothyroidism
biogrid:biogrid:688093	0.024386	8	Hypothyroidism
biogrid:biogrid:688507	0.024386	8	Hypothyroidism
biogrid:biogrid:689514	0.024386	8	Hypothyroidism
biogrid:biogrid:719822	0.024386	8	Hypothyroidism
biogrid:biogrid:719823	0.024386	8	Hypothyroidism
biogrid:biogrid:719824	0.024386	8	Hypothyroidism
biogrid:biogrid:719826	0.024386	8	Hypothyroidism
biogrid:biogrid:733711	0.024386	8	Hypothyroidism
biogrid:biogrid:753085	0.024386	8	Hypothyroidism
biogrid:biogrid:809430	0.024386	8	Hypothyroidism
biogrid:biogrid:826510	0.024386	8	Hypothyroidism
biogrid:biogrid:826666	0.024386	8	Hypothyroidism
biogrid:biogrid:831216	0.024386	8	Hypothyroidism
biogrid:biogrid:835515	0.024386	8	Hypothyroidism
biogrid:biogrid:837191	0.024386	8	Hypothyroidism
biogrid:biogrid:894703	0.024386	8	Hypothyroidism
biogrid:biogrid:940200	0.024386	8	Hypothyroidism
go:cellular_response_to_lipopolysaccharide	0.024386	8	Hypothyroidism
go:common_myeloid_progenitor_cell_proliferation	0.024386	8	Hypothyroidism
go:dinitrosyl-iron_complex_binding	0.024386	8	Hypothyroidism
go:JUN_kinase_binding	0.024386	8	Hypothyroidism
go:kinase_regulator_activity	0.024386	8	Hypothyroidism
go:negative_regulation_of_acute_inflammatory_response	0.024386	8	Hypothyroidism
go:negative_regulation_of_biosynthetic_process	0.024386	8	Hypothyroidism
go:negative_regulation_of_ERK1_and_ERK2_cascade	0.024386	8	Hypothyroidism

go:negative_regulation_of_ extrinsic_apoptotic_signaling_pathway	0.024386	8	Hypothyroidism
go:negative_regulation_of_ fibroblast_proliferation	0.024386	8	Hypothyroidism
go:negative_regulation_of_ interleukin-1_beta_production	0.024386	8	Hypothyroidism
go:negative_regulation_of_JUN_kinase_activity	0.024386	8	Hypothyroidism
go:negative_regulation_of_leukocyte_ proliferation	0.024386	8	Hypothyroidism
go:negative_regulation_of_ MAPK_cascade	0.024386	8	Hypothyroidism
go:negative_regulation_of_ MAP_kinase_activity	0.024386	8	Hypothyroidism
go:negative_regulation_of_monocyte _chemotactic_protein-1_production	0.024386	8	Hypothyroidism
go:negative_regulation_of_ nitric-oxide_synthase_biosynthetic_process	0.024386	8	Hypothyroidism
go:negative_regulation_of_ protein_kinase_activity	0.024386	8	Hypothyroidism
go:negative_regulation_of _stress-activated_MAPK_cascade	0.024386	8	Hypothyroidism
go:nitric_oxide_binding	0.024386	8	Hypothyroidism
go:nitric_oxide_storage	0.024386	8	Hypothyroidism
go:positive_regulation_of_superoxide_ anion_generation	0.024386	8	Hypothyroidism
go:regulation_of_ERK1_and_ERK2_cascade	0.024386	8	Hypothyroidism
go:regulation_of_stress-activated_ MAPK_cascade	0.024386	8	Hypothyroidism
go:S-nitrosoglutathione_binding	0.024386	8	Hypothyroidism
go:TRAF2-GSTP1_complex	0.024386	8	Hypothyroidism
mint:mint:MINT-63445	0.024386	8	Hypothyroidism
mint:mint:MINT-63446	0.024386	8	Hypothyroidism
go:vesicle	0.024771	24	Hypothyroidism
reactome:REACT_13450	0.024854	45	Hypothyroidism
biogrid:biogrid:809411	0.027052	16	Hypothyroidism
biogrid:biogrid:817562	0.027052	16	Hypothyroidism
biogrid:biogrid:817563	0.027052	16	Hypothyroidism
biogrid:biogrid:817564	0.027052	16	Hypothyroidism
biogrid:biogrid:817566	0.027052	16	Hypothyroidism
biogrid:biogrid:817567	0.027052	16	Hypothyroidism
biogrid:biogrid:817568	0.027052	16	Hypothyroidism
biogrid:biogrid:817569	0.027052	16	Hypothyroidism
biogrid:biogrid:817570	0.027052	16	Hypothyroidism
biogrid:biogrid:817571	0.027052	16	Hypothyroidism
biogrid:biogrid:817572	0.027052	16	Hypothyroidism
biogrid:biogrid:817573	0.027052	16	Hypothyroidism

biogrid:biogrid:817574	0.027052	16	Hypothyroidism
biogrid:biogrid:817575	0.027052	16	Hypothyroidism
biogrid:biogrid:817576	0.027052	16	Hypothyroidism
biogrid:biogrid:817577	0.027052	16	Hypothyroidism
biogrid:biogrid:817578	0.027052	16	Hypothyroidism
biogrid:biogrid:817579	0.027052	16	Hypothyroidism
biogrid:biogrid:817580	0.027052	16	Hypothyroidism
biogrid:biogrid:817581	0.027052	16	Hypothyroidism
biogrid:biogrid:817582	0.027052	16	Hypothyroidism
biogrid:biogrid:817583	0.027052	16	Hypothyroidism
biogrid:biogrid:817584	0.027052	16	Hypothyroidism
biogrid:biogrid:817585	0.027052	16	Hypothyroidism
biogrid:biogrid:817586	0.027052	16	Hypothyroidism
biogrid:biogrid:817587	0.027052	16	Hypothyroidism
biogrid:biogrid:817588	0.027052	16	Hypothyroidism
biogrid:biogrid:817589	0.027052	16	Hypothyroidism
biogrid:biogrid:817590	0.027052	16	Hypothyroidism
biogrid:biogrid:817591	0.027052	16	Hypothyroidism
biogrid:biogrid:817592	0.027052	16	Hypothyroidism
biogrid:biogrid:817593	0.027052	16	Hypothyroidism
biogrid:biogrid:817594	0.027052	16	Hypothyroidism
biogrid:biogrid:817595	0.027052	16	Hypothyroidism
biogrid:biogrid:817596	0.027052	16	Hypothyroidism
biogrid:biogrid:817597	0.027052	16	Hypothyroidism
biogrid:biogrid:817598	0.027052	16	Hypothyroidism
biogrid:biogrid:817599	0.027052	16	Hypothyroidism
biogrid:biogrid:817600	0.027052	16	Hypothyroidism
biogrid:biogrid:817602	0.027052	16	Hypothyroidism
biogrid:biogrid:817603	0.027052	16	Hypothyroidism
biogrid:biogrid:817605	0.027052	16	Hypothyroidism
biogrid:biogrid:817606	0.027052	16	Hypothyroidism
biogrid:biogrid:817607	0.027052	16	Hypothyroidism
biogrid:biogrid:817608	0.027052	16	Hypothyroidism
biogrid:biogrid:817609	0.027052	16	Hypothyroidism
biogrid:biogrid:817610	0.027052	16	Hypothyroidism
biogrid:biogrid:817611	0.027052	16	Hypothyroidism
biogrid:biogrid:817612	0.027052	16	Hypothyroidism
biogrid:biogrid:817613	0.027052	16	Hypothyroidism
biogrid:biogrid:817614	0.027052	16	Hypothyroidism
biogrid:biogrid:817615	0.027052	16	Hypothyroidism
biogrid:biogrid:817616	0.027052	16	Hypothyroidism
biogrid:biogrid:817617	0.027052	16	Hypothyroidism
biogrid:biogrid:817618	0.027052	16	Hypothyroidism
biogrid:biogrid:817619	0.027052	16	Hypothyroidism
biogrid:biogrid:817620	0.027052	16	Hypothyroidism
biogrid:biogrid:817621	0.027052	16	Hypothyroidism
biogrid:biogrid:817622	0.027052	16	Hypothyroidism

biogrid:biogrid:817623	0.027052	16	Hypothyroidism
biogrid:biogrid:817624	0.027052	16	Hypothyroidism
biogrid:biogrid:817625	0.027052	16	Hypothyroidism
biogrid:biogrid:817626	0.027052	16	Hypothyroidism
biogrid:biogrid:817627	0.027052	16	Hypothyroidism
biogrid:biogrid:817628	0.027052	16	Hypothyroidism
biogrid:biogrid:817629	0.027052	16	Hypothyroidism
biogrid:biogrid:817630	0.027052	16	Hypothyroidism
biogrid:biogrid:817631	0.027052	16	Hypothyroidism
biogrid:biogrid:817632	0.027052	16	Hypothyroidism
biogrid:biogrid:817633	0.027052	16	Hypothyroidism
biogrid:biogrid:817634	0.027052	16	Hypothyroidism
biogrid:biogrid:817636	0.027052	16	Hypothyroidism
biogrid:biogrid:817637	0.027052	16	Hypothyroidism
biogrid:biogrid:817638	0.027052	16	Hypothyroidism
biogrid:biogrid:817639	0.027052	16	Hypothyroidism
biogrid:biogrid:817640	0.027052	16	Hypothyroidism
biogrid:biogrid:817641	0.027052	16	Hypothyroidism
biogrid:biogrid:817643	0.027052	16	Hypothyroidism
biogrid:biogrid:817645	0.027052	16	Hypothyroidism
biogrid:biogrid:941402	0.027052	16	Hypothyroidism
biogrid:biogrid:943918	0.027052	16	Hypothyroidism
go:bone_development	0.027052	16	Hypothyroidism
go:peptidyl-glutamic_acid_carboxylation	0.027052	16	Hypothyroidism
mint:mint:MINT-8171260	0.027052	16	Hypothyroidism
pfam:Vitamin_K_epoxide_reductase_family	0.027052	16	Hypothyroidism
reactome:REACT_1132	0.027052	16	Hypothyroidism
biogrid:biogrid:2006	0.030524	11	Hypothyroidism
biogrid:biogrid:282802	0.030524	11	Hypothyroidism
biogrid:biogrid:282807	0.030524	11	Hypothyroidism
biogrid:biogrid:715396	0.030524	11	Hypothyroidism
biogrid:biogrid:715399	0.030524	11	Hypothyroidism
biogrid:biogrid:835955	0.030524	11	Hypothyroidism
biogrid:biogrid:857490	0.030524	11	Hypothyroidism
biogrid:biogrid:905131	0.030524	11	Hypothyroidism
biogrid:biogrid:905136	0.030524	11	Hypothyroidism
go:adenylate_cyclase-activating_adrenergic_receptor_signaling_pathway	0.030524	11	Hypothyroidism
go:alpha-2A_adrenergic_receptor_binding	0.030524	11	Hypothyroidism
go:beta-adrenergic_receptor_activity	0.030524	11	Hypothyroidism
go:positive_regulation_of_cAMP-mediated_signaling	0.030524	11	Hypothyroidism
go:Ras_guanyl-nucleotide_exchange_factor_activity	0.030524	11	Hypothyroidism
go:receptor_signaling_protein_activity	0.030524	11	Hypothyroidism
mint:mint:MINT-58357	0.030524	11	Hypothyroidism
mint:mint:MINT-58358	0.030524	11	Hypothyroidism

mint:mint:MINT-58359	0.030524	11	Hypothyroidism
mint:mint:MINT-58360	0.030524	11	Hypothyroidism
mint:mint:MINT-58361	0.030524	11	Hypothyroidism
go:negative_regulation_of_tumor_necrosis_factor_production	0.031017	11	Hypothyroidism
biogrid:biogrid:1037442	0.032255	8	Hypothyroidism
biogrid:biogrid:1037443	0.032255	8	Hypothyroidism
biogrid:biogrid:1037444	0.032255	8	Hypothyroidism
biogrid:biogrid:1037445	0.032255	8	Hypothyroidism
biogrid:biogrid:1037446	0.032255	8	Hypothyroidism
biogrid:biogrid:1037447	0.032255	8	Hypothyroidism
biogrid:biogrid:1037448	0.032255	8	Hypothyroidism
biogrid:biogrid:1037449	0.032255	8	Hypothyroidism
biogrid:biogrid:609562	0.032255	8	Hypothyroidism
biogrid:biogrid:749396	0.032255	8	Hypothyroidism
go:cytidine_deaminase_activity	0.032255	8	Hypothyroidism
go:cytidine_deamination	0.032255	8	Hypothyroidism
go:cytosine_metabolic_process	0.032255	8	Hypothyroidism
go:negative_regulation_of_nucleotide_metabolic_process	0.032255	8	Hypothyroidism
go:nucleoside_binding	0.032255	8	Hypothyroidism
go:pyrimidine-containing_compound_salvage	0.032255	8	Hypothyroidism
pfam:Cytidine_and_deoxycytidylate_deaminase_zinc-binding_region	0.032255	8	Hypothyroidism
go:neurotransmitter_secretion	0.035038	56	Hypothyroidism
biogrid:biogrid:817604	0.035565	18	Hypothyroidism
go:neuron_projection	0.037679	7	Hypothyroidism
biogrid:biogrid:442570	0.038862	19	Hypothyroidism
biogrid:biogrid:626632	0.038862	19	Hypothyroidism
biogrid:biogrid:632516	0.038862	19	Hypothyroidism
reactome:REACT_267863	0.038862	19	Hypothyroidism
biogrid:biogrid:1053841	0.039705	9	Hypothyroidism
biogrid:biogrid:1057600	0.039705	9	Hypothyroidism
biogrid:biogrid:242742	0.039705	9	Hypothyroidism
biogrid:biogrid:446010	0.039705	9	Hypothyroidism
biogrid:biogrid:446104	0.039705	9	Hypothyroidism
biogrid:biogrid:446439	0.039705	9	Hypothyroidism
biogrid:biogrid:446595	0.039705	9	Hypothyroidism
biogrid:biogrid:604735	0.039705	9	Hypothyroidism
biogrid:biogrid:632272	0.039705	9	Hypothyroidism
biogrid:biogrid:689055	0.039705	9	Hypothyroidism
biogrid:biogrid:689362	0.039705	9	Hypothyroidism
biogrid:biogrid:904077	0.039705	9	Hypothyroidism
biogrid:biogrid:906253	0.039705	9	Hypothyroidism
biogrid:biogrid:937629	0.039705	9	Hypothyroidism
go:oxidoreductase_activity__acting_on_NAD(P)H__quinone_or_similar_compound_as_acceptor	0.039705	9	Hypothyroidism

mint:mint:MINT-63481	0.039705	9	Hypothyroidism
go:extracellular_matrix_organization	0.040285	7	Hypothyroidism
reactome:REACT_1069	0.041053	24	Hypothyroidism
go:response_to_reactive_oxygen_species	0.041978	31	Hypothyroidism
reactome:REACT_264249	0.041978	31	Hypothyroidism
go:aldehyde_oxidase_activity	0.042216	7	Hypothyroidism
go:post-translational_protein_modification	0.042883	25	Hypothyroidism
reactome:REACT_22161	0.042883	25	Hypothyroidism
biogrid:biogrid:817601	0.043563	23	Hypothyroidism
reactome:REACT_15391	0.043684	21	Hypothyroidism
reactome:REACT_15532	0.043684	21	Hypothyroidism
kegg:Steroid_biosynthesis	0.043967	50	Hypothyroidism
kegg:Primary_bile_acid_biosynthesis	0.044718	28	Hypothyroidism
biogrid:biogrid:478465	0.047196	10	Hypothyroidism
biogrid:biogrid:478466	0.047196	10	Hypothyroidism
pfam:SEA_domain	0.047891	6	Hypothyroidism
pfam:Sodium_Bile_acid_symporter_family	0.049606	17	Hypothyroidism
biogrid:biogrid:664197	0.007722	52	Type II Diabetes
biogrid:biogrid:1030343	0.007722	52	Type II Diabetes
biogrid:biogrid:892786	0.007722	52	Type II Diabetes
mint:mint:MINT-24751	0.007722	52	Type II Diabetes
go:neurotrophin_TRKB_receptor_binding	0.007722	52	Type II Diabetes
biogrid:biogrid:892868	0.007722	52	Type II Diabetes
biogrid:biogrid:894020	0.007722	52	Type II Diabetes
biogrid:biogrid:893410	0.007722	52	Type II Diabetes
biogrid:biogrid:739742	0.007722	52	Type II Diabetes
pfam:Nerve_growth_factor_family	0.007722	52	Type II Diabetes
go:regulation_of_neuron_differentiation	0.007722	52	Type II Diabetes
go:positive_regulation_of_synapse_assembly	0.007722	52	Type II Diabetes
reactome:REACT_150420	0.010564	126	Type II Diabetes
go:nervous_system_development	0.011894	62	Type II Diabetes
pfam:Organic_Anion_Transporter_ Polypeptide_(OATP)_family	0.014508	241	Type II Diabetes
biogrid:biogrid:833263	0.014767	97	Type II Diabetes
biogrid:biogrid:305778	0.014767	97	Type II Diabetes
go:leukotriene_metabolic_process	0.017357	91	Type II Diabetes
netpath:IL5	0.018362	58	Type II Diabetes
go:oxidative_deethylation	0.018451	26	Type II Diabetes
go:demethylase_activity	0.018451	26	Type II Diabetes
biogrid:biogrid:838618	0.018451	26	Type II Diabetes
reactome:REACT_13721	0.018451	26	Type II Diabetes
go:toxin_biosynthetic_process	0.018451	26	Type II Diabetes
go:steroid_catabolic_process	0.019027	60	Type II Diabetes
reactome:REACT_23988	0.019144	231	Type II Diabetes
go:neuron_projection_morphogenesis	0.019579	54	Type II Diabetes
go:organic_anion_transmembrane_ transporter_activity	0.020338	221	Type II Diabetes

go:cytoplasmic_membrane-bounded_vesicle	0.020674	74	Type II Diabetes
go:sodium-independent_organic_anion_transport	0.021034	246	Type II Diabetes
go:electron_carrier_activity	0.024277	38	Type II Diabetes
pfam:SEA_domain	0.024391	6	Type II Diabetes
reactome:REACT_19118	0.02451	655	Type II Diabetes
go:monocarboxylic_acid_metabolic_process	0.026173	45	Type II Diabetes
reactome:REACT_18334	0.028319	229	Type II Diabetes
biogrid:biogrid:824781	0.028565	13	Type II Diabetes
pfam:TMPIT-like_protein	0.028565	13	Type II Diabetes
mint:mint:MINT-64803	0.028565	13	Type II Diabetes
biogrid:biogrid:809629	0.028565	13	Type II Diabetes
go:voltage-gated_calcium_channel_complex	0.028728	228	Type II Diabetes
reactome:REACT_18312	0.028728	228	Type II Diabetes
go:calcium_ion_import	0.028728	228	Type II Diabetes
go:high_voltage-gated_calcium_channel_activity	0.028728	228	Type II Diabetes
kegg:Huntington's_disease	0.028738	63	Type II Diabetes
pfam:SAM_domain_(Sterile_alpha_motif)	0.029203	7	Type II Diabetes
reactome:REACT_22285	0.03049	305	Type II Diabetes
biogrid:biogrid:738466	0.031799	93	Type II Diabetes
go:estrogen_catabolic_process	0.032254	5	Type II Diabetes
biogrid:biogrid:894166	0.032254	5	Type II Diabetes
kegg:Vascular_smooth_muscle_contraction	0.032861	203	Type II Diabetes
netpath:FSH	0.033506	223	Type II Diabetes
go:proton_transport	0.035114	72	Type II Diabetes
go:iron_ion_binding	0.035168	62	Type II Diabetes
go:protein_sulfation	0.037174	11	Type II Diabetes
reactome:REACT_18339	0.038845	177	Type II Diabetes
go:caffeine_oxidase_activity	0.039335	85	Type II Diabetes
reactome:REACT_268561	0.03997	28	Type II Diabetes
biogrid:biogrid:317012	0.040343	28	Type II Diabetes
go:nuclear_matrix	0.040343	28	Type II Diabetes
reactome:REACT_150209	0.040343	28	Type II Diabetes
biogrid:biogrid:1036829	0.040343	28	Type II Diabetes
biogrid:biogrid:283096	0.040343	28	Type II Diabetes
biogrid:biogrid:304063	0.040343	28	Type II Diabetes
biogrid:biogrid:818890	0.040343	28	Type II Diabetes
biogrid:biogrid:903970	0.040343	28	Type II Diabetes
biogrid:biogrid:1036830	0.040343	28	Type II Diabetes
biogrid:biogrid:914388	0.040343	28	Type II Diabetes
biogrid:biogrid:739796	0.040343	28	Type II Diabetes
go:arachidonate_5-lipoxygenase_activity	0.040343	28	Type II Diabetes
biogrid:biogrid:1036833	0.040343	28	Type II Diabetes
biogrid:biogrid:1036831	0.040343	28	Type II Diabetes
biogrid:biogrid:1036835	0.040343	28	Type II Diabetes
biogrid:biogrid:1036834	0.040343	28	Type II Diabetes
biogrid:biogrid:818887	0.040343	28	Type II Diabetes

go:nuclear_envelope_lumen	0.040343	28	Type II Diabetes
biogrid:biogrid:854149	0.040343	28	Type II Diabetes
biogrid:biogrid:914389	0.040343	28	Type II Diabetes
biogrid:biogrid:818889	0.040343	28	Type II Diabetes
biogrid:biogrid:1036832	0.040343	28	Type II Diabetes
biogrid:biogrid:9397	0.040343	28	Type II Diabetes
biogrid:biogrid:1036836	0.040343	28	Type II Diabetes
go:leukotriene_biosynthetic_process	0.040343	28	Type II Diabetes
biogrid:biogrid:904084	0.040343	28	Type II Diabetes
go:sodium-independent_organic_ anion_transmembrane_transporter_activity	0.040864	131	Type II Diabetes
kegg:cGMP-PKG_signaling_pathway	0.041183	226	Type II Diabetes
go:lipoxygenase_pathway	0.041756	29	Type II Diabetes
pfam:PLAT/LH2_domain	0.041756	29	Type II Diabetes
reactome:REACT_150320	0.041756	29	Type II Diabetes
go:lipoxin_metabolic_process	0.041756	29	Type II Diabetes
pfam:Lipoxygenase	0.041756	29	Type II Diabetes
go:extracellular_region	0.041968	211	Type II Diabetes
reactome:REACT_18325	0.043076	189	Type II Diabetes
reactome:REACT_1505	0.043076	189	Type II Diabetes
go:brush_border_membrane	0.04377	19	Type II Diabetes
kegg:cAMP_signaling_pathway	0.043788	477	Type II Diabetes
kegg:Alzheimer's_disease	0.04532	176	Type II Diabetes
kegg:Cholinergic_synapse	0.04532	176	Type II Diabetes
pfam:Voltage_gated_ calcium_channel_IQ_domain	0.04532	176	Type II Diabetes
kegg:GABAergic_synapse	0.045697	177	Type II Diabetes
kegg:Retrograde_endocannabinoid_signaling	0.046574	178	Type II Diabetes
biogrid:biogrid:121107	0.049204	21	Type II Diabetes
mint:mint:MINT-67530	0.049204	21	Type II Diabetes
reactome:REACT_6258	0.049739	11	Type II Diabetes
go:respiratory_electron_transport_chain	0.049739	11	Type II Diabetes
reactome:REACT_6341	0.049739	11	Type II Diabetes
reactome:REACT_6305	0.049739	11	Type II Diabetes
reactome:REACT_6196	0.049739	11	Type II Diabetes
pfam:Mitochondrial_carrier_protein	0.049739	11	Type II Diabetes
biogrid:biogrid:1031876	4.38E-05	6	Uterine Fibroids
biogrid:biogrid:336699	4.38E-05	6	Uterine Fibroids
reactome:REACT_150417	0.000394	130	Uterine Fibroids
kegg:Linoleic_acid_metabolism	0.000477	140	Uterine Fibroids
go:omega-hydroxylase_P450_pathway	0.000529	136	Uterine Fibroids
reactome:REACT_150134	0.000529	136	Uterine Fibroids
reactome:REACT_20506	0.00161	118	Uterine Fibroids
reactome:REACT_unknown_1749	0.00161	118	Uterine Fibroids
reactome:REACT_19305	0.001876	275	Uterine Fibroids
reactome:REACT_22345	0.002539	137	Uterine Fibroids
biogrid:biogrid:740138	0.003746	22	Uterine Fibroids

biogrid:biogrid:740214	0.003746	22	Uterine Fibroids
biogrid:biogrid:740238	0.003746	22	Uterine Fibroids
biogrid:biogrid:740258	0.003746	22	Uterine Fibroids
biogrid:biogrid:740295	0.003746	22	Uterine Fibroids
biogrid:biogrid:892323	0.003746	22	Uterine Fibroids
biogrid:biogrid:892324	0.003746	22	Uterine Fibroids
go:cellular_amide_metabolic_process	0.003746	22	Uterine Fibroids
go:urea_metabolic_process	0.003746	22	Uterine Fibroids
pfam:Sugar_(and_other)_transporter	0.005111	130	Uterine Fibroids
biogrid:biogrid:259490	0.006744	48	Uterine Fibroids
biogrid:biogrid:259491	0.006744	48	Uterine Fibroids
biogrid:biogrid:302311	0.006744	48	Uterine Fibroids
biogrid:biogrid:306198	0.006744	48	Uterine Fibroids
biogrid:biogrid:435981	0.006744	48	Uterine Fibroids
biogrid:biogrid:435982	0.006744	48	Uterine Fibroids
biogrid:biogrid:435983	0.006744	48	Uterine Fibroids
biogrid:biogrid:435984	0.006744	48	Uterine Fibroids
biogrid:biogrid:471747	0.006744	48	Uterine Fibroids
biogrid:biogrid:556550	0.006744	48	Uterine Fibroids
biogrid:biogrid:716196	0.006744	48	Uterine Fibroids
biogrid:biogrid:716197	0.006744	48	Uterine Fibroids
biogrid:biogrid:726891	0.006744	48	Uterine Fibroids
biogrid:biogrid:736918	0.006744	48	Uterine Fibroids
biogrid:biogrid:736919	0.006744	48	Uterine Fibroids
biogrid:biogrid:736921	0.006744	48	Uterine Fibroids
biogrid:biogrid:736924	0.006744	48	Uterine Fibroids
biogrid:biogrid:857524	0.006744	48	Uterine Fibroids
go:ammonium_transmembrane_transport	0.006744	48	Uterine Fibroids
go:cation_transmembrane_transport	0.006744	48	Uterine Fibroids
go:dopamine_transmembrane_transporter_activity	0.006744	48	Uterine Fibroids
go:dopamine_transport	0.006744	48	Uterine Fibroids
mint:mint:MINT-73279	0.006744	48	Uterine Fibroids
mint:mint:MINT-73280	0.006744	48	Uterine Fibroids
mint:mint:MINT-73281	0.006744	48	Uterine Fibroids
mint:mint:MINT-73284	0.006744	48	Uterine Fibroids
mint:mint:MINT-73294	0.006744	48	Uterine Fibroids
mint:mint:MINT-8055798	0.006744	48	Uterine Fibroids
go:monoterpenoid_metabolic_process	0.006797	192	Uterine Fibroids
reactome:REACT_13723	0.007437	84	Uterine Fibroids
go:neuronal_cell_body	0.01007	51	Uterine Fibroids
go:epoxygenase_P450_pathway	0.011262	275	Uterine Fibroids
reactome:REACT_15418	0.01173	81	Uterine Fibroids
biogrid:biogrid:305775	0.012949	104	Uterine Fibroids
reactome:REACT_147851	0.014643	396	Uterine Fibroids
biogrid:biogrid:894519	0.014799	58	Uterine Fibroids

go:heme_catabolic_process	0.014799	58	Uterine Fibroids
reactome:REACT_22297	0.014799	58	Uterine Fibroids
reactome:REACT_268618	0.014799	58	Uterine Fibroids
kegg:Arachidonic_acid_metabolism	0.015632	342	Uterine Fibroids
biogrid:biogrid:1033905	0.01565	44	Uterine Fibroids
biogrid:biogrid:1036332	0.01565	44	Uterine Fibroids
biogrid:biogrid:1036333	0.01565	44	Uterine Fibroids
biogrid:biogrid:1054450	0.01565	44	Uterine Fibroids
biogrid:biogrid:1100959	0.01565	44	Uterine Fibroids
biogrid:biogrid:243739	0.01565	44	Uterine Fibroids
biogrid:biogrid:243785	0.01565	44	Uterine Fibroids
biogrid:biogrid:245750	0.01565	44	Uterine Fibroids
biogrid:biogrid:253707	0.01565	44	Uterine Fibroids
biogrid:biogrid:253708	0.01565	44	Uterine Fibroids
biogrid:biogrid:253733	0.01565	44	Uterine Fibroids
biogrid:biogrid:255694	0.01565	44	Uterine Fibroids
biogrid:biogrid:255695	0.01565	44	Uterine Fibroids
biogrid:biogrid:255696	0.01565	44	Uterine Fibroids
biogrid:biogrid:255697	0.01565	44	Uterine Fibroids
biogrid:biogrid:255698	0.01565	44	Uterine Fibroids
biogrid:biogrid:255702	0.01565	44	Uterine Fibroids
biogrid:biogrid:255768	0.01565	44	Uterine Fibroids
biogrid:biogrid:256005	0.01565	44	Uterine Fibroids
biogrid:biogrid:258662	0.01565	44	Uterine Fibroids
biogrid:biogrid:258663	0.01565	44	Uterine Fibroids
biogrid:biogrid:260418	0.01565	44	Uterine Fibroids
biogrid:biogrid:260419	0.01565	44	Uterine Fibroids
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go:cellular_response_to_steroid_hormone_stimulus	0.01565	44	Uterine Fibroids
go:glucocorticoid-activated_RNA_polymerase_II_transcription_factor_binding_transcription_factor_activity	0.01565	44	Uterine Fibroids

go:glucocorticoid_receptor_activity	0.01565	44	Uterine Fibroids
go:steroid_hormone_binding	0.01565	44	Uterine Fibroids
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pfam:Glucocorticoid_receptor	0.01565	44	Uterine Fibroids
kegg:Choline_metabolism_in_cancer	0.015889	157	Uterine Fibroids
reactome:REACT_22310	0.015966	41	Uterine Fibroids
go:monocarboxylic_acid_metabolic_process	0.016278	48	Uterine Fibroids
reactome:REACT_22357	0.016338	96	Uterine Fibroids
biogrid:biogrid:1067424	0.016352	105	Uterine Fibroids
biogrid:biogrid:618500	0.016369	11	Uterine Fibroids
biogrid:biogrid:824769	0.016369	11	Uterine Fibroids
biogrid:biogrid:876362	0.016369	11	Uterine Fibroids
go:glutathione_peroxidase_activity	0.016369	11	Uterine Fibroids
go:L-phenylalanine_catabolic_process	0.016369	11	Uterine Fibroids
go:maleylacetoacetate_isomerase_activity	0.016369	11	Uterine Fibroids
mint:mint:MINT-67189	0.016369	11	Uterine Fibroids
reactome:REACT_1786	0.016369	11	Uterine Fibroids
biogrid:biogrid:905780	0.017693	50	Uterine Fibroids
reactome:REACT_13583	0.01812	185	Uterine Fibroids
go:porphyrin-containing_compound_metabolic_process	0.01819	61	Uterine Fibroids
reactome:REACT_9431	0.01819	61	Uterine Fibroids
mint:mint:MINT-4789619	0.018425	83	Uterine Fibroids
mint:mint:MINT-4789636	0.018425	83	Uterine Fibroids
mint:mint:MINT-4789661	0.018425	83	Uterine Fibroids
mint:mint:MINT-4789680	0.018425	83	Uterine Fibroids
go:axon	0.018498	84	Uterine Fibroids
go:anion_transmembrane_transport	0.019803	103	Uterine Fibroids
kegg:Neuroactive_ligand-receptor_interaction	0.020071	193	Uterine Fibroids
go:heterocycle_metabolic_process	0.020217	191	Uterine Fibroids
go:drug_metabolic_process	0.021419	484	Uterine Fibroids
reactome:REACT_13477	0.023099	247	Uterine Fibroids

kegg:Amphetamine_addiction	0.023212	222	Uterine Fibroids
biogrid:biogrid:279878	0.023488	28	Uterine Fibroids
biogrid:biogrid:892291	0.023488	28	Uterine Fibroids
go:retinoic_acid_binding	0.024876	130	Uterine Fibroids
reactome:REACT_13685	0.026231	287	Uterine Fibroids
go:monoamine_transmembrane_transporter_activity	0.026783	84	Uterine Fibroids
go:monoamine_transport	0.026783	84	Uterine Fibroids
kegg:Parkinson's_disease	0.026851	111	Uterine Fibroids
go:caffeine_oxidase_activity	0.027996	88	Uterine Fibroids
go:inorganic_anion_exchanger_activity	0.028436	32	Uterine Fibroids
go:arachidonic_acid_metabolic_process	0.029996	436	Uterine Fibroids
pfam:Sodium:neurotransmitter_symporter_family	0.030874	92	Uterine Fibroids
go:enzyme_binding	0.031403	604	Uterine Fibroids
go:organic_cation_transmembrane_transporter_activity	0.031575	91	Uterine Fibroids
go:caveola	0.032963	83	Uterine Fibroids
kegg:Cocaine_addiction	0.033199	184	Uterine Fibroids
biogrid:biogrid:316204	0.035242	94	Uterine Fibroids
go:flavonoid_biosynthetic_process	0.035292	145	Uterine Fibroids
go:flavonoid_glucuronidation	0.035292	145	Uterine Fibroids
go:glucuronosyltransferase_activity	0.035292	145	Uterine Fibroids
pfam:UDP-glucoronosyl_and_UDP-glucosyl_transferase	0.035292	145	Uterine Fibroids
go:cellular_glucuronidation	0.035396	139	Uterine Fibroids
kegg:Starch_and_sucrose_metabolism	0.036629	143	Uterine Fibroids
reactome:REACT_6784	0.036629	143	Uterine Fibroids
go:transcription_from_RNA_polymerase_II_promoter	0.037356	74	Uterine Fibroids
biogrid:biogrid:681456	0.038172	5	Uterine Fibroids
biogrid:biogrid:681665	0.038172	5	Uterine Fibroids
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go:brain_development	0.038172	5	Uterine Fibroids
go:histamine_N-methyltransferase_activity	0.038172	5	Uterine Fibroids
go:positive_regulation_of_protein_targeting_to_mitochondrion	0.038172	5	Uterine Fibroids
go:respiratory_gaseous_exchange	0.038172	5	Uterine Fibroids
pfam:Methyltransferase_domain	0.038172	5	Uterine Fibroids
go:organic_cation_transport	0.039286	98	Uterine Fibroids
go:monooxygenase_activity	0.039622	374	Uterine Fibroids
kegg:Ascorbate_and_aldarate_metabolism	0.040218	153	Uterine Fibroids
kegg:Pentose_and_glucuronate_interconversions	0.040218	153	Uterine Fibroids
go:synaptic_transmission	0.041154	342	Uterine Fibroids
biogrid:biogrid:892337	0.041341	11	Uterine Fibroids

kegg:Serotonergic_synapse	0.042894	510	Uterine Fibroids
kegg:Porphyrin_and_chlorophyll_metabolism	0.043324	146	Uterine Fibroids
biogrid:biogrid:26852	0.043845	6	Uterine Fibroids
go:cellular_homeostasis	0.043845	6	Uterine Fibroids
go:urate_transmembrane_transporter_activity	0.043845	6	Uterine Fibroids
go:neurotransmitter_secretion	0.0444	56	Uterine Fibroids
go:excretion	0.047097	89	Uterine Fibroids
go:peptide_transport	0.047495	21	Uterine Fibroids
go:mitochondrial_matrix	0.047924	81	Uterine Fibroids
go:brush_border_membrane	0.048809	19	Uterine Fibroids