Supporting Information:

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"Proxy-Phenotype Method Identifies Common Genetic Variants Associated with Cognitive Performance"

This document provides further details about materials, methods and additional analyses to accompany the research report "Proxy-Phenotype Method Identifies Common Genetic Variants Associated with Cognitive Performance."

Contents

Materials and Methods

1. Meta-analyses and selection of education-associated candidate SNPs

The first stage of our two-stage procedure consisted of conducting a GWAS meta-analysis on years of schooling, using the same analysis plan as Rietveld et al. (1) for the years-of-schooling variable (referred to in Rietveld et al. as "EduYears") and the same cohorts, except omitting the individuals that we include in the Cognitive Performance Sample (all individuals in the cohorts ALSPAC, ERF, LBC1921, LBC1936, and MCTFR, and subsamples of the cohorts QIMR and STR) described in section "Cognitive Performance Sample" below. Thus, compared with the meta-analysis sample size of $N = 126{,}559$ in Rietveld et al., the sample size for our meta-analysis of years of schooling is $N = 106{,}736$. We obtained permission to use these data under the SSGAC data sharing policy (http://ssgac.org/documents/DatasharingpolicySSGAC.pdf). Our meta-analysis found 927 single-nucleotide polymorphisms (SNPs) meeting the inclusion threshold of $p\text{-value} < 10^{-5}$, which was chosen based on power calculations prior to conducting our study (see section 15.E of this SI Appendix). We pruned this set of SNPs for linkage disequilibrium using the clumping command in PLINK and the HapMap II CEU (r23) data. The physical threshold for clumping was 1000 kB, and the R^2 threshold for clumping was 0.01. This pruning procedure resulted in a set of 69 approximately independent SNPs, which is our set of "education-associated SNPs." These are listed in Supplementary Table S4.

We note that the education-associated SNPs (Table S4) are independent from *APOE*, a gene that has previously been associated with cognitive decline in older individuals (2–6). The *APOE* gene is located on chromosome 19, while none of our education-associated SNPs are located on that chromosome; thus, *APOE* status is inherited independently from all of our education-associated SNPs.

For the polygenic-score analyses in the Health and Retirement Study (HRS) described in section 14 below, we conducted the same meta-analysis, except that we additionally exclude the HRS cohort. The sample size of this meta-analysis is $N = 98{,}110$.

2. Cognitive Performance Sample

The Cognitive Performance Sample that we use in the second stage of our two-stage procedure consists of CHIC (the Childhood Intelligence Consortium (7)) and five additionally recruited GWA samples. CHIC consists of six studies: the Avon Longitudinal Study of Parents and Children (ALSPAC, $N = 5{,}517$), the Lothian Birth Cohorts of 1921 and 1936 (LBC1921, $N = 464$; LBC1936, $N = 947$), the Brisbane Adolescent Twin Study subsample of Queensland Institute of Medical Research (QIMR, $N = 1{,}752$), the Western Australian Pregnancy Cohort Study (Raine, $N = 936$), and the Twins Early Development Study (TEDS, $N = 2{,}825$). The five additional samples are the Erasmus Rucphen Family Study (ERF, $N = 1{,}076$), the Generation R Study (GenR, $N = 3{,}701$), the Harvard/Union Study (HU, $N = 389$), the Minnesota Center for Twin and Family Research Study (MCTFR, $N = 3{,}367$) and the Swedish Twin Registry Study (STR, $N = 3{,}215$). This brings the total sample size to 24,189 individuals from 11 studies.

In most of these cohorts, cognitive performance was elicited before participants completed schooling (for details, see section 3). Exceptions are ERF and HU, which constitute ≈6% of the Stage 2 sample. In STR, cognitive performance was measured among males during military conscription at the age of 18. Some of these individuals may have also already completed schooling. However, some of the individuals in ERF and HU may have still been in school when cognitive performance was measured.

Participating studies were recruited from January 2013 – March 2013, and summary results were uploaded before the end of April 2013. All participants provided written informed consent, and the studies were performed in accordance with the respective Local Research Ethics Committees or Institutional Review Boards. The descriptive statistics and study designs are provided in Table S1.

To provide additional data for examining the within-family explanatory power of the polygenic score (see section 13), an additional cohort was recruited: Generation Scotland (GS). The sample consists of 1,081 siblings.

3. Cognitive performance measures

Measures of cognitive performance for the studies that are part of CHIC, and the cognitive performance measures for the other five GWA studies, are as follows:

ALSPAC: Cognitive performance at the age of 8 years was measured with the Wechsler Intelligence Scale for Children (WISC-III). A short version of the test consisting of alternate items only (except the Coding task) was applied by trained psychologists. Verbal (information, similarities, arithmetic, vocabulary, comprehension) and performance (picture completion, coding, picture arrangement, block design, object assembly) subscales were administered. Each subtest was age-scaled according to population norms, and a summary score for total cognitive performance was derived. We calculated the first two principal components of the genome-wide data using Eigenstrat. As inputs to the analysis reported here, we generated sex- and principal-component-adjusted Z-standardized cognitive performance scores for unrelated ALSPAC children for whom total cognitive performance and genome-wide data were available. To do so, cognitive performance scores within a range of ±4 SD relative to the total ALSPAC sample were regressed on sex and the principal components. The residuals were Z-transformed. Using the resulting data, genome-wide association analysis was conducted.

ERF: Scores on the following cognitive tests were used to create the fluid-type general cognitive ability factor: Stroop 3 (time needed to complete Stroop color-word card), TMT-B (time needed to complete Trailmaking Test part B), phonemic fluency (with D, A, T, number of words mentioned beginning with each letter, one minute each, sum of the three trials), 15-word Auditory Verbal Learning Test (AVLT-sum) (sum of immediate (5 iterations) and delayed recall (once)), WAIS block design test (*n* of correct answers, Wechsler scoring). The tests, the method of application, and key references are described in (8). Principal components analysis was applied to these 5 tests. The first unrotated principal component, which accounted for 50.1% of the total test variance, is the measure of *g*. The mean age at reporting is 33.2 (SD = 7.1).

GenR: The phenotype has been constructed using assessments of the Snijders-Oomen Non-Verbal Intelligence Test (SON-R 2.5–7). The overall cognitive performance score was calculated based on two subtests: Mosaics (performance) and Categories (reasoning). The mean age at reporting is 6.17 (SD = 0.50).

GS: Scores on the following cognitive ability tests were used to create the general cognitive ability factor: Wechsler Digit Symbol Substitution Task, Wechsler Logical Memory Test, Verbal Fluency (sum of letters C, F, and L), and the Mill Hill Vocabulary Scale. The tests, the method of application and key references have been described in detail elsewhere (9). The number of siblings used in the analysis was 1081 (mean age 41.1 (SD 11.0), range 18-77). The Pearson correlations (*r*s) among the 4 tests ranged from 0.07 to 0.40 (mean 0.22). Principal components analysis was applied to these 4 tests. The first unrotated principal component (FUPC) accounted for 42% of the total test variance. Loadings on the FUPC were as follows:

Wechsler Digit Symbol Substitution Task = 0.56, Wechsler Logical Memory Test = 0.63, Verbal Fluency = 0.71, Mill Hill Vocabulary Scale = 0.68.

HU: A composite score of several cognitive performance subtests was generated in the following way. A shortened version of Raven's Advanced Progressive Matrices (RAPM) (10); a 10-item vocabulary test; the Vocabulary, Similarities, and Arithmetic subtests of the Multidimensional Aptitude Battery II; and the number correct in a speeded version of the Shepard-Metzler Mental Rotation (SMMR) task were administered. RAPM, Arithmetic, and SMMR were standardized to have mean zero and variance one in the sample. The Vocabulary, Similarities, and separate 10-item vocabulary test were factor analyzed, and Bartlett's method was used to calculate a verbal factor score on the basis of the three observed scores. This verbal score was then standardized. The standardized verbal, RAPM, Arithmetic, and SMMR scores were added to form a raw composite, which was itself standardized separately for each sex. The composite IQ formed in this way showed a correlation of ~0.70 with self-reported SAT scores, which is quite good considering the restriction of range in SAT scores (a standard deviation only two-thirds of that observed in the total population of European-descent SAT examinees). The mean age at reporting is 25.48 (SD = 6.63).

LBC1921 and LBC1936: The measure of cognitive performance was the Moray House Test (MHT) No. 12. This is one of a series of tests of cognitive performance devised by Godfrey Thomson at the Moray House College, University of Edinburgh, from the late 1920s onwards. The MHT is a group test of cognitive performance with a time limit of 45 minutes. The test has 71 items and a maximum possible score of 76. It was also known as the "Verbal Test" because the items have a predominance of verbal reasoning. The test has a variety of items, as follows: following directions (14 items), same–opposites (11), word classification (10), analogies (8), practical items (6), reasoning (5), proverbs (4), arithmetic (4), spatial items (4), mixed sentences (3), cypher decoding (2), and other items (4). Mean age at reporting is 10.9 years (SD = 0.28).

MCTFR: Measurement of general cognitive ability in the Minnesota sample was based on an abbreviated form of the Wechsler Intelligence Scale for Children-Revised (WISC-R) for those 16 years or younger or Wechsler Adult Intelligence Scale-Revised (WAIS-R) for those older than 16 years. The short forms consisted of two Performance subtests (Block Design and Picture Arrangement) and two Verbal subtests (Information and Vocabulary), the scaled scores on which were prorated to determine Full-Scale IQ (FSIQ). FSIQ estimates from this short form have been shown to correlate greater than 0.90 with FSIQ from the complete test. The mean age at reporting is 14.2 (SD = 2.7).

QIMR: Cognitive performance was measured using a shortened version of the computerized Multi-dimensional Aptitude Battery (MAB), a general intelligence test similar to Wechsler Adult Intelligence Scale-Revised. The shortened MAB includes three verbal subtests (information, arithmetic, vocabulary) and two performance subtests (spatial, object assembly). Scaled scores for cognitive performance were computed in accordance with the manual.

Raine: Cognitive performance was estimated based on four cognitive tests carried out at approximately 10 years of age (Peabody Picture Vocabulary Test, Raven's Colored Progressive Matrices, Symbol Digits Modalities Test (SDMT) written score and SDMT oral score. The first principal component from the four cognitive measures was used for analyses.

STR: Men in the sample were matched to conscription data provided by the Military Archives of Sweden. Data on cognitive ability are available for most men in the sample born in 1936 or later. These men were required by law to participate in military conscription around the age of 18. They enlisted at a point in time when exemptions from military duty were rare and typically only granted to men who could document a serious handicap that would make it impossible to complete training. For the men born after 1950, the military data have been digitalized. For men born 1936-1950, we manually retrieved the information from the Military Archives. The first test of cognitive ability used by the Swedish Military was implemented in 1944, and it has subsequently been revised and improved on a few occasions. (11) discusses the history of psychometric testing in the Swedish military and provides evidence that the measure of cognitive ability is a good measure of *g*. For men in the sample who did the military conscription before 1959, the cognitive ability test consisted of 5 subtests: logical, verbal, mathematical, spatial, and technical. The first subtest about logical ability was called "Instructions" and measured the ability to understand complicated instructions. The second subtest about verbal ability was called "Selection," and in these questions the subjects had to pick out one out of five words that differed from the four other words. The third subtest was called "Multiplication" and consisted of multiplying a two-digit number by a one-digit number. The fourth subtest was called "Levers." With the guidance of a graph depicting a system of levers, the subjects answered questions about the effect of a force applied to a specific point in the system. The final test was called "Technical comprehension," in which the subjects answered questions about technical problems with the guidance of graphs. In 1959 the cognitive ability test was revised, and men in the sample who did the military conscription in 1959 or later took this revised test. The logical and verbal ability subtests were kept. The mathematical subtest ("Multiplication") was dropped from the test. The spatial ability test ("Levers") was replaced by a test of spatial ability called "Composition," in which the subjects had to indicate which pieces fit with a specific figure. The technical ability test ("Technical comprehension") was revised (it was modernized). For both men who did the military conscription before and after 1959, we use data for the 4 subtests of logical, verbal, spatial, and technical ability (since subtests of these abilities were included at the military conscription both before and after 1959). We do not include the mathematical ability test since it was only given to subjects who did the military conscription in 1959 and later. At the military conscription, each subtest was given a raw score and a standardized 1-9 stanine score. The norm tables for the stanine scores were updated each year to ensure that there was no trend in the stanine scores over time. We use the stanine scores of the four subtests of logical, verbal, spatial and technical ability. We use the first principal component of these four stanine scores as the measure of cognitive performance.

TEDS: Individuals were tested at 12 years using two verbal and two nonverbal measures: WISC-III-PI Multiple Choice Information (General Knowledge) and Vocabulary Multiple Choice subtests (12), the WISC-III-UK Picture Completion (12) and Raven's Standard Progressive Matrices (13). Test scores were adjusted for age within each testing period, and the first principal component was derived.

Within each cohort the cognitive performance measure was adjusted for sex and age and standardized to have mean 0 and standard deviation 1.

4. Genotyping and imputation

All cohorts were genotyped using commercially available genotyping arrays. The study-specific details on genotype platform, genotype calling algorithm, imputation software, and imputation reference dataset are provided in Table S2.

5. Quality control

In CHIC extensive quality control has been performed at the meta-analysis stage (for details, see (7)). We followed CHIC's protocol and cleaned each GWA summary file from the five additionally recruited replication studies. First, the SNPs with a Minor Allele Frequency

(MAF) < 1%, imputation quality score < 40%, Hardy-Weinberg *p*-value < 10^{-6} and call rate < 0.95 were excluded. Quantile-Quantile plots of the cleaned summary files were visually inspected, and the genomic control (GC) inflation factor λ (14) was calculated for each cleaned summary file. The Quantile-Quantile plots (Supplementary Figure 1) did not reveal stratification problems. This is confirmed by the values of λ's, which are all close to 1. Second, following (7), we calculated the average effective sample size per cohort (as a function of the allele frequency and the standard error of the effect size from the association) and compared it with the actual sample size. We found that the average effective sample sizes were consistent with the reported sample sizes in all cohorts.

6. Association analysis

Each cohort was asked to follow a prespecified analysis plan (preregistered on the Open Science Framework website prior to conducting our study; see https://osf.io/z7fe2/). This plan requested from each study summary results of the ordinary least squares regression of the standardized measure of cognitive performance on the imputed SNPs. At least four principal components of the Identity-by-State (IBS) matrix (to control for subtle population stratification) were either added as covariates, or used in the standardization of the phenotype. Only individuals from recent Caucasian descent were included. Association software used by the studies is reported in Table S2.

7. Meta-analysis

The meta-analysis was performed with inverse-variance weighting using METAL (15). The necessary inputs from the study-specific GWA summary results were: SNP ID, coded allele (allele to which regression coefficient refers), non-coded allele, strand, beta (regression coefficient), standard error, *p*-value, and allele frequency for the coded allele.

8. Correction of effect sizes for winner's curse

The "winner's curse" refers to the fact that the estimated effect size for a SNP (and therefore the R^2 associated with the SNP) newly discovered to be statistically significant tends to be much higher than the unbiased effect size estimated subsequently in replication samples. It occurs because, although OLS gives an unbiased *unconditional* estimate of the true parameter value, the expected value of the estimate is biased away from zero conditional on the parameter meeting a threshold for statistical significance. This bias is more highly pronounced the more stringent the significance threshold (and therefore especially pronounced in GWAS because the significance threshold for "genome-wide significant" is especially stringent). In Subsection A, we walk through the (well-known) derivation of the analytic form for the expected value of the winner's curse. In Subsection B, we discuss several known methods for correcting for it. Subsection C contains a comparison of these methods in a simulation study of the current analysis of cognitive performance. We conclude in Subsection D by applying the winner's curse corrections to both Rietveld et al.'s (1) findings—a context where we can compare the winner's-curse-corrected estimates to the unbiased, replication-sample estimates—and to the findings from the current analysis of cognitive performance.

A. Derivation of the winner's curse

We derive the winner's curse for the simple case where outcome Y is truly related to a SNP's genotype $g \in \{0,1,2\}$ in accordance with the simple linear regression model:

$$Y = cons + \beta g + \varepsilon$$

where $\varepsilon \sim N(0,\sigma^2)$, and σ^2 and the SNP's MAF *m* are known. If the sample size *n* is large and if the SNP is in Hardy-Weinberg equilibrium, then the OLS estimate is drawn from the normal distribution $\hat{\beta} \mid \beta \sim N(\beta, v^2)$, where $\upsilon^2 \equiv \frac{\sigma^2}{2nm(1-m)}$ (and υ^2 is known because σ^2, *m*, and *n* are all known). Given statistical significance threshold α, the null hypothesis $\beta = 0$ is rejected if the test statistic, $\frac{\hat{\beta}}{\upsilon}$, falls within the $\left(1-\frac{\alpha}{2}\right)$ percentile right or left tail of this distribution:

$$\frac{\hat{\beta}}{\upsilon} > \Phi^{-1}\left(1-\frac{\alpha}{2}\right),$$

where Φ is the cdf of a standard normal distribution (that has corresponding pdf ϕ). Therefore, conditional on the SNP having been identified as statistically significant at size α, its coefficient $\hat{\beta}$ is distributed as a truncated standard normal distribution with the mass removed in a neighborhood of zero, with pdf:

$$f(\hat{\beta} \mid \beta, sig_\alpha) = \begin{cases} \dfrac{\frac{1}{\upsilon}\phi\left(\frac{\hat{\beta}-\beta}{\upsilon}\right)}{1-[\Phi(T^+(\beta))-\Phi(T^-(\beta))]} & if \left|\hat{\beta}\right| > \upsilon\Phi^{-1}\left(1-\frac{\alpha}{2}\right) \\ 0 & if \left|\hat{\beta}\right| \le \upsilon\Phi^{-1}\left(1-\frac{\alpha}{2}\right) \end{cases}, \tag{1}$$

where $T^+(\beta) \equiv \Phi^{-1}\left(1-\frac{\alpha}{2}\right) - \frac{\beta}{\upsilon}$ and $T^-(\beta) \equiv -\Phi^{-1}\left(1-\frac{\alpha}{2}\right) - \frac{\beta}{\upsilon}$. The mean of the distribution described by equation (1) is

$$E(\hat{\beta} \mid \beta, sig_\alpha) = \beta + \upsilon \frac{\Phi(T^+(\beta)) - \Phi T^-(\beta)}{1-[\Phi(T^+(\beta))-\Phi(T^-(\beta))]}. \tag{2}$$

The bias due to the winner's curse is the second term in equation (2). The numerator of this term signs the bias: if $\beta > 0$, then the bias is positive, while if $\beta < 0$, then it is negative. The bias therefore always pushes the estimate away from zero. In order to obtain a more accurate estimate of the SNP's effect size, it is necessary to apply a correction procedure that "shrinks" the OLS estimate toward zero. If α is smaller (that is, the significance threshold is more stringent), then the denominator of the bias term is smaller and hence the bias is larger in magnitude.

B. Correcting for the winner's curse

There are several methods that one might consider to correct for this bias. Here we briefly describe four: inverting the conditional expectation of the OLS estimator, maximum likelihood estimation (MLE), Bayesian estimation, and empirical-Bayes estimation.

B.1. Inverting the conditional expectation of the OLS estimator

One approach is motivated by the seemingly straightforward idea of inverting the above conditional expectation equation (2) that is a function of the true parameter value:

$$E(\hat{\beta} \mid \beta, sig_\alpha) \equiv g(\beta) = \beta + \upsilon \frac{\Phi(T^+(\beta)) - \Phi(T^-(\beta))}{1 - [\Phi(T^+(\beta)) - \Phi(T^-(\beta))]}.$$

While $g(\beta)$ is not analytically invertible, it can be inverted numerically. However, $E(\hat{\beta} \mid \beta, sig_\alpha)$ is not observed and so cannot be plugged into $g^{-1}(\cdot)$. The feasible version of this estimator must instead use the observed value $\hat{\beta}$. Unfortunately, though, the estimator $g^{-1}(\hat{\beta})$ is biased: that is, generically $E[g^{-1}(\hat{\beta}) \mid \beta, sig_\alpha] \neq \beta$. To see this, note that $g^{-1}[E(\hat{\beta} \mid \beta, sig_\alpha)] = \beta$, and Jensen's inequality implies that $E[g^{-1}(\hat{\beta}) \mid \beta, sig_\alpha]$ is generically *not* equal to $g^{-1}[E(\hat{\beta} \mid \beta, sig_\alpha)]$ since $g(\beta)$ is non-linear. Furthermore, it is difficult to assess the direction and amount of bias.

B.2. Maximum Likelihood Estimation

Some researchers have used MLE to correct for the winner's curse (16, 17). To estimate a MLE, we use the pdf of $\hat{\beta} \mid (\beta, sig_\alpha)$, which is equation (1) above. Since we only have one observation of $\hat{\beta}$, the likelihood function in this case is simply equation (1). Taking the first-order condition with respect to β and rearranging terms, the ML estimator β_{MLE} is implicitly defined by the equation:

$$\hat{\beta} = \beta_{MLE} + \upsilon \frac{\Phi(T^+(\beta_{MLE})) - \Phi(T^-(\beta_{MLE}))}{1 - [\Phi(T^+(\beta_{MLE})) - \Phi(T^-(\beta_{MLE}))]}.$$

The right-hand side of this equation is identical to the right-hand side of equation (2) above. Therefore, the MLE is the same as the estimate obtained from inverting the conditional expectation of the OLS estimator, and thus the MLE will be biased in an identical manner. Via simulation, (16) shows that these methods will over-correct when β is large and under-correct when β is small.

We note a few observations about the bias correction implied by this estimator; similar points will hold for the Bayesian estimators that follow, but we make these observations here because they are particularly straightforward to see for the MLE estimator. First, when the estimated coefficient is large in magnitude, the bias correction is small; that is, the MLE-corrected estimate will be approximately equal to the uncorrected estimate. This can be seen in the above formula: since $\lim_{|\beta|\to\infty} \phi(T^{+}(\beta)) - \phi(T^{-}(\beta)) = 0$ and $\lim_{|\beta|\to\infty} \Phi(T^{+}(\beta)) - \Phi(T^{-}(\beta)) = 0$, it follows that $\lim_{|\hat{\beta}|\to\infty} \beta_{MLE}(\hat{\beta}) = \hat{\beta}$. Intuitively, when the uncorrected estimate is large in magnitude, it is very likely to have been resulted from a true β that is large in magnitude and hence very likely that we would have observed a statistically significant estimate regardless of our sample realization; therefore, the fact that the observed estimate was statistically significant provides little additional information about the value of β.

Second and on the flipside, when the estimated coefficient is close to the significance threshold, the bias correction may be quite large. Intuitively, it is actually fairly likely that a barely statistically significant estimate resulted from a true β that is below the threshold.

B.3. Bayesian and Empirical-Bayes Estimation

Two alternative approaches are Bayesian and are closely related. We follow a derivation similar to (18), who adjust the winner's curse of the odds ratio in a binary setting. However, we consider a more general setting, correcting the underlying β parameters, which are defined over the real line and therefore require a different class of priors and posteriors (for a closely related approach, see (19)). For a normally-distributed prior $\beta \sim N(\mu, \tau^2)$, the posterior is given by the pdf

$$f(\beta \mid \hat{\beta}, sig_{\alpha}) = \frac{\dfrac{\phi\left(\left(\beta - \dfrac{\tau^2\hat{\beta} + \upsilon^2\mu}{\tau^2 + \upsilon^2}\right) / \sqrt{\dfrac{\tau^2\upsilon^2}{\tau^2 + \upsilon^2}}\right)}{1 - [\Phi(T^{+}(\beta)) - \Phi(T^{-}(\beta))]}}{\displaystyle\int_b \dfrac{\phi\left(\left(b - \dfrac{\tau^2\hat{\beta} + \upsilon^2\mu}{\tau^2 + \upsilon^2}\right) / \sqrt{\dfrac{\tau^2\upsilon^2}{\tau^2 + \upsilon^2}}\right)}{1 - [\Phi(T^{+}(b)) - \Phi(T^{-}(b))]} db}$$

The mean of this distribution is

$$E(\beta \mid \hat{\beta}, sig_{\alpha}) = \frac{E[g_1(X)]}{E[g_2(X)]}, \tag{3}$$

where $X \sim N\left(\dfrac{\tau^2\hat{\beta} + \upsilon^2\mu}{\tau^2 + \upsilon^2}, \dfrac{\tau^2\upsilon^2}{\tau^2 + \upsilon^2}\right)$, $g_1(x) = \dfrac{x}{1 - [\Phi(T^{+}(x)) - \Phi(T^{-}(x))]}$, and $g_2(x) = \dfrac{1}{1 - [\Phi(T^{+}(x)) - \Phi(T^{-}(x))]}$.

The right-hand side of equation (3) can be evaluated numerically by taking a set of M draws of the random variable X, $\{x_m\}$, and taking the ratio of the sample means of $\{g_1(x_m)\}$ and $\{g_2(x_m)\}$. In the implementations below, we use M = 10 million.

The Bayesian and empirical Bayes approaches are distinguished by the way that the parameters of the prior distributions, μ and τ^2, are chosen. The Bayesian method we consider is to assume an uninformative prior: $\tau \to \infty$ (and in this case, the choice of μ does not matter). Using this method, equation (3) is evaluated using $X \sim N(\hat{\beta}, \upsilon^2)$. Similar to with the MLE correction, the Bayesian (and empirical Bayes) correction will be small when the uncorrected estimate is far from the significance threshold and large when it is close. Intuitively, when the observed estimate is large in magnitude, the probability that the true β that is below the threshold is negligible, so the bias correction has very little impact on the posterior mean.

In the empirical Bayes approach, the data are used to estimate appropriate values for μ and τ^2 . To develop intuition, we first consider a method (simpler than the method we use) that would be appropriate if one had access to OLS estimates for a large random sample of SNPs (for example, from complete GWAS meta-analysis results), $s = 1, \ldots, S$. Since for each SNP the choice of reference allele is arbitrary, the mean of the true effects across the S SNPs is zero: $\mu = 0$. Now, note that since $\hat{\beta}_s \mid \beta_s \sim N(\beta_s, \upsilon_s^2)$ and $\beta_s \sim N(0, \tau^2)$, it follows that $\hat{\beta}_s \sim N(0, \tau^2 + \upsilon_s^2)$. Therefore, τ^2 can be estimated as the variance of all of the $\hat{\beta}_s$ estimates minus the mean of the square of their estimated standard errors:

$$\hat{\tau}^2 = \frac{1}{S-1} \sum_{s=1}^{S} \hat{\beta}_s^2 - \overline{\hat{\upsilon}_s^2} \, .$$

We do not use this approach because assuming $\mu = 0$ would be extremely conservative in our context, where the SNPs we study are not a random sample—rather, they were selected as candidates for cognitive performance because they had strong impacts in a previous GWAS on educational attainment.

The empirical-Bayes approach that we employ exploits information available from the GWAS results on educational attainment to inform our choice of μ. Specifically, we set μ equal to the magnitude of a SNP's effect that would be needed in order for the SNP to explain the same fraction of variance in cognitive performance as it explains in educational attainment. To be more precise, let $\hat{\beta}_{educ,s}$ be the estimated effect of SNP *s* on years of schooling taken from Rietveld et al. (2013). The fraction of variance in years of schooling explained by the SNP can be calculated as $R^2_{educ,s} = \frac{2m_s(1-m_s)\hat{\beta}_{educ,s}}{\sigma^2_{educ}}$, where m_s is the MAF of SNP *s* and σ^2_{educ} is the variance of years of schooling. We can calculate that SNP *s* would have the same R^2 for cognitive performance if $\beta_{cog,s} = \frac{\sigma_{cog}}{\sigma_{educ}} \hat{\beta}_{educ,s}$, where $\beta_{cog,s}$ is the putative effect of SNP *s* on cognitive performance, and σ^2_{cog} is the variance of cognitive performance. Thus, we set the mean of our prior for the effect of the SNP on cognitive performance as $\mu = \frac{\sigma_{cog}}{\sigma_{educ}} \hat{\beta}_{educ,s}$.

While not as conservative as setting a prior of zero, this prior mean is still likely to be conservative (i.e., too close to zero) to the extent that a SNP's effect on educational attainment works through a more direct effect on the mediating phenotype of cognitive performance; in that case, the SNP would be expected to explain a *larger* fraction of variance in cognitive performance than in years of schooling. We calculate the prior parameter τ^2 similarly as in the mean-zero empirical-Bayes procedure above (but rather than estimating the variance about zero, we estimate the variance about the mean of the prior):

$$\hat{\tau}^2 = \frac{1}{S-1}\sum_{s=1}^{S}(\hat{\beta}_s - \mu)^2 - \overline{\hat{\upsilon}_s^2}.$$

(18) prove that there is no winner's curse correction that is unbiased for all values of β, but an advantage of a Bayesian approach is that the estimates will be on average unbiased. As an intuitive rationale for a choice for a prior, note that the Bayesian method with a diffuse prior will be unbiased on average across all real-valued effect sizes, while the empirical Bayes method is unbiased across a weighted average of effect sizes with the weights given by the prior. Thus, the empirical-Bayes-corrected estimate should be less biased if the true effect size is local to the mean of the selected prior but more biased if the true value is distant from the mean.

As a final note on implementation: all of the above approaches require a value for $\upsilon^2 \equiv \frac{\sigma^2}{2nm(1-m)}$, which we have assumed is known, but it is in fact not known because *m* and σ^2 are not known. For *m*, we just use the empirical frequency of the minor allele in our data. We estimate σ^2 iteratively, starting with the naive estimate of β, $b_0 = \hat{\beta}$. Then we calculate $\sigma_0^2 = \text{var}(Y) - 2b_0^2 m(1-m)$. Using σ_0^2, we estimate $b_1(\sigma_0)$. We iterate this procedure until it converges, giving us estimates of both σ^2 and $\hat{\beta}$. (In the implementations below, we ran the algorithm for ten iterations, but convergence was virtually always apparent after only two.)

C. Simulation Study

We now examine and compare the MLE and Bayesian methods via simulation. To roughly match the analysis of the top three SNP associations with cognitive performance from the main text, we set the sample size n = 25,000, MAF m = 0.4734, dependent-variable variance $\sigma^2 = 1$ (that is, the dependent variable is standardized), and significance threshold α = 0.05/69 (the conventional significance threshold after Bonferroni correction for analysis of 69 SNPs). For each fixed true value of β, in each iteration *i* of the simulation, we draw an *n*-length genotype vector g_i, and we draw an *n*-length error $\varepsilon_i \sim N(0, \sigma^2 I_n)$. In each iteration, we estimate the naïve $\hat{\beta}_i$, which we keep if it passes the significance threshold and ignore otherwise. If we keep $\hat{\beta}_i$, we then estimate $\tilde{\beta}_{MLE,i}$ using maximum likelihood and $\tilde{\beta}_{Bayes,i}$ using the diffuse-prior Bayesian method described above. (We do not perform simulations for an empirical Bayes approach since it is not clear what the right choice should be for an empirical prior for the simulation.) We perform 1,000,000 replications of this simulation.

Supplementary Figure 3 below shows the winner's-curse corrected estimate as a function of the true β, grouped in bins of the true β that are 0.002 units wide. For each estimate, the light dotted lines in the corresponding color show the interval that contains 95% of the estimates. The figure suggests that there can be significant bias from the winner's curse in this parameterization when the true β is less than 0.04, but this bias becomes negligible for higher values. It is also evident that neither correction procedure gives an unbiased estimate of the true β for every particular value of β. In this example, it seems that MLE performs slightly better when the true β is very small, while the Bayesian method performs better for medium values of β. If an empirical-Bayes approach were used, it would perform better than the Bayesian approach for the more common values of β and worse elsewhere.

D. Applications

We now apply these winner's-curse-correction methods to actual data. We begin with the findings of (1) for educational attainment, where we can compare the unbiased replication-stage estimates to the results from applying the winner's-curse-correction methods to the inflated discovery-stage estimates. The first and fourth columns of Supplementary Table S5, respectively, report the discovery-stage estimates and the replication-stage estimates for the three SNPs that (1) report passed a significance threshold of $p < 5 \times 10^{-8}$ (the linear regression coefficients for the SNP associated with years of education are from (1)'s Table 1, and the logistic regression coefficients for the SNPs associated with college completion have been provided by the SSGAC). The second and third columns, respectively, show the discovery-stage estimates corrected by MLE and by the Bayesian method with a diffuse prior. Supplementary Table S6 is the same, except that it shows the 10 SNPs that passed a suggestive significance threshold of $p < 10^{-6}$ (including the three that are genome-wide significant). The results in the tables indicate that in these data, both correction methods do a reasonable job of predicting the effect size that is estimated in the replication.

Finally, we apply the winner's-curse-correction methods to the cognitive performance findings reported in the main text. The first column of Supplementary Table S7 shows the effect size estimates for the three education-based SNPs that passed the (Bonferroni-corrected) significance threshold of $p < 0.05/69$. The second, third, and fourth columns, respectively, show the estimates corrected by MLE, by the Bayesian method with a diffuse prior, and by empirical Bayes.

There are two reasons why the corrections as applied to the cognitive performance findings are large relative to the corrections as applied to Rietveld et al.'s (1) findings (despite the fact that the more stringent significance threshold of genome-wide significance used in (1) would tend to generate a larger correction, all else equal). First, the sample size on which the uncorrected estimates are based is much larger in (1) than for the cognitive performance estimates (approximately 100,000 versus 25,000, respectively). Second and more subtly, simulations (not reported here) show that the uncorrected estimates for the cognitive performance results fall within the region around the significance threshold where the corrections are relatively large.

To provide another way of assessing the magnitude of the SNP associations with cognitive performance, the fifth and sixth columns of Supplementary Table S7 show the R^2 associated with the uncorrected estimates and with the empirical-Bayes-corrected estimates. The R^2, which is defined as the ratio of the variance explained by the SNP to the total phenotypic variance, is here simply equal to the variance explained by the SNP, because the phenotypic variance has been normalized to 1:

$$R^2 = 2m(1-m)\hat{\beta}^2 ,$$

where $\hat{\beta}$ is either the uncorrected (naïve) effect size estimate or the empirical-Bayes-corrected estimate. The results reported in the table suggest that the winner's curse adjustment reduces the SNPs' R^2 from ≈0.0006 to ≈0.0002.

9. Bayesian analysis of the credibility of the SNP associations

Here, we report a heuristic Bayesian calculation along the lines of (20) and (21) to assess the likelihood that the three individual SNP associations we find with cognitive performance are false positives attributable to sampling variation. Several simplifying assumptions make the calculations especially straightforward. First, we assume that each SNP has only two (rather than three) possible genotypes. Second, we assume for each of the three SNPs, there are only two possibilities: either there is no true association (the null hypothesis H_0), or there is a true association that explains a known fraction of phenotypic variance, R^2 (the alternative hypothesis H_1). Let the prior probability of H_1 be denoted by π; hence the prior probability of H_0 is $1–\pi$. Third, we assume the information available to us is that for each SNP, using a two-sided t-test, we rejected the null hypothesis of no association at the standard significance threshold after Bonferroni correction for testing 69 SNPs, i.e., we rejected H_0 at the significance threshold $\alpha = 0.05/69 \approx 0.00072$.

By Bayes' Rule, the probability that there is a true association given that we observed a significant association is:

$$P(H_1 \| t |> t_{\alpha/2}) = \frac{P(| t |> t_{\alpha/2} \mid H_1)P(H_1)}{P(| t |> t_{\alpha/2} \mid H_1)P(H_1) + P(| t |> t_{\alpha/2} \mid H_0)P(H_0)} = \frac{(power)(\pi)}{(power)(\pi) + (\alpha)(1-\pi)},$$

where "power" (as well as the significance test) is two-sided. Using (22) (http://pngu.mgh.harvard.edu/~purcell/gpc/qtlassoc.html), we calculate statistical power for several different values of R^2 and for the sample size of $N = 24,189$ (the actual sample size of the Cognitive Performance Sample).

Supplementary Table S8 shows posterior probabilities that there is a true association, given specific values for R^2 and π. The larger value for R^2 is 0.0006, which roughly corresponds to the estimated magnitude of the association in the Cognitive Performance Sample for each of the three SNPs that are statistically significant after Bonferroni correction (their R^2's are 0.00064, 0.00058, and 0.00056; see Supplementary Table S4). Because this estimate is likely to be inflated by the winner's curse, we also examine the smaller value of $R^2 = 0.0002$. This value roughly corresponds to the estimated magnitude of the association for each of the three SNPs after adjustment for the winner's curse, as discussed in Supplementary Information section 8 (these winner's-curse-adjusted R^2's are 0.00027, 0.00019, and 0.0017; see Supplementary Table S7).

In the simple set-up here, we view a prior probability π in the range of 0.2% to 2% as the right order of magnitude for an *arbitrarily* selected SNP to be associated with cognitive performance with effect sizes of order of magnitude $R^2 = 0.0002$. To see why, begin by taking one extreme: suppose all independent associated SNPs had effect sizes $R^2 = 0.0002$. Since the proportion of variance in cognitive performance explained by the linear, additive effect of all SNPs jointly is roughly 0.40 (23, 24), there would be 0.40 / 0.0002 = 2,000 independent associated SNPs. Given that there are approximately 1 million independent loci in the human genome (25), each of the loci would have prior probability 2,000 / 1 million = 0.2%. However, in reality, most SNPs associated with cognitive performance surely have smaller effect sizes than $R^2 = 0.0002$. In this simple set-up with only two hypotheses, if we consider any SNP whose association is more than an order of magnitude smaller than $R^2 = 0.0002$ as consistent with the "null hypothesis," then the largest number of independent SNPs that are non-null is 20,000 (because 0.40 / 0.00002 = 20,000). In that case, each locus has prior probability 20,000 / 1 million = 2%.

Since the 69 SNPs we study are not arbitrary but are instead selected from those most strongly associated with educational attainment, the prior probability for each of those SNPs should be much higher than for a randomly selected locus in the genome—indeed, this observation is what motivates the proxy-phenotype method in the first place. Therefore, we view $\pi = 0.1\%$ as an extremely conservative lower bound for the prior probability on the three SNPs being true positives. Since we suspect that a number of the 69 SNPs we study are probably truly associated with cognitive performance, we believe that priors of $\pi = 5\%$ and $\pi = 10\%$ are more reasonable.

Given priors of $\pi = 5\%$ or $\pi = 10\%$, together with a reasonable assumption about the true effect size (the winner's-curse-adjusted R^2 of 0.0002), Supplementary Table S8 indicates that the evidence very strongly evidence favors H_1 over H_0: the posterior probability of each SNP association being a true positive is 90% or 95%, respectively. According to the table, a proper Bayesian thinker should be skeptical only when the prior probability becomes so conservative that the first stage of selecting SNPs on the basis of their being associated with years of schooling is treated as uninformative (π less than 1%).

10. Selection of theory-based candidate SNPs

To select a set of SNPs that would fairly represent those that would be nominated as candidates on theoretical grounds, we required a method of constraining the search. One challenge for candidate-gene approaches is that any of the thousands of genes that are expressed in the central nervous system could be selected as a theoretical candidate for association with cognitive performance. Therefore, we chose to use only SNPs that had at least one published positive association with IQ, *g*, or a measure of general cognitive ability, including higher-order facets of IQ such as verbal or spatial IQ (but *not* episodic memory, working memory, dementia, MMSE, autism, schizophrenia, etc.) in a healthy sample, regardless of whether there are any published negative associations (non-replications), as of May 2013. PubMed was used for the searches, and the results were required to be publications in peer-reviewed journals (not conference abstracts, etc.). This selection method should be biased in favor of "good candidates" in the sense that they are more likely to be true associations than would be a randomly chosen set of common SNPs in central-nervous-system-expressed genes. We excluded SNPs that originated as discoveries in GWAS studies, SNPs that were only significant in association with IQ as large haplotypes, and polymorphisms that are not SNPs. The first exclusion was applied because GWAS-discovered SNPs are not traditional candidates, since they were by definition derived in an atheoretical manner. The latter two were applied so as to restrict our set of theory-based candidates to individual SNPs that could be compared directly to the set of SNPs nominated from the results of the years-of-schooling (proxy phenotype) GWAS. Finally, we confirmed that none of the positive associations reported in the literature for the theory-based SNPs used a cohort included in the Cognitive Performance Sample. Our set of theory-based SNPs is listed in Supplementary Table S3.

(While the SNPs comprising the two-SNP haplotype for *APOE*, rs429358 + rs7412, were retained on our initial list, these SNPs were not available in the cohort GWAS results.)

11. Testing the Q–Q plots for the education-associated and the theory-based candidates

To test whether the Q–Q plot for the education-associated SNPs (Figure 2 in the main text) differs from the null of a uniform distribution, we use as our test statistic

$$Z = \frac{\frac{1}{S}\sum_{s=1}^{S} z_s^2 - 1}{\sqrt{2/S}},$$

where s indexes the $S = 69$ education-associated SNPs, and z_s^2 is the squared z-statistic from the regression of cognitive performance on SNP s. This squared z-statistic captures the strength of the association between cognitive performance and SNP s (while ignoring the sign of the association, which depends on the arbitrary choice of reference allele). Under the null hypothesis, each $z_s \sim N(0,1)$, and thus $z_s^2 \sim \chi^2(1)$, which has mean 1 and variance 2. Therefore, under the null:

$$E(Z) = 0, \mathrm{var}(Z) = \frac{(1/S)^2 S \,\mathrm{var}(z_s^2)}{2/S} = 1.$$

We calculate a p-value for the test of whether the realized value of the test statistic, $Z = z$, differs from zero using the inverse cdf of the standard normal distribution. As reported in the main text, for the education-associated SNPs, we calculate $z = 5.98$, corresponding to p-value $= 1.12\times10^{-9}$.

We test the theory-based SNPs analogously, but with $S = 24$. As reported in the main text, we calculate $z = 1.19$, corresponding to p-value = 0.12.

To calculate the 95% confidence bounds around the null hypothesis shown in Figure 2, we use the fact that the s^{th} order statistic out of S from a Uniform(0,1) random variable has a Beta(s, $S–s+1$) distribution (*33*, p. 230). These confidence bounds differ for the two sets of SNPs because S differs.

12. Biological annotation

In this section, we describe the methods used in our biological annotation analyses. In order to focus on the SNPs most strongly implicated in cognitive performance, we study a subset of the 69 education-associated SNPs described in Supplementary Information section 1. Specifically, we analyze the 14 SNPs that reach a nominal significance level of 5% in the meta-analysis of cognitive performance in the Cognitive Performance Sample. (A more stringent significance threshold would retain too few SNPs for substantial analysis.) Throughout, we refer to these SNPs as the *Nominally-Significant Education-Associated SNPs* (the *NSEA* SNPs).

We conduct five types of analyses. In Subsection A, we examine which non-synonymous coding variants are known to be in strong linkage disequilibrium with the *NSEA* SNPs. In Subsections B and C, we investigate if the *NSEA* SNPs are associated with gene expression levels in, respectively, blood and three distinct brain regions. In Subsection D, to shed light on the biological function of the genes implicated in our analyses, we conduct a gene function prediction analysis. Subsection E, which builds on the analysis from Subsection D, tests whether the loci implicated in our analyses are more enriched for nervous system functioning than SNPs that are similar to our 14 SNPs in terms of minor allele frequency, gene proximity, and gene density, but that are otherwise randomly selected from the GWAS data.

Our analyses here differ in a number of ways from those reported in (1), in which similar biological annotation analyses were conducted in an expanded version of our Education Sample on SNPs reaching $p < 5\times10^{-8}$ (genome-wide significance) or $p < 10^{-5}$ (suggestive significance) for association with educational attainment (with the p-value threshold depending on the biological analysis). First and most importantly, by restricting attention to the *NSEA* SNPs, all of our analyses are based on a set of SNPs for which there is especially strong reason to believe that at least some are related to cognitive performance (as opposed to other endophenotypes that matter for educational attainment). Second, our eQTL look-ups (in Subsections B and C) have substantially more statistical power because our gene-expression databases have larger sample sizes. In particular, the brain sample we work with is four times larger than the one analyzed in (1). Third, the gene-prediction analyses we conduct (in Subsection D) are more expansive. Specifically, our analyses include predictions from mouse models about the phenotypic effects of a gene and inferences about the types of tissue in which the gene is expressed. Finally, we report (in Subsection E) formal tests of the hypothesis that the loci implicated in our analyses are more likely than would be expected by chance for otherwise-similar SNPs to be in the vicinity of genes with neuronal functionality. Such formal tests are novel, as far as we are aware. Subsection F provides a summary of the evidence for biological candidates.

A. Non-Synonymous Variants in Strong LD with Candidate SNPs

We used the software tool HaploReg to identify missense variants in close linkage disequilibrium ($r^2 \geq 0.5$) with at least one of the 14 *NSEA* SNPs. In total we identified 8 such non-synonymous variants in the 1000 Genomes database tagged by 6 *NSEA* SNPs. These 8 variants are within 8 genes: *JMJD1C*, *RECQL4*, *LRRC14*, *SH2B1*, *SDCCAG8*, *DNAJC28*, *GART*, and *SBNO1*. See Supplementary Table S9 for more information about these variants.

B. Blood *cis*-eQTL Lookup

We conducted gene expression analyses from blood using publicly available data (downloadable from http://genenetwork.nl/bloodeqtlbrowser/) from a recently published paper by (27). (27) conducted *cis*-eQTL mapping by testing, for a large set of genes, all SNPs within 250 kb of the transcription start site of the gene for association with total RNA expression level of the gene. The publicly available data contain, for each gene, a list of all SNPs that were found to be significantly associated with gene expression using a False Discovery Rate (FDR) of 5%. For a detailed description of the quality control measures applied to the original data and an overview of the statistical framework, see (27). Their meta-analysis is based on a pooled sample of 5,311 individuals with gene expression levels measured from full blood. We looked up the 14 *NSEA* SNPs in this publicly available data and found 8 that were significantly associated with gene expression levels in a total of 19 different genes and transcripts: *LRRC24*, *GPT*/*PPP1R16A*, *VPS28*, *MFSD3*, *TUFM*, *SPNS1*, *CCDC101*, *SULT1A2*/*SULT1A1*, *LAT*, *SDCCAG8*, *GART*, *ITSN1*, *RILPL2*, *SETD8*, *STK24*, *TANK*, and *PSMD14*. The effect sizes and statistical significance for the *NSEA* SNPs and strongest eQTL signal for each gene are presented in Supplementary Table S10.

C. Brain *cis*-eQTL Lookup

To investigate if any of the *NSEA* SNPs are associated with gene expression levels in human neural tissue, we utilized data from the Harvard Brain Tissue Research Center. The total sample of 742 individuals is comprised of 376 Alzheimer patients, 193 Huntington patients, and 173 individuals without a known neurological disorder. The dataset contains data on expression probes obtained from postmortem brains and measured in three distinct neural regions: prefrontal cortex, visual cortex, and cerebellum (28). The probe data on the Huntington patients have not previously been reported.

The quality control and probe-data normalization steps are each extensive and are described in detail in Zhang et al. After these steps, 39,579 probes were taken forward as dependent variables for subsequent eQTL analysis.

As is standard, we tested the probes for association with all of the SNPs in the GWAS data; below, we report the results from "looking up" our prioritized SNPs in the results. We eliminated SNPs with a minor allele frequency below 0.01, SNPs that failed a test of Hardy-Weinberg equilibrium at a nominal p-value < 10^{-6}, and SNPs with a call rate below 95%. After quality control, 838,958 SNPs remained. We used a Kruskal-Wallis test to test all SNPs within one Mb of the transcription start site of each gene for association with gene expression level of a given probe. We adjusted the resulting p-values to control for testing of many SNPs and probes. To take into account the correlation structures among the probes and among the SNP genotypes, we estimated an empirical FDR: the ratio of the average number of eQTLs found in datasets with randomly permuted sample labels to the number of eQTLs identified in the original data set. Since the number of tests was large, we found that the empirical null distribution converges after a relatively small number of permutation runs; thus, we used ten permutation runs to estimate the empirical FDR. We focus on the associations that survive after constraining the empirical FDR to be less than 10% (which corresponds to a nominal p-value cutoff of approximately 5×10^{-5}).

In the meta-analytic results for the three different brain regions, we looked up a total of 580 SNPs: the original 14 SNPs together with all SNPs in high linkage disequilibrium ($r^2 > 0.5$) with one of these 14 SNPs. We observed 40 significant *cis*-effects for 27 of these 580 SNPs (significant at FDR 10%, as described in the previous paragraph): 13 for prefrontal cortex, 10 for visual cortex, and 15 for cerebellum. These 27 SNPs, which proxy for 6 of the 14 *NSEA* SNPs, regulate gene expression for 18 distinct transcripts (some of which are genes and some of which are non-coding, regulatory RNAs): *LRRC14*, *LRRC24*, *KIFC2*, *AF075035*, *EIF3C*, *LAT*, *NUPR1*, *NFATC2IP*, *TUFM*, *SDCCAG8*, *SBNO1*, *C12ORF65*, *MPHOSPH9*, *TMEM50B*, *GART*, *IFNGR2*, *AK026896*, and *AF33979*. Supplementary Table S11 lists the effect-sizes, p-values, LD metrics, and brain regions.

D. Co-expression-driven Gene Functional Prediction

We used a recently developed method (extensively described and implemented by (29)) to gain insight into the putative functions of the genes in the vicinity of the *NSEA* SNPs. Gene function prediction is based on the idea that genes with shared expression profiles are likely to have related biological functions. For example, if there are 50 genes known to play a role in apoptosis, then a gene with unknown function that is strongly co-expressed with these 50 genes is likely to be part of apoptotic pathways as well. The method described in (29) uses data on co-expression profiles to predict the likely functions of as-of-yet uncharacterized genes and refine our understanding of the function of other genes (achieving this by reconstituting the existing gene sets – described below). In addition to proposing the method, (29) also report evidence that a prediction coming out of the framework was validated by subsequent wet-lab experiments.

To apply the method, we queried the co-expression database described by (29) with our list of genes (our list is explained below). The query for each gene returned the probable function of the gene or the reconstituted pathway in which it operates (more specific details are given below). In the remainder of this paragraph, we briefly summarize the information from which the co-expression database was generated. The database was generated by linking information about gene expression obtained from published data on approximately 80,000 gene expression profiles (from the database Gene Expression Omnibus (GEO) (30), which itself was generated using data from humans, animals, and/or cell lines) with three other distinct types of information:

1. A list of pathways and gene sets that a given gene is believed to be involved in, obtained from the databases: REACTOME pathways (31), Gene Ontology terms (32), and KEGG pathways (33).
2. The phenotypic effects of perturbing the normal functioning of a given gene in mice (e.g., knock-out models, overexpression), obtained from the Mouse Genetics Initiative database (http://www.informatics.jax.org).
3. More than 200 specific tissues, organs, or cell types within which a given gene is highly expressed in the co-expression dataset, for which annotation was obtained from searching the U.S. National Library of Medicine's Medical Subject Headings (MeSH) database (http://www.nlm.nih.gov/mesh/).

(In contrast to the functional prediction analysis that we describe here, the analogous analysis in (1) was conducted at a time when the co-expression database included only information from #1 in the above list.)

In our analyses, we queried a list of 83 genes that were derived from the list of 14 *NSEA* SNPs: we included every gene that is located within 250 kb of the 14 SNPs; and if the SNP is located within a gene desert (defined by having no gene located within 250 kb base pairs of the SNP), we included the nearest gene. Two of the 14 SNPs were located within a gene desert: rs1487441 (nearest annotated gene *POU3F2* is located ~700kb away) and rs1606974 (nearest annotated gene *NRXN1* is located ~600kb away).

Among the 83 genes we queried, we found that 15 genes are in relevant gene sets related to reconstituted pathways and biological functions (for specific predictions, see Supplementary Table S12), 23 genes are predicted to cause relevant neuronal phenotypes in mouse models (for specific predictions, see Supplementary Table S13), and 29 genes are highly expressed in nervous-system-related tissues and cell types (for specific tissues and cell types, see Supplementary Table S14). Given that there is overlap between the genes in these three sets, our co-expression analyses identified 36 genes in total as potential biological candidates for cognitive performance (see Supplementary Table S15 for a list of these genes). (Note that *APOE*, which may be associated with cognitive decline in older individuals (*6*) is *not* among our list of genes. This is perhaps as expected given our results from section 'Polygenic score analyses in the Health and Retirement Study', in which we find that a polygenic score comprised of our educated-associated SNPs is associated with the *level* of cognitive function in older individuals but not with cognitive decline.)

While the full list of all implicated reconstituted pathways is available online at http://www.ssgac.org[1], we conclude our discussion of this analysis by listing the top 5 most frequently occurring search terms from the analysis for each category (with the count given in square brackets) listed in the Supplementary Tables S12, S13 and S14:

1. **Gene Ontology: Biological Processes** – neuron-neuron synaptic transmission [3]; neurotransmitter secretion [3]; regulation of neurotransmitter levels [3]; synaptic transmission, glutamatergic [3]; axonogenesis [2].

2. **Gene Ontology: Cellular Compound** – synapse [6]; dendrite [5]; synapse part [5]; cation channel complex [4]; synaptic membrane [4].

3. **Gene Ontology: Molecular Function** – cation channel activity [5], gated channel activity [5]; voltage-gated cation channel activity [5]; voltage-gated channel activity [5]; voltage-gated ion channel activity [5].

4. **KEGG** – Calcium signaling pathway [4], Neuroactive ligand-receptor interaction [3], axon guidance [2], Long-term potentiation [2].

5. **REACTOME** – Neuronal System [6] Potassium Channels [5]; Transmission across Chemical Synapses [5]; Voltage gated Potassium channels [5]; Ras activation uopn Ca2+ infux through NMDA receptor [4]; Unblocking of NMDA receptor, glutamate binding and activation [4].

6. **Mouse Genome Informatics** – abnormal brain wave pattern [5]; abnormal excitatory postsynaptic currents [5]; abnormal excitatory postsynaptic potential [5]; abnormal inhibitory postsynaptic currents [5]; abnormal CNS synaptic transmission [4].

7. **Site-specific expression** – Prefrontal Cortex [12]; Visual Cortex [12]; Occipital Lobe [12]; Cerebral Cortex [11]; Entorhinal Cortex [11].

E. Evaluating for Enrichment of Genes Related to Neuronal Function

Our prediction analyses showed that all 12 *NSEA* SNPs not located in a gene desert were within 250 kb of at least one gene predicted to be related to neuronal function. While this finding seems impressive, it is well understood that many genes can been linked to neuronal function. It is therefore important to evaluate whether the 12 non-desert *NSEA* SNPs in our analysis are more associated with neuronal function than would be expected by chance. To do so, we calculated an empirical *p*-value using a matching procedure that we describe in this section.

As a first step, for each of the 12 non-desert *NSEA* SNPs, we randomly sampled a vector of 1,000 “matched SNPs” that resembled the *NSEA* SNPs in terms of minor allele frequency, gene density, and distance to nearest gene. For each *NSEA* SNP, we generated the 1,000 matched SNPs using the following algorithm:

1. We identified the set of all SNPs covered by our GWAS data that have a minor allele frequency within 5 percentage points of the given *NSEA* SNP’s minor allele frequency.

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[1] The link will be activated on the day of publication of this article. The materials that will be posted online are included as a separate appendix to the submitted manuscript.

2. We discarded SNPs from this set whose gene density differed from the given *NSEA* SNP's gene density by more than 10%, where "gene density" is defined as the total number of genes containing a SNP that is in LD $r^2 > 0.5$ with the focal SNP.

3. We then further discarded SNPs from the set whose distance to the nearest gene exceeds the given *NSEA* SNP's distance to nearest gene by more than 20 kb.

4. Finally, from the remaining SNPs in the set, we randomly sampled 1,000 of them. (Up to this point in the algorithm, there were always more than 1,000 SNPs remaining in the set.)

As a second step, for each of the 12 *NSEA* SNPs and each of their respective 1,000 matched SNPs, we coded a SNP as either "enriched for neuronal functioning" or "not enriched for neuronal functioning." We did so using a version of the gene function prediction procedure outlined in section 4, but we modified the procedure in two ways. First, to make our definition of "enriched for neuronal functioning" in this analysis more stringent and specific to reconstituted *pathways*, we only used the type of information listed in bullet point #1 from section 4: the pathways and gene sets that a given gene is believed to be involved in. Specifically, we manually annotated *all* of the 6,004 functionality terms from the relevant databases (737 REACTOME pathways, 5,083 Gene Ontology terms, and 184 KEGG pathways), categorizing each as either "related to neuronal function" or "not related to neuronal function" depending on the direct or indirect involvement in the central nervous system via anatomy, cellular structure, or physiological processes (information drawn from published literature). We have posted this annotated list on the following website: http://www.ssgac.org[2]. Second, rather than identifying genes in the vicinity of a SNP as those genes containing a SNP within a window of 250 kb around the focal SNP (as we did in section 4), here we identify genes in the vicinity of a SNP as those genes containing a SNP that is in LD $r^2 > 0.5$ with the focal SNP; this latter definition is generally more stringent and therefore may be considered more appropriate for the kind of enrichment analysis we conduct here. For each gene in the vicinity of one of the *NSEA* SNPs or in the vicinity of one of the matched SNPs, we code the gene as "related to neuronal function" if and only if at least one of its predicted functionality terms is categorized as "related to neuronal function." We then code each *NSEA* SNP as "enriched for neuronal functioning" if and only if at least one of the genes in its vicinity is "related to neuronal function," and we code each of its respective matched SNPs analogously.

In the final step, we tested the null hypothesis that the 12 *NSEA* SNPs are no more "enriched for neuronal functioning" than would be expected by chance. Using the definition of "enriched for neuronal functioning" from the previous paragraph, 10 out of the 12 *NSEA* SNPs are "enriched for neuronal functioning." For comparison, among the 1,000 random matched sets, we observed 88 sets with at least 10 out of 12 SNPs "enriched for neuronal functioning." Hence, the empirical *p*-value is 0.088. While this *p*-value does not reach the standard statistical significance threshold of 0.05, we nonetheless view it as fairly strong evidence in favor of the biological significance of the *NSEA* SNPs: our procedure of matching the SNPs on minor allele frequency, gene density, and distance to nearest gene leads to a very conservative test because if the properties of the *NSEA* SNPs—say, their distance to nearest gene—is typical of functional SNPs, then the SNPs matched to them are also reasonably likely to be functional. Thus, our test does not just require that the *NSEA* SNPs are more likely to be "enriched for neuronal functioning" than any randomly chosen SNPs, but more likely than SNPs that are already chosen to be reasonably likely to be functional.

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[2] The link will be activated on the day of publication of this article. The materials that will be posted online are included as a separate appendix to the submitted manuscript.

(We note that our approach is an improvement compared to current standard practice in enrichment analysis. Instead of investigating only established functions and links to pathways, we apply functional prediction, which extends over known biology and is likely more accurate and stringent. It is not common practice yet to conduct the kind of statistical test that we introduce here, and we suspect that our results are statistically stronger than those that would be obtained from many published findings using related bioinformatics procedures.)

F. Summary of the Evidence for Biological Candidates

In this section we briefly summarize the cumulative evidence arising from our extensive bioinformatics annotation analyses regarding which genes are associated with cognitive performance. In Supplementary Table S15 we outline the positive findings from our 4 different computational approaches (described above), in total 8 distinct categories: (1) non-synonomous variants; (2) blood eQTL; (3) brain eQTL–prefrontal; (4) brain eQTL–visual; (5) brain eQTL–cerebellum; (6) functional prediction–GO, KEGG, REACTOME; (7) functional prediction–mouse phenotypes; and (8) functional prediction–tissue expression. In the last two columns of Supplementary Table S15, we additionally report the results from looking for overlap between our list of 83 genes and the genes implicated in two recent analyses of neural function:

1. (28) report functional modules constructed using brain-derived gene expression profiles from three regions (prefrontal cortex, visual cortex and cerebellum). We looked up which if any of our 83 genes were reported as clustered into any of the 62 network modules containing at least 50 genetic nodes as defined in (28). Here, we find that six of the genes (*POU3F2*, *CPSF1*, *AKT3*, *NMS*, *TMED2* and *TMEM50B)* map to the neuropeptide hormone specific module (Fisher's exact test (FET) enrichment *p*-value = 0.004, analytical framework explained extensively at (28). Furthermore, we combined all neuronal specific modules (synaptic transmission; neurogenesis; neuropeptide hormone and/or nerve myelination) from (28): this approach implicates 12 of the following genes – *POU3F2*, *CPSF1*, *KCNMA1*, *AKT3*, *KIFC2*, *FARP1*, *NMS*, *NRXN1*, *SCRT1*, *TBR1*, *TMED2* and *TMEM50B*, in neuronal-related module functions (FET enrichment *p*-value = 0.015).

2. (34) identifies genes that code for proteins isolated from the postsynaptic density from human neocortex [hPSD]. We looked up which if any of our 83 genes were reported as part of this protein complex. This exercise implicates the following genes: *FARP1*, *ITSN1*, NRXN1, and *TUFM*.

In total we found some supportive evidence for 56 out of the 83 genes. Furthermore, 21 genes were prioritized by at least 3 of the methods, 12 genes by at least 4 methods, and 6 genes by up to 5 methods. These 6 genes that have highly convergent evidence of biological functionality are: *LRRC14*, *KIFC2*, *NRXN1*, *C12ORF65*, *ITSN1* and *TMEM50B*. Furthermore, the results from the above two analyses of blood and brain *cis*-eQTLs indicate that the *NSEA* SNPs or respective proxies affect the gene expression levels of almost half of the 21 top-ranking implicated genes, and hence these analyses may reveal potential regulatory mechanisms. As noted in the main text, in total 4 of the highly prioritised genes (*KCNMA1*, *NRXN1*, *POU3F2*, and *SCRT*) are predicted (in the analysis in the section "Co-expression-driven Gene Functional Prediction" above) to be involved in a particular reconstituted neurotransmitter pathway, labeled in REACTOME as "unblocking of NMDA receptor, glutamate binding and activation."

13. Polygenic score analyses in family samples

A. Results from analyses in family samples

We used a polygenic score to explain cognitive performance in MCTFR, QIMR, STR, and in the additionally recruited cohort Generation Scotland (GS). To construct the weights for the polygenic score used for each of these cohorts, we performed a meta-analysis on cognitive performance, excluding respectively MCTFR, QIMR, STR, and no cohorts (for GS, we use the complete cognitive performance meta-analysis since GS was not included in the meta-analysis). This resulted in a meta-analysis of $N = 20,822$ for MCTFR, $N = 22,437$ for QIMR, $N = 20,974$ for STR, and $N = 24,189$ for GS. We constructed a linear polygenic score by weighting the 69 education-associated SNPs by the coefficient estimates obtained from these meta-analyses (in QIMR, the SNP rs2970992 was excluded because it exhibited a very high number of Mendelian errors and extreme Hardy-Weinberg irregularity: HWE test $p = 1.98\times10^{-17}$). In MCTFR the sample is restricted to 1,346 siblings from 673 families. In QIMR the sample is restricted to 5 siblings from 1 family, 4 siblings from 19 families, 3 siblings from 129 families, and 2 siblings from 479 families, yielding a total of 1469 pseudo-independent siblings. In STR the sample is restricted to 810 DZ twins from 405 distinct families. In GS there are 1,081 siblings from 476 independent families. In each regression the standard errors are clustered (35) at the family level to take into account the non-independence of individuals within a family. The results are reported in Supplementary Table S16. Using both within-family and between-family variation (the top panel: "Without family dummies"), pooling the coefficients across GS, MCTFR, QIMR, and STR with inverse-variance weighting (the right-most column), we find that the score is significantly protectively associated with cognitive performance (p-value = 8.17×10^{-4}). Using only within-family variation (the bottom panel: "With family dummies"), the pooled coefficient has the same sign but is smaller with a larger standard error, and is thus not statistically significant (p-value = 0.36).

B. Power calculations for within-family analysis

In the main text, we claim that "even without stratification, the non-significance of the within-family coefficient is not surprising given the low power of this test." Here we substantiate that claim.

We estimate the power of this analysis by simulation. We assume that cognitive performance Y of sibling i from family j is determined according to the following simple model:

$$Y_{ij} = \beta s_{ij} + z_j + \varepsilon_{ij},$$

where s_{ij} is the polygenic score, z_j is a family effect, and ε_{ij} is the residual from a projection of Y_{ij} on s_{ij} and z_j in the population and is therefore uncorrelated with both by construction. The variables Y_{ij} and s_{ij} are standardized to have mean 0 and variance 1. We assume that $\varepsilon_{ij} \sim N(0,\sigma_\varepsilon^2)$ and that the family effects are distributed normally in the population: $z_j \sim N(0,\sigma_z^2)$. Since we are interested in testing our power to detect a polygenic score effect within families under the assumption that the size of the effect is the same as it is without family effects, we assume that s_{ij} is uncorrelated with z_j.

To match the empirical fact that the correlation of cognitive performance between siblings is about 0.5, we assume that $\sigma_z^2 = \sigma_\varepsilon^2 \equiv \sigma^2$. Now, note that the explanatory power of the polygenic score is given by:

$$R^2 = \frac{\beta^2 \operatorname{var}(s_{ij})}{\beta^2 \operatorname{var}(s_{ij}) + \operatorname{var}(z_j) + \operatorname{var}(\varepsilon_{ij})} = \frac{\beta^2}{\beta^2 + 2\sigma^2}.$$

In the simulations below, we examine two different values for β, 0.045 and 0.065. For each β, the value of σ^2 is set to satisfy $\beta^2 + 2\sigma^2 = 1$ (which ensures that Y_{ij} has variance 1 and that $R^2 = \beta^2$). Given this, the two values of β correspond to R^2 equal to 0.20% and 0.42%, respectively, which roughly correspond to the lower and upper end of the range of R^2's we estimate for the score across samples (in Table S16).

For each assumed true value of β, we conduct 500 simulation runs. In each run, we generate data as follows for a sample of 2,182 families that matches the data used in our estimation: 1,950 two-sibling families, 181 three-sibling families, 42 four-sibling families, 4 five-sibling families, 3 six-sibling families, and 2 seven-sibling families. We generate SNP-level data for the parents by assuming that the allele frequency for 69 SNPs matches the empirical frequency measured in our data, that parental genotypes are drawn independently, and that all SNPs are in Hardy-Weinberg equilibrium. Children are then simulated by drawing one allele from each parent with equal probability. The weights to calculate the score are drawn from a normal distribution (with mean 0 and variance scaled such that s_{ij} has variance 1). This data-generating process produces scores that have a within-family correlation of 0.5.

Given the data in each run, we estimate β in two regressions. In the first, we regress Y_{ij} on s_{ij} (i.e., we not include family dummies as covariates); this is the "Without family dummies" model in table S17 discussed below. In the second, we regress Y_{ij} on s_{ij} and z_j; this is the "With family dummies" model in table S17 discussed below. Note that in the second model, we are estimating the family effect as a fixed effect (even though we model it as a random effect, which is normally distributed, for the purpose of doing the power calculation) because in the analysis of the actual data we estimate the family effect as a fixed effect. In both regressions, we take into account the non-independence of individuals within a family by clustering standard errors within family (35), just as we do in the analysis of the actual data.

We estimate power as the fraction of the 500 runs in which we reject the null hypothesis $\beta = 0$ with a p-value less than 0.05. Table S17 shows the average regression output over the 500 simulations for the two different values of β, 0.045 and 0.065.

As can be seen in table S17, power is much higher in the model estimated without family dummies; it is very nearly 80% even at the lower end of the range of R^2's. With family dummies, however, the range of R^2's corresponds to power between 31.2% and 64.2%. Thus, our power to detect a significant effect in the within-family analysis is relatively low even if the true effect size is at the upper end of our range of estimates.

14. Polygenic score analyses in the Health and Retirement Study

A. HRS data description

The Health and Retirement Study (HRS; (36)) is a representative sample of Americans over the age of 50 who have been surveyed every two years since 1992. The survey data from all 10 waves of the study are publicly available. The total sample size of the HRS is 30,671, including respondents who entered the sample in wave 1, replenishment samples who entered in subsequent waves, and spouses of respondents. However, for all analyses using the HRS described in this section and elsewhere in this paper, the sample is restricted to genotyped individuals from European ancestry (*N* = 8,652). Because testing individual SNPs in a sample of this size would have low power, we instead analyze a polygenic score.

To combine the education-associated SNPs into a linear polygenic score that exploits their joint explanatory power, we generated a linear combination of the SNPs' number of reference alleles, weighted by their coefficient estimates from the GWAS meta-analysis of years-of-schooling (as in (37)). In particular, we use the results from the meta-analysis that excludes the HRS; this meta-analysis is described in section 1 above. We construct the score in the HRS using the 60 out of 69 education-associated candidate SNPs available in the imputed genotype data.

We obtained the cognitive measures from the HRS datafile as prepared by RAND (RAND v.L, available at http://hrsonline.isr.umich.edu). This datafile contains cognitive scores harmonized across all waves of the study in which the data were collected. We use the two summary cognitive-health measures that are available in more than one wave: Total Word Recall (TWR) and Total Mental Status (TMS). TWR is the sum of scores on immediate and delayed word-recall tasks. In each task, the recall list contains 10 words, and scores ranged from 0-20. TMS is a dementia battery. It is the sum of scores for the following tasks: serial 7's (repeatedly subtracting the number 7), backwards counting from 20, and naming objects, the current date, and the current President and Vice-President. The resulting range is 0-15. Because these batteries focus on identifying cognitive problems and early signs of dementia (rather than measuring cognitive ability among healthy individuals), the resulting variables are viewed as measures of cognitive health (for discussion, see (38) p.10, which is posted online as part of the HRS data documentation: http://hrsonline.isr.umich.edu/sitedocs/dmc/Lachman_hrscognitive.pdf). Below, we also report results for Total Cognition (TC), which is the sum of TWR and TMS, resulting in a range of 0-35. Consistent measures for TWR, TMS, and TC are available in wave 3-9.

Prior to wave 4, all cognitive tests were administered to all respondents. Starting in wave 4, all cognitive tests were administered to new respondents, but for those who had participated in a prior wave, the respondent's age determined which cognitive measures were administered. Respondents 65 years or older received the full set of cognitive tests. Respondents under 65 received the full TWR battery but only two of the tasks comprising TMS (serial 7's and backwards counting from 20). For this reason, we have more observations for the TWR measure than for the TMS and TC measures.

B. HRS regression results

For each of the cognitive measures—TWR, TMS, and TC—we run two sets of regressions: one in which the dependent variable is the cognitive measure itself (the "levels" regressions), and one in which the dependent variable is the difference between the cognitive measure in the current wave and the previous wave (the "changes" regressions). All dependent variables are standardized to have mean 0 and standard deviation 1. In all analyses we control for gender and an age spline. Knots of the age spline are at 60, 70, and 80, except for the changes regressions for TMS and TC, in which the knots are at 70 and 80 because there are only 9 respondent-wave observations with age < 60. We exclude these nine observations from the analysis. For each dependent variable we run two regression specifications. The first includes as a regressor (in addition to gender and the age spline) the polygenic score, and the second additionally includes as regressors the interactions of the polygenic score with the age spline. Because the data include observations from the same respondent in multiple waves, we cluster the standard errors (35) at the respondent level.

Supplementary Table S18 displays the regression results, with each column representing a different regression specification. The odd-numbered columns include only controls for sex and an age spline, while the even-numbered columns additionally control for interactions between the score and the age spline. For each column, the "ΔR^2" row shows the increase from including the score variables (either just the score, or the score and its interactions, depending on the specification) in the regression.

In the levels regressions (columns 1-6), the increasingly negative coefficients on the age spline indicate that cognitive performance is decreasing with age, as expected. The coefficients on the indicator for being female show that females on average have higher scores in TWR and lower scores on TMS, with the net effect on TC being higher scores. Turning to the main coefficient of interest, in all of the levels regressions a higher value for the score is associated with a higher level of cognitive performance. In terms of magnitude, a one standard-deviation increase in the score is associated with approximately a 0.04 increase in TWR, a 0.06 increase in TMS, and a 0.06 increase in TC.

In the levels regressions that include an interaction between the score and the age spline (columns 2, 4, and 6), we find that the effect of the score is approximately unaffected by age, except possibly for the age category ≥80, where there appears to be some reduction in the magnitude of the protective effect of the score (but statistically significantly only for TWR). This pattern is consistent with the results shown in Figure 3 in the main text.

In the changes regressions (columns 7-12), the negative coefficients on the age spline again reflect that cognitive performance is decreasing with age, and indeed at an increasing rate. The negative coefficient on the indicator for being female in the ΔTMS regressions suggests that the decline is slower for females for this measure, but the coefficients are not statistically distinguishable from zero for the other measures. The coefficient on the score is not significantly distinguishable from zero for any of the measures in the changes regressions. Thus, even though the score is associated with a higher *level* of cognitive performance, it does not appear to be protective against *declines* in cognitive performance.

In the changes regressions that include an interaction between the score and the age spline (columns 8, 10, and 12), we again find a negative coefficient for the age category ≥80 (statistically significant for ΔTWR and ΔTC). This negative coefficient means that cognitive performance declines more quickly for those respondents over the age of 80 who have higher values of the score—and hence had higher cognitive performance on average at younger ages. This negative coefficient in the changes regressions is thus consistent with the negative coefficient on the analogous interaction term in the levels regressions.

To probe the robustness of the results to population stratification, we repeated the levels regressions for TWR, TMS, and TC, omitting the interaction between the polygenic score and the age spline as a regressor, and instead including different numbers of principal components of the genome-wide data. For each dependent variable, 20 additional regressions are performed, in which principal components are iteratively added. Supplementary Figure S4 shows how the coefficients for the polygenic score change as principal components are added. The coefficients for the polygenic score may decline slightly as principal components are added, but the decline is very small, and the coefficients with 20 principal components and essentially the same as those without any principal components. Thus, we find no evidence that population stratification is driving the HRS results.

Table S19 presents the same analyses as those in Table S18, however, in these analyses years of education (0-17+) is added as control variable to the model. There is a slight decrease in sample size, because years of education is missing for a few individuals. In the levels regressions (columns 1-6), the coefficient for the polygenic score remains statistically significant, but the magnitude of the coefficient is about half as large as when educational attainment is not included as a control, and ΔR^2 is much smaller. In the changes regressions (columns 7-12), the polygenic score is not statistically significant.

C. HRS sign tests on the education-associated SNPs

We also tested whether the direction of the SNPs' effects on educational attainment generally coincide with the direction of their effects on cognitive performance. For each of the three dependent variables, we ran 60 regressions, using the 60 out of 69 SNPs available in the HRS data as regressors instead of the polygenic score in regression specifications (2), (4), and (6) from Table S18. For each SNP, we compared the sign of the SNP's coefficient with the sign of the same SNP's coefficient from the meta-analysis of educational attainment that excludes the HRS. We computed the *p*-value using a binomial distribution with probability 50% of matching the sign. The resulting *p*-values are: 0.0067 for TWR (39 out of 60 SNPs with identical sign), 0.0775 for TMS (35 out of 60 SNPs with identical sign), and 0.0775 for TC (35 out of 60 SNPs with identical sign).

15. Statistical Framework for the Proxy-Phenotype Method as Applied to Cognitive Performance

A. Statistical power of GWAS vs. candidate-SNP (including proxy-phenotype) method for gene discovery

Consider the problem of estimating the association between a phenotype of interest Y, say cognitive performance, and the genotype g_k of each of $k = 1, 2, \ldots, K$ SNPs. The standard approach is to estimate K separate linear regressions of Y on each g_k. After standardizing Y and g_k so that each has mean 0 and variance 1, the regression equations to be estimated can be written as

(1) $Y = \beta_k g_k + \varepsilon_k$,

for $k = 1, 2, \ldots, K$. (For simplicity, we omit the covariates, which would typically include age, sex, and possibly principal components of genetic data, and to avoid cluttering notation, we suppress indexing variables by individual.) Because Y and g_k are standardized, in a large sample the estimated regression coefficient β_k is equal to the correlation between Y and g_k, and the coefficient of determination is $R^2{}_{Y,g_k} = \beta_k^2$.

In terms of statistical power, the key difference between a GWAS approach to gene discovery and a candidate-SNP approach is the size and composition of the set of K SNPs. In GWAS, the set includes all SNPs measured by the dense SNP genotyping platform (typically 0.5-2.5 million). The statistical significance threshold is set at the "genome-wide significance" level of $\alpha = 5\times10^{-8}$, which can be interpreted as a Bonferroni correction for the effective number of independent loci in European populations (25, 39). In contrast, in a candidate-SNP approach—either theory-based or proxy-phenotype-based—K is a much smaller number of SNPs that the researcher considers to be reasonable candidates for association with the phenotype. In a theory-based method, the candidates are chosen on the basis of what is known or believed about their biological function, while in a proxy-phenotype method, the candidates are chosen on the basis of their association with a proxy phenotype. Either way, in terms of statistical power, the advantage of a candidate-SNP approach is that the Bonferroni-corrected significance threshold can be set at the much less stringent level of $\alpha = 0.05 / K$. The potential disadvantage is that the effect sizes of the most strongly associated SNPs in a candidate-SNP approach may be smaller than in a GWAS, since the method of choosing the candidates may not succeed in selecting those that are most strongly associated with the phenotype of interest.

Table S20 calculates power for GWAS vs. candidate-SNP methods of gene discovery that could be pursued in our Cognitive Performance Sample of size $N = 24{,}189$. The columns show different effect sizes for a SNP: $R^2 \in \{0.02\%, 0.04\%, 0.06\%, 0.08\%\}$, a range from the size of our estimated winner's-curse-adjusted effect size for cognitive performance of $R^2 \approx 0.02\%$ up to four times that size. The top row shows statistical power to detect each of these effect sizes at the genome-wide significance threshold, $\alpha = 5\times10^{-8}$. The bottom row shows statistical power to detect each of these effect sizes at the experiment-wide significance threshold for 69 SNPs, $\alpha = 0.05 / 69 \approx 0.00072$.

As explained in the next subsection below, our calculations prior to the study (based on the results of Rietveld et al., (1)) led us to expect an effect size of $R^2 \approx 0.08\%$ for the strongest associations in our set of proxy-based candidate SNPs. In that case, our power to detect such associations would have been 85%. In contrast, a direct GWAS on cognitive performance in our Cognitive Performance Sample would have had power of 15% to detect these SNPs. Given our estimated winner's-curse-adjusted effect size for cognitive performance of $R^2 \approx 0.02\%$, our actual power to detect the largest associations we found was 12%–which in turn suggests that there are roughly 8 times as many SNPs with the same effect sizes as the 3 significant SNPs we identified (since 1/0.12 = 8.33). A direct GWAS on cognitive performance in our sample would have had power of only 0.06% to detect these SNPs. Therefore, even if there are 25 SNPs with associations of magnitude $R^2 \approx 0.02\%$ with cognitive performance, a GWAS with the available sample size would very likely not have detected any of them.

B. Statistical power of proxy-phenotype method under plausible effect sizes for cognitive performance

Prior to conducting this study, we calculated expected effect sizes using the formal framework introduced by Rietveld et al. (1) (SOM pp. 22-27) and the results reported in that paper. Here we sketch a slightly simplified version of that framework (also note that our notation here differs somewhat). Let $s = 1, \ldots, S$ index the SNPs that are causally related to cognitive performance or any other genetically-influenced factor that matters for educational attainment.

We assume that cognitive performance is a simple linear function of the individual's genotype and determined by:

$$(2) Y = \sum_{s=1}^{S} \beta_{Y,s} g_s + \varepsilon_Y ,$$

where g_s is the individual's genotype at SNP *s* (as above, normalized to have mean zero and variance one), $\beta_{Y,s}$ is the effect of g_s on *Y*, and ε_Y is a random variable with mean zero that we assume is independent of the g_s's. The error term ε_Y captures all other factors besides the SNPs, including exogenous environmental factors, that affect cognitive performance.

We assume that the proxy phenotype *P*, in this context educational attainment, is determined by a simple linear function of cognitive performance and other factors:

$$(3) P = \gamma_Y Y + \gamma_X X + \varepsilon_P .$$

X captures genetically-influenced factors that affect educational attainment, including personality traits (such as perseverance) and early-life health conditions. The error term ε_P captures all other factors, including exogenous environmental factors that affect *P*. We assume that ε_P is a random variable with mean zero and is independent of *Y* and *X*. We normalize *P*, *Y*, and *X* so that they have mean zero and variance one (hence regression coefficients are equal to partial correlation coefficients). Without loss of generality, we assume that both *Y* and *X* are oriented in the direction that increases educational attainment: $\gamma_Y > 0$ and $\gamma_X > 0$.

To complete the model, we write *X* as an analogous linear function of the individual's genotype:

$$(4) X = \sum_{s=1}^{S} \beta_{X,s} g_s + \varepsilon_X ,$$

where $\beta_{X,s}$ is the partial correlation coefficient of g_s with *X*, and ε_X is a random variable with mean zero that we assume is independent of the g_s's. Now, educational attainment *P* can be expressed as a function of the SNP genotypes by substituting equations (2) and (4) into equation (3):

$$(5) P = \sum_{s=1}^{S} (\gamma_Y \beta_{Y,s} + \gamma_X \beta_{X,s}) g_s + (\gamma_Y \varepsilon_Y + \gamma_X \varepsilon_X + \varepsilon_P) = \sum_{s=1}^{S} \delta_s g_s + u_Y ,$$

where $\delta_s \equiv (\gamma_Y \beta_{Y,s} + \gamma_X \beta_{X,s})$ is the effect of SNP *s* on educational attainment, and $u_Y \equiv \gamma_Y \varepsilon_Y + \gamma_X \varepsilon_X + \varepsilon_P$ is a mean-zero composite error term that is independent of the g_s's. Note that a GWAS of educational attainment *P* estimates the δ_s's in equation (5). Note that if $\delta_s \neq 0$, then either $\beta_{Y,s} \neq 0$ or $\beta_{X.s} \neq 0$ or both. Therefore, if the GWAS of *P* credibly identifies a SNP, then that SNP can serve as a plausible "candidate SNP" for genetically influenced factors that matter for *P*.

To generate a first-pass estimate of the effect size of SNPs associated with cognitive performance, we begin with the special case in which genetic factors matter for educational attainment exclusively through cognitive performance: $\gamma_X = 0$. In that case, $\delta_s = \gamma_Y \beta_{Y,s}$. Rearranging, the R^2 from a regression of cognitive performance on SNP *s* is equal to the R^2 from a regression of educational attainment on SNP *s* is divided by the squared phenotypic correlation: $\beta_{Y,s}^2 = \delta_s^2 / \gamma_Y^2$. The largest SNP effects on educational attainment are likely to have a coefficient of determination of roughly 0.0003 (see Table S20), and since $\gamma_X = 0$, these same SNPs will be the ones with the largest effects on cognitive performance. Using $\delta_s^2 \approx$ 0.0003 and an estimated phenotypic correlation of γ_Y = 0.6 (40, 41) gives $\beta_{Y,s}^2 \approx$ 0.0008 (our reading of the evidence is that estimates of the phenotypic correlation have generally been in the range 0.4-0.6; our high-end estimate of the correlation yields a lower, and hence more conservative, estimate of the SNP effect size). As mentioned in the previous subsection, this was our best guess of the effect size before we conducted our study and was the basis of our ex ante power calculations. Although we anticipated that the largest SNP effects on cognitive performance would have $\beta_{Y,s}^2 \approx$ 0.0008, what we found was $\beta_{Y,s}^2$ = 0.0006, which became $\beta_{Y,s}^2$ = 0.0002 after correction for the winner's curse (Table S7).

The more realistic case where $\gamma_X > 0$ opens up the possibility that the SNPs most strongly associated with cognitive performance are not the same SNPs as those most strongly associated with educational attainment. To see this, note that since $\delta_s = \gamma_Y \beta_{Y,s} + \gamma_X \beta_{X,s}$, the SNPs with the largest effect on educational attainment—those most likely to be picked out from a GWAS of educational attainment as candidate SNPs—will tend to be those for which *both* $\beta_{Y,s}$ and $\beta_{X,s}$ are positive and large in magnitude. Rietveld et al. use the term "mono-directional" to refer to such a SNP: a SNP that has pleiotropic effects on *Y* and *X* such that it affects *P* in the same direction through both pathways. A SNP has a stronger association with educational attainment than it does with cognitive performance if $\delta_s > \beta_{Y,s}$.

C. Explaining the negative correlation between coefficients for educational attainment and cognitive performance

As noted in the main text, Figure 1 shows a negative correlation between the coefficients on educational attainment and the coefficients on cognitive performance. Also as mentioned in the text, this negative correlation seems somewhat robust to dropping the most conspicuous possible outlier, although we view the evidence for negative correlation as relatively weak. Here we note that according to the framework developed in this section, a negative correlation between δ_s and $\beta_{Y,s}$ implies that $\beta_{Y,s}$ and $\beta_{X,s}$ are negatively correlated. In words, SNPs that affect cognitive performance more strongly tend to affect other factors that matter for educational attainment (such as personality traits) less strongly, and vice-versa.

D. Relating the genetic correlation between educational attainment and cognitive performance to the above framework

According to the framework above, a GWAS of educational attainment (EA) generates good candidate SNPs for cognitive performance (CP) because CP is an important causal factor in determining EA. Moreover, if CP is the primary genetically-influenced factor that matters for EA ($\gamma_X \approx 0$), then the effect size of the SNPs on CP is expected to be larger when the phenotypic correlation between EA and CP (γ_Y) is *smaller*, because the smaller phenotypic correlation means that the effect of the SNP on EA is more attenuated relative to its more direct and larger effect on CP.

Intuitively, it might seem that the *genetic* correlation between EA and CP would be at least as relevant as the phenotypic correlation. In this subsection, we address the relevance of the genetic correlation within the context of our formal framework; we conclude that the high genetic correlation can be viewed as providing a justification for using EA as a proxy phenotype for EA, but the argument is somewhat loose.

What *can* be shown formally and straighforwardly is that the statistical power of the proxy-phenotype approach is increasing in $\mathrm{corr}(\delta_s, \beta_{Y,s})$. The assumption that CP is the only genetically-influenced factor that matters for EA ($\gamma_X = 0$) implies that $\mathrm{corr}(\delta_s, \beta_{Y,s}) = 1$. If other genetically-influenced factors also matter for EA ($\gamma_X > 0$), then $\mathrm{corr}(\delta_s, \beta_{Y,s})$ can be smaller than 1, and the SNPs with the largest effects on EA may not be those with the largest effects on CP.

The genetic correlation is a different object: $\mathrm{corr}\left(\sum_{s=1}^{S} \delta_s g_s, \sum_{s=1}^{S} \beta_{Y,s} g_s\right)$. In words, the genetic correlation is the correlation between the population polygenic score for EA and the population polygenic score for CP. It follows from this definition that if the genetic correlation is high, a polygenic score estimated from EA is likely to explain more of the variance in CP. However, the genetic correlation does not have direct implications about the statistical power for identifying individual SNPs unless the (unconditional) genetic correlation is equal to the genetic correlation *conditional* on including only the SNPs with largest effect sizes in the polygenic score. The evidence discussed in subsection C above casts some doubt on this assumption. Therefore, while in general we view the high genetic correlation between EA and CP as supportive of our use of EA as a proxy phenotype, we view our overall framework as providing a more solid justification.

E. Setting the *p*-value threshold for the proxy-based SNPs

The power calculations in Table S21 take as given the fact that we included 69 SNPs in the set of proxy-based candidates. We used 69 SNPs because this is the number that passed our inclusion threshold of $p < 10^{-5}$ from the first-stage GWAS on educational attainment. In this subsection, we explain why we chose this particular inclusion threshold.

We chose our inclusion threshold of $p < 10^{-5}$ prior to conducting any analyses on cognitive performance, on the basis of power calculations using the results from the first-stage GWAS on educational attainment. Our goal was to design the study in a way that would maximize the expected number of true positive results in the second stage analyses on cognitive performance. The optimal threshold trades off between two opposing effects. On the one hand, a less stringent threshold yields a larger number of candidates that are forwarded to the second stage. A larger set of candidates is more likely to contain true positives. On the other hand, a larger number of candidates requires that a more stringent experiment-wide significance level needs to be applied in the second stage to adjust for multiple testing, which decreases power to pick out the true positives from among the set of candidates.

Our calculations are reported in Table S21. Row (1) reports the number of LD-pruned SNPs in the first stage GWAS on EA that passed the *p*-value threshold of the respective column. Row (2) is the observed average R^2 of these SNPs on EA. The R^2 estimates deviate slightly from those reported in (1) due to the slightly different set of subjects that were included in the two analyses. The ex-post power (i.e., assuming that the observed average R^2 is the true effect size) to find such an effect size in our EA sample is reported in row (3), again always for the *p*-value threshold of the respective column. Row (4) reports the posterior belief that a randomly chosen SNP from the set included in the column is truly associated with EA. To calculate this value, we used Bayes' formula, with a conservative prior belief equal to 0.01%, power equal to row (3), and α equal to the respective *p*-value threshold of the column (see Section 9 for the formula we use, as well as a discussion of why we consider the larger prior belief of 0.02% to be quite conservative).

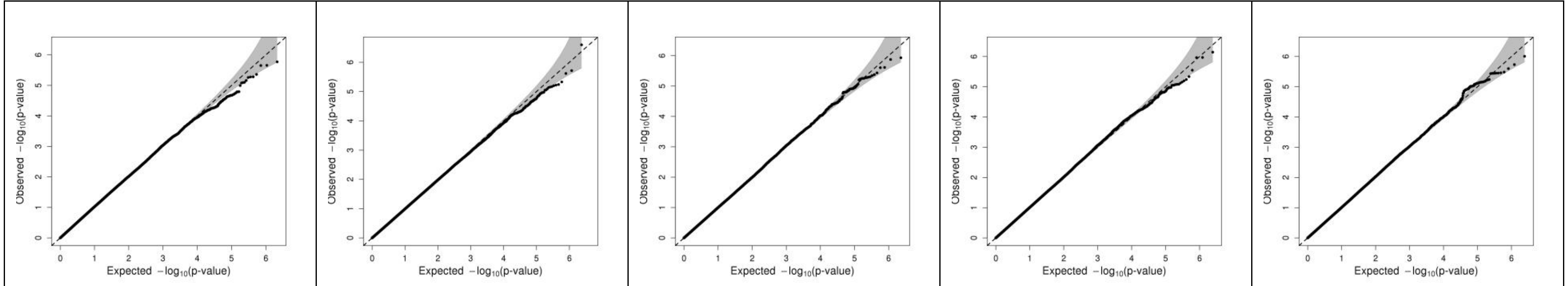
Row (5) reports the Bonferroni-adjusted *p*-value threshold for stage 2, given a family-wide significance level of 0.05 and the number of independent hypotheses that will be tested, given by row (1). Row (6) uses the statistical proxy-phenotype framework reported above to calculate the expected average R^2 of SNPs in the second stage on CP. We assumed a phenotypic correlation of 0.6 between EA and CP, and we assumed that the selected SNPs influence EA only through their influence on CP. Row (7) calculates the expected power for a two-sided test given the available sample size in the second stage on CP, as well as the *p*-value threshold given by row (5) and the expected effect size given by row (6).

Row (8) reports the expected number of true positive SNPs that would be discovered in the study overall, given by multiplying the number of candidate SNPs given by row (1), the posterior belief that these candidates are truly associated with EA (row 4), and the expected power of stage 2 (row 7). The choice of the *p*-value threshold we have chosen for our study ($p < 10^{-5}$) was given by the column that maximized the value of row (8). The optimal *p*-value threshold turns out to depend only on the results of the first-stage GWAS on EA, and not on our assumptions about prior beliefs, phenotypic correlation, or available sample size in stage 2. These assumptions influence the absolute magnitudes in row (8) but not their relative magnitudes.

Finally, row (9) reports the expected posterior belief that a SNP associated with CP at the Bonferroni-adjusted *p*-value is truly associated with CP, using Bayes' formula, prior beliefs equal to row (4) and power equal to row (7). These calculations were included with the analysis plan that was forwarded to cohorts participating in early 2013. The analysis plan was also posted on Open Science Framework on 14 Apr 2013 (see https://osf.io/z7fe2/).

Supplementary Figures

Figure S1. Quantile-Quantile plots and Genomic Control λ for the summary results of the five GWA studies after quality control.



ERF, λ = 1.039

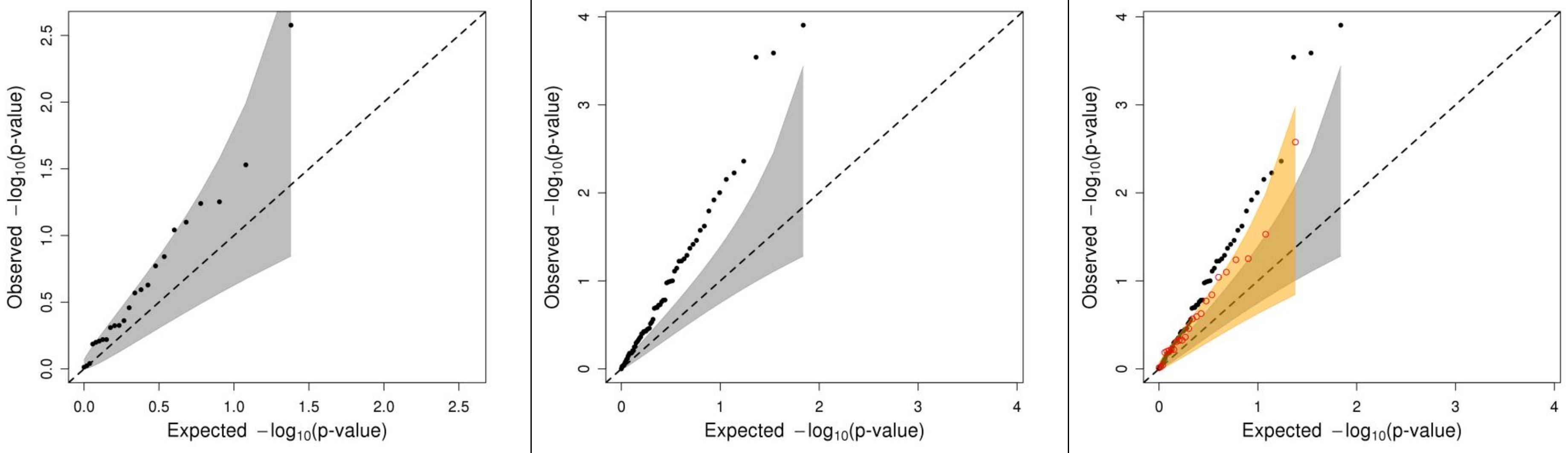
GenR, λ = 0.975

HU, λ = 1.001

MCTFR, λ = 1.006

STR, λ = 1.015

Figure S2. Quantile-Quantile plots of the cognitive performance meta-analysis results for the theory-based and education-associated candidate SNPs. The joint plots show in black the QQ-plot for the education-associated candidate SNPs, and in red the theory-based candidate SNPs.



Theory-based candidate SNPs

Education-associated candidate SNPs

Joint plot

Figure S3. Simulation study of winner's curse corrections: MLE versus diffuse-prior Bayesian. The *x*-axis is the true effect size β, grouped in bins that are 0.002 standard-deviation units wide. The *y*-axis is the estimated effect size. The dots show the naïve OLS estimate (red), the MLE-corrected effect size estimate (green), and the Bayesian-corrected effect size estimate (blue). The light dotted lines are 95% confidence intervals around the estimates. For the simulation parameters, see section 8.

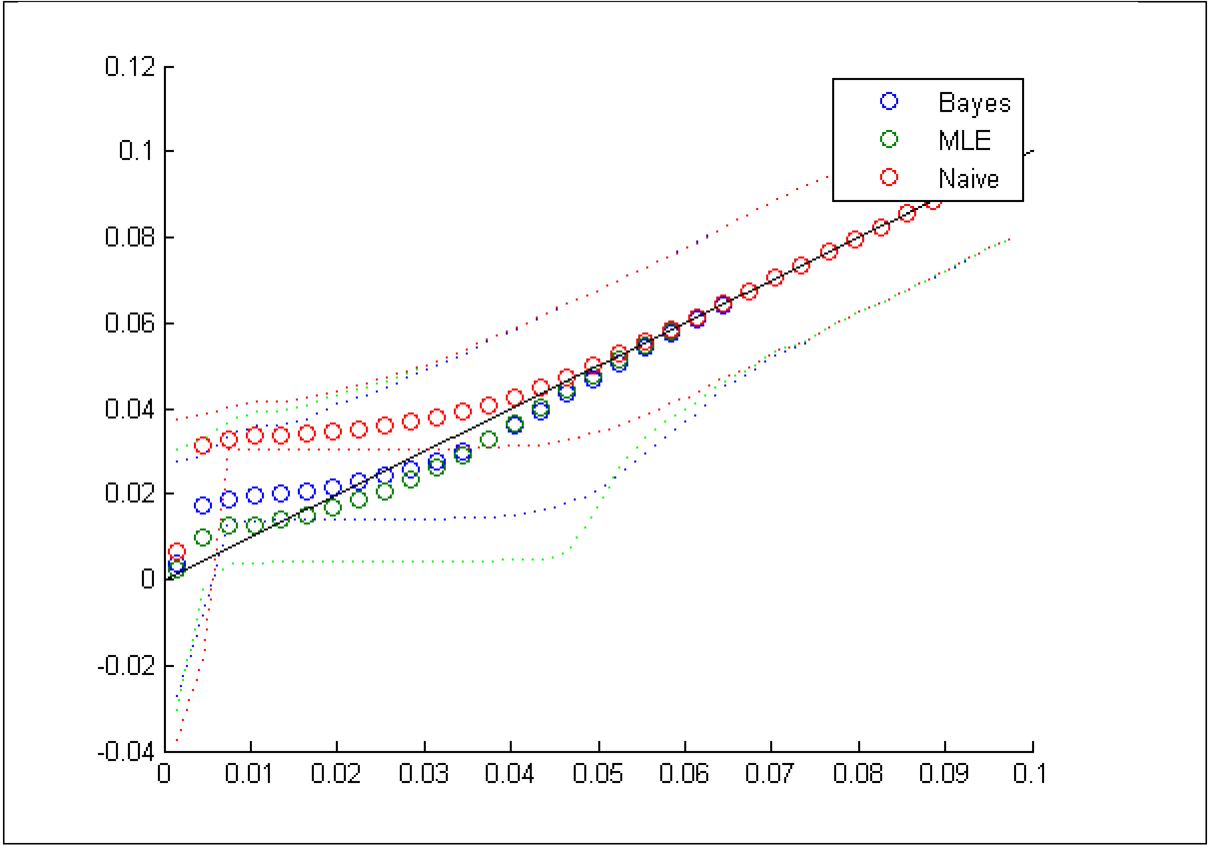
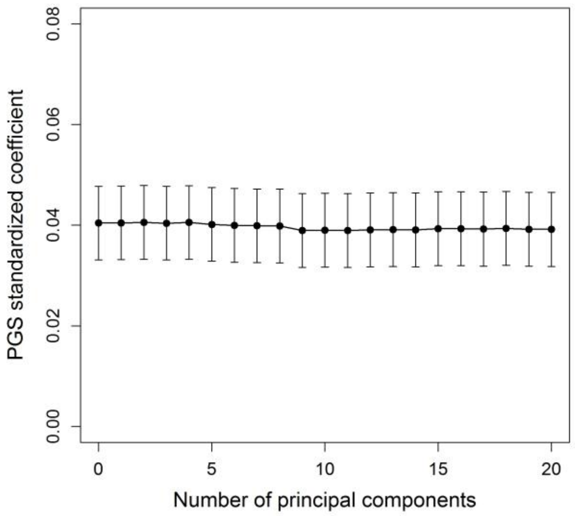
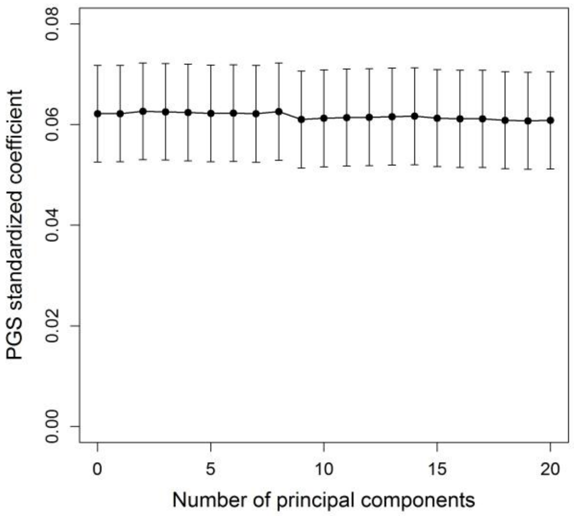
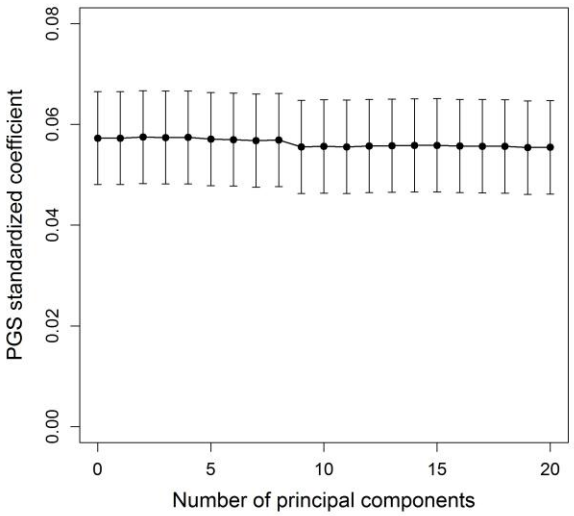


Figure S4. Coefficient on the polygenic score in the regressions explaining the level of TWR, TMS, and TC and controlling for an increasing number of principal components. TWR = Total Word Recall, TMS = Total Mental Score.

		
TWR	TMS	TC

Supplementary Tables

Table S1. Study design, numbers of individuals, and quality control for GWAS cohorts. "Call rate" refers to the genotyping success rate, i.e., the minimum percentage of successfully genotyped SNPs.

Study				Sample QC			
Short name	Full name	Study design	Total sample size (*N*)	Call rate	Other exclusions	Sample in analysis (*N*)	References
ALSPAC	Avon Longitudinal Study of Parents and Children	Prospective pregnancy cohort	8,340	≥97%	1) Gender mismatches 2) Minimal or excessive heterozygosity 3) Cryptic relatedness (IBD > 0.1 and IBD < 0.8) 4) Non-European ancestry 5) Missing cognitive performance phenotype	5,517	(42)
ERF	Erasmus Rucphen Family study	Family-based	3,658	≥95%	1) Failing IBS checks 2) Sex chromosome checks 3) Ethnic outliers removed 4) Age < 45 years 5) Missing cognitive performance phenotype	1,076	(43)
GenR	Generation R	Birth-cohort	6,135	≥97.5%	1) Duplicate samples 2) Gender mismatch 3) Relatedness 4) Missing cognitive performance phenotype	3,701	(44)
GS	Generation Scotland	Family-based	10,000	≥98%	1) Sample call rate 0.95 2) SNPs diverging from HWE with a significance $p<1\times10^{-3}$ 3) SNPs with a MAF <0.01 4) Missing cognitive performance phenotype 5) Only siblings	1,081	(45)
HU	Harvard/Union Study	Population-based	415	≥93%	1) Ethnic outliers removed 2) Participants more than 6 SD away from any of the top 10 principal components	389	(46)

					3) Missing cognitive performance phenotype		
LBC1921	Lothian Birth Cohort 1921	Population-based birth-cohort	517	≥95%	1) Unresolved gender discrepancy 2) Relatedness 3) Non-Caucasian descent 4) Missing cognitive performance phenotype	464	(47)
LBC1936	Lothian Birth Cohort 1936	Population-based birth-cohort	1,005	≥95%	1) Unresolved gender discrepancy 2) Relatedness 3) Non-Caucasian descent 4) Missing cognitive performance phenotype	947	(48)
MCTFR	Minnesota Center For Twin and Family Research	Family-based	7,438	≥99%	1) >5000 uncalled SNPs 2) Low GenCall score 3) Extreme hetero- or homozygosity 4) Sample mix-up or unable to confirm known genetic relationships 5) Missing cognitive performance phenotype	3,367	(49)
QIMR	Brisbane Adolescent Twin Study, Queensland Institute of Medical Research	Population-based	3,899	≥95%	1) Non-European ancestry 2) Missing cognitive performance phenotype	1,752	(50)
Raine	Western Australian Pregnancy Cohort Study	Prospective pregnancy cohort	1,593	≥97%	1) Gender mismacht 2) Relatedness 3) Low heterozygosity 4) Missing cognitive performance phentoype	936	(51)
STR	Swedish Twin Registry	Family-based	9,836	≥97%	1) Sex-check (heterozygosity of X-chomosomes) 2) Deviations in heterozygosity of more then 5 SD from the population mean 3) Cryptic relatedness check 4) Missing cognitive performance phenotype	3,215	(52)
TEDS	Twins of Early Development Study	Family-based	3,747	Exact percentage unknown (done by	1) Low call rate 2) Heterozygosity outliers 3) Intensity outliers 4) Ancestry outliers	2,825	(53)

external genotyping center)	5) Relatedness/duplicates 6) Gender mismatches 7) Samples were re-genotyped on a panel of 30 SNPs using Sequenom and were excluded because of low concordance (<90%). 8) Missing cognitive performance phenotype

Table S2. Information on genotyping methods, imputation, and assocation analysis.

Study	Genotyping platform	Genotyping calling algorithm	Imputation software	Imputation reference dataset	Association software
ALSPAC	Illumina HumanHap550	GenomeStudio	MACH	HapMap 2 CEU	Mach2QTL
ERF	Illumina 318K, Affymetrix 250K, Illumina 350K, Illumina 610K	GenCall & BRLMM	MACH/Minimac	1000Genomes I v3 (GIANT)	ProbABEL
GenR	Illumina 610K Quad, 660W Quad	GenomeStudio	MACH	HapMap2	PLINK
GS	Illumina HumanOmniExpressExome-8 v1.0	GenomeStudio	MACH	HapMap 2 CEU	N.A.
HU	Affymetrix 6.0	Birdseed	MACH	HapMap2	PLINK
LBC1921	Illumina Human610_Quadv1	GenomeStudio	MACH	HapMap 2 CEU	Mach2QTL
LBC1936	Illumina Human610_Quadv1	GenomeStudio	MACH	HapMap 2 CEU	Mach2QTL
MCTFR	Illumina 660W Quad	BeadStudio	Minimac	HapMap2 CEU	RFGLS (R)
QIMR	Illumina 610, Illumina 370, Illumina 317	BeadStudio	MACH	HapMap 2 CEU	Merlin
Raine	Illumina Human660W	BeadStudio	MACH	HapMap 2 CEU	Mach2QTL
STR	Illumina HumanOmniExpress-12v1_A	GenomeStudio	IMPUTE	HapMap2 CEU	Merlin-offline
TEDS	Affymetrix GeneChip 6.0	Affymetrix Genotyping Console	IMPUTE2	HapMap 2/3 CEU	SNPTEST

Table S3. Results for the theory-based candidate SNPs; SNPs are ordered according to their *p*-value in the cognitive performance meta-analysis. The chromosome and basepair position are from the NCBI genome annotation (build 36). The frequency of the coded allele is from the cognitive performance meta-analysis.

						Years of Education		Cognitive Performance	
SNP ID	Chromosome	Basepair	Coded allele	Non-coded allele	Frequency coded allele	Beta coeff. (standardized)	*p*-value	Beta coeff. (standardized)	*p*-value
rs1042713	5	148186633	a	g	0.380	-0.004	4.05×10^{-1}	0.029	2.65×10^{-3}
rs1800497	11	112776038	a	g	0.201	-0.004	5.16×10^{-1}	-0.025	2.95×10^{-2}
rs2830102	21	26456898	t	c	0.314	-0.005	2.62×10^{-1}	0.021	5.59×10^{-2}
rs1612902	19	56191007	t	c	0.566	0.008	7.60×10^{-2}	-0.020	5.75×10^{-2}
rs2274185	1	158587804	c	g	0.942	-0.001	8.94×10^{-1}	0.037	7.95×10^{-2}
rs2251621	8	31007504	a	g	0.041	0.010	3.83×10^{-1}	-0.052	9.09×10^{-2}
rs1799990	20	4628251	a	g	0.636	0.011	2.16×10^{-2}	0.015	1.44×10^{-1}
rs4680	22	18331271	a	g	0.522	-0.002	6.10×10^{-1}	0.013	1.69×10^{-1}
rs1800855	4	26100215	a	t	0.785	-0.007	2.07×10^{-1}	-0.016	2.35×10^{-1}
rs8191992	7	136351848	a	t	0.542	0.001	7.93×10^{-1}	-0.012	2.55×10^{-1}
rs237895	3	8782423	t	c	0.394	0.006	2.41×10^{-1}	-0.012	2.70×10^{-1}
rs714939	2	75688615	a	g	0.385	-0.006	1.56×10^{-1}	0.009	3.48×10^{-1}
rs821616	1	230211221	a	t	0.719	0.010	4.71×10^{-2}	0.008	4.35×10^{-1}
rs6489630	12	5474885	t	c	0.191	0.000	9.40×10^{-1}	0.009	4.72×10^{-1}
rs1130214	14	104330779	a	c	0.297	-	-	0.008	4.74×10^{-1}
rs2725385	8	31047688	t	c	0.291	-0.015	1.33×10^{-3}	-0.007	4.90×10^{-1}
rs2760118	6	24611569	t	c	0.349	-0.003	5.61×10^{-1}	0.005	6.03×10^{-1}
rs9536314	13	32526138	t	g	0.844	-0.009	1.41×10^{-1}	0.007	6.03×10^{-1}
rs363043	20	10174146	t	c	0.294	-0.002	6.33×10^{-1}	0.005	6.19×10^{-1}
rs17571	11	1739170	a	g	0.081	-0.015	5.80×10^{-2}	0.009	6.32×10^{-1}
rs760761	6	15759111	a	g	0.212	-0.003	5.56×10^{-1}	0.006	6.51×10^{-1}
rs12239747	1	158587689	a	g	0.939	-0.005	6.61×10^{-1}	0.002	9.11×10^{-1}
rs6265	11	27636492	t	c	0.186	0.010	7.65×10^{-2}	-0.001	9.48×10^{-1}
rs16944	2	113311338	a	g	0.347	-0.003	5.43×10^{-1}	0.000	9.71×10^{-1}

Table S4. Results for the education-associated candidate SNPs; SNPs are ordered according to their *p*-value in the cognitive performance meta-analysis. The chromosome and basepair position are from the NCBI genome annotation (build 36). The frequency of the coded allele is from the cognitive performance meta-analysis.

						Years of Education		Cognitive performance	
SNP ID	Chromosome	Basepair	Coded allele	Non-coded allele	Frequency coded allele	Beta coeff. (standardized)	*p*-value	Beta coeff. (standardized)	*p*-value
rs1487441	6	98660615	a	g	0.473	0.026	1.78×10^{-9}	0.036	1.24×10^{-4}
rs7923609	10	64803828	a	g	0.521	-0.021	1.06×10^{-6}	-0.034	2.58×10^{-4}
rs2721173	8	145715237	t	c	0.473	-0.020	8.61×10^{-6}	-0.034	2.88×10^{-4}
rs8049439	16	28745016	t	c	0.595	0.021	1.48×10^{-6}	0.027	4.36×10^{-3}
rs1606974	2	51727103	a	g	0.124	0.031	5.39×10^{-6}	0.042	5.93×10^{-3}
rs2970992	2	100688741	a	c	0.493	-0.020	8.27×10^{-6}	-0.025	7.03×10^{-3}
rs3127447	10	78923267	a	c	0.529	0.020	6.21×10^{-6}	0.024	9.95×10^{-3}
rs7847231	9	117248892	a	c	0.620	-0.020	6.73×10^{-6}	-0.024	1.20×10^{-2}
rs4658552	1	241479559	t	c	0.632	0.021	2.01×10^{-6}	0.023	1.61×10^{-2}
rs1892700	21	33938007	a	g	0.256	-0.023	2.96×10^{-6}	-0.024	2.39×10^{-2}
rs7980687	12	122388664	a	g	0.200	0.029	7.14×10^{-8}	0.028	2.66×10^{-2}
rs1187220	18	33605724	t	c	0.323	-0.024	3.48×10^{-7}	-0.027	3.47×10^{-2}
rs3783006	13	97909210	c	g	0.457	0.023	3.11×10^{-7}	0.022	3.84×10^{-2}
rs7309	2	161800886	a	g	0.491	-0.022	2.21×10^{-7}	-0.019	4.26×10^{-2}
rs10166311	2	162575859	a	g	0.326	0.023	9.50×10^{-7}	0.019	5.13×10^{-2}
rs3789044	1	202855724	a	g	0.219	0.028	5.44×10^{-8}	0.022	5.62×10^{-2}
rs2635047	18	42990334	t	c	0.483	0.020	5.76×10^{-6}	0.019	5.94×10^{-2}
rs17176043	14	36064553	a	g	0.946	0.043	7.17×10^{-6}	-0.045	5.98×10^{-2}
rs1198575	1	98334848	t	c	0.189	-0.026	2.37×10^{-6}	-0.025	7.17×10^{-2}
rs889956	2	57258338	a	g	0.397	-0.023	1.52×10^{-7}	-0.017	7.76×10^{-2}
rs7594192	2	199159337	a	g	0.250	0.026	1.28×10^{-7}	0.018	9.98×10^{-2}
rs3753275	1	8348487	t	c	0.824	-0.030	3.97×10^{-7}	-0.020	1.01×10^{-1}
rs9289301	3	128627683	c	g	0.155	0.031	7.77×10^{-7}	0.024	1.03×10^{-1}
rs9858213	3	49706865	t	g	0.288	0.028	4.85×10^{-9}	0.018	1.05×10^{-1}
rs11191193	10	103792398	a	g	0.653	0.023	5.65×10^{-7}	0.014	1.65×10^{-1}
rs6732189	2	161281027	a	g	0.526	-0.023	8.44×10^{-8}	0.013	1.66×10^{-1}
rs4073894	7	104254200	a	g	0.202	0.024	9.32×10^{-6}	0.017	1.73×10^{-1}
rs2066955	12	80614747	a	c	0.237	0.023	4.77×10^{-6}	0.015	1.87×10^{-1}
rs2966	6	33797498	t	c	0.452	0.022	3.60×10^{-7}	-0.012	1.89×10^{-1}
rs188133	15	45489734	a	g	0.683	-0.021	9.29×10^{-6}	-0.013	2.01×10^{-1}
rs11742741	5	24198698	a	t	0.515	-0.022	2.61×10^{-7}	-0.012	2.02×10^{-1}
rs10783779	12	54778147	t	g	0.607	-0.021	6.25×10^{-6}	-0.012	2.05×10^{-1}
rs4468007	9	123634160	t	c	0.554	0.021	3.38×10^{-6}	0.011	2.74×10^{-1}

rs9940536	16	77713418	t	c	0.321	0.022	3.47×10^{-6}	0.011	2.94×10^{-1}
rs3731896	2	219854646	t	c	0.174	0.029	5.21×10^{-6}	-0.013	3.06×10^{-1}
rs1970584	9	125150127	a	c	0.060	0.048	4.64×10^{-7}	-0.021	3.45×10^{-1}
rs6712515	2	100172946	t	c	0.471	-0.026	2.21×10^{-9}	-0.009	3.51×10^{-1}
rs1478110	9	1711478	t	c	0.480	-0.023	3.54×10^{-7}	-0.011	3.59×10^{-1}
rs1239771	18	75666608	t	c	0.218	0.024	9.54×10^{-6}	0.011	3.72×10^{-1}
rs12640626	4	176863266	a	g	0.570	0.022	7.63×10^{-7}	0.009	3.75×10^{-1}
rs2955259	4	171110419	a	g	0.569	0.024	7.04×10^{-8}	0.009	3.77×10^{-1}
rs2053831	14	84049789	a	g	0.776	0.023	8.35×10^{-6}	-0.010	3.94×10^{-1}
rs7788657	7	13888666	t	c	0.436	0.056	8.78×10^{-7}	0.018	4.86×10^{-1}
rs4451621	10	12471373	t	c	0.536	-0.023	9.73×10^{-7}	0.008	4.37×10^{-1}
rs1056667	6	26618543	t	c	0.628	0.023	5.25×10^{-7}	0.007	4.45×10^{-1}
rs10028773	4	120484707	c	g	0.675	0.020	7.45×10^{-6}	0.007	4.63×10^{-1}
rs1360382	9	23369719	a	g	0.042	-0.024	3.41×10^{-7}	-0.007	4.81×10^{-1}
rs17013497	1	207061559	t	c	0.135	0.030	6.78×10^{-6}	0.010	4.95×10^{-1}
rs6984449	8	19372239	a	g	0.601	0.022	1.40×10^{-6}	-0.006	5.09×10^{-1}
rs6882046	5	88004620	a	g	0.727	-0.024	8.63×10^{-7}	-0.006	5.57×10^{-1}
rs10519388	5	113879949	t	c	0.835	-0.029	5.21×10^{-7}	0.007	5.64×10^{-1}
rs362987	20	10225452	a	c	0.522	0.020	7.80×10^{-6}	0.005	6.19×10^{-1}
rs9537938	13	57551696	a	g	0.672	0.023	4.85×10^{-7}	-0.005	6.21×10^{-1}
rs7729356	5	107425114	a	c	0.341	0.021	3.53×10^{-6}	-0.004	6.55×10^{-1}
rs11590526	1	116229090	t	c	0.077	-0.039	8.50×10^{-6}	0.008	6.63×10^{-1}
rs1875714	8	68590101	t	c	0.628	0.022	2.07×10^{-6}	0.004	6.63×10^{-1}
rs12075	1	157441978	a	g	0.577	-0.022	1.33×10^{-6}	-0.004	6.64×10^{-1}
rs1105881	15	39859822	c	g	0.643	0.020	6.67×10^{-6}	0.004	6.92×10^{-1}
rs10904180	10	4127661	t	g	0.820	0.026	8.00×10^{-6}	0.005	7.18×10^{-1}
rs13401104	2	236770257	a	g	0.176	-0.032	2.74×10^{-8}	-0.004	7.67×10^{-1}
rs4818225	21	41551765	a	g	0.338	0.021	5.61×10^{-6}	0.003	7.79×10^{-1}
rs334147	2	127972527	t	g	0.929	-0.046	8.67×10^{-6}	-0.005	8.16×10^{-1}
rs6025281	20	54994407	t	c	0.566	-0.021	1.75×10^{-6}	-0.002	8.36×10^{-1}
rs10500871	11	20172332	t	c	0.322	-0.022	3.31×10^{-6}	-0.002	8.73×10^{-1}
rs1995082	16	75564938	t	g	0.865	-0.029	1.97×10^{-6}	-0.002	9.12×10^{-1}
rs247929	12	44581175	c	g	0.513	-0.020	8.36×10^{-6}	0.001	9.13×10^{-1}
rs12134600	1	72408584	a	c	0.116	0.038	6.18×10^{-8}	-0.001	9.38×10^{-1}
rs1550582	8	135611266	a	g	0.262	0.022	7.16×10^{-6}	-0.001	9.38×10^{-1}
rs2930713	9	7639442	t	g	0.523	0.021	2.47×10^{-6}	0.000	9.97×10^{-1}

Table S5. Winner's curse corrections (MLE and Bayesian) applied to Rietveld et al.'s (2013) SNPs associated with educational attainment at the genome-wide significance threshold ($p < 5\times10^{-8}$). Standard errors are reported in parentheses.

SNP	Discovery-stage estimates			Replication- stage estimates
	Naïve (Uncorrected)	MLE Corrected	Bayesian (diffuse) Corrected	
rs9320913	0.106 (0.018)	0.070	0.065	0.077 (0.034)
rs11584700	-0.014 (0.002)	-0.011	-0.009	-0.016 (0.005)
rs4851266	0.012 (0.002)	0.009	0.008	0.011 (0.004)

Table S6. Winner’s curse corrections (MLE and Bayesian) applied to Rietveld et al.’s (1) SNPs associated with educational attainment at a suggestive significance threshold ($p < 10^{-6}$). The SNPs are listed in the same order as in (1) Table 1 (the first four in order of increasing *p*-value for association with years of schooling, and the last six in order of increasing *p*-value for association with college completion). SNPs rs9320913, rs11584700, and rs4851266 are also listed in Supplementary Table S5 above (though the corrected estimates here are different because the significance threshold is different). Standard errors are reported in parentheses.

SNP	Discovery-stage estimates			Replication- stage estimates
	Naïve (Uncorrected)	MLE Corrected	Bayesian (diffuse) Corrected	
rs9320913	0.106 (0.018)	0.096	0.087	0.077 (0.034)
rs3783006	0.096 (0.018)	0.035	0.050	0.056 (0.035)
rs8049439	0.090 (0.018)	0.008	0.039	0.065 (0.033)
rs13188378	-0.136 (0.027)	-0.011	-0.058	0.091 (0.067)
rs11584700	-0.014 (0.002)	-0.013	-0.012	-0.016 (0.005)
rs4851266	0.012 (0.002)	0.011	0.010	0.011 (0.004)
rs2054125	0.023 (0.004)	0.011	0.010	0.006 (0.008)
rs3227	0.011 (0.002)	0.008	0.007	0.002 (0.004)
rs4073894	0.012 (0.002)	0.008	0.006	0.000 (0.005)
rs12640626	0.010 (0.002)	0.001 0.096	0.005	0.000 (0.004)

Table S7. Winner's curse corrections (MLE, Bayesian, and empirical Bayes) applied to the cognitive-performance associations that pass the significance threshold ($p < .05/69$). Standard errors are reported in parentheses. Since the phenotypic variance has been normalized to 1, the estimated R^2 is calculated simply as the amount of phenotypic variance explained: $R^2 = 2m(1-m)\beta^2$, where m is the MAF and β is the effect size estimate.

SNP	Effect size estimates				Estimated R^2	
	Naïve (Uncorrected)	MLE Corrected	Bayesian (diffuse) Corrected	Empirical Bayes Corrected	Naïve (Uncorrected)	Empirical Bayes Corrected
rs1487441	0.036 (0.009)	0.022	0.023	0.023	0.064%	0.027%
rs7923609	-0.034 (0.009)	-0.013	-0.020	-0.020	0.058%	0.019%
rs2721173	-0.034 (0.009)	-0.008	-0.019	-0.018	0.056%	0.017%

Table S8. Posterior probability of true association as a function of effect size (R^2) and prior probability (π).

		Effect size (R^2)	
		$R^2 = 0.0002$ (power = .1186)	$R^2 = 0.0006$ (power = .6658)
Prior (π)	0.1%	14%	48%
	1%	62%	90%
	5%	90%	98%
	10%	95%	99%

Table S9. Results for the functional annotation analysis for the 14 *NSEA* SNPs and respective proxies at consderable LD ($r^2 > 0.5$).

SNP ID	Proxy SNP	LD	Coded Allele	Non-coded allele	Minor allele freqency	Gene name	Sequence change	Amino acid change
rs7923609	rs1935	0.75	c	g	0.47	*JMJD1C*	GA**G** ⇒ GA**C**	E [Glu] ⇒ D [Asp]
rs2721173	rs4251691	0.9	c	t	0.46	*RECQL4*	C**G**G ⇒ C**A**G	R [Arg] ⇒ Q [Gln]
	rs13277542	0.8	t	g	0.47	*LRRC14*	G**A**A ⇒ G**C**A	E [Glu] ⇒ A [Ala]
rs8049439	rs7498665	0.69	a	g	0.34	*SH2B1*	**A**CA ⇒ **G**CA	T [Thr] ⇒ A [Ala]
rs4658552	rs2275155	0.64	a	t	0.33	*SDCCAG8*	GA**A** ⇒ GA**T**	E [Glu] ⇒ D [Asp]
rs1892700	rs139852262	0.55	caatta	c	0.25	*DNAJC28*		Frameshift
	rs8971	0.58	t	c	0.25	*GART*	G**A**T ⇒ G**G**T	D [Asp] ⇒ G [Gly]
rs7980687	rs1060105	0.95	c	t	0.23	*SBNO1*	A**G**T ⇒ A**A**T	S [Ser] ⇒ N [Asn]

Table S10. Results for the gene expression *cis*-eQTL analysis in blood. SNP ID – nominally significant cognitive performance associated variant; FDR – false discovery rate; LD – linkage disequilibrium; ArrayID – Illumina probe identifier; * – denotes a probe not annotated; NSEA - *Nominally-Significant Education-Associated SNPs*: Best eQTL-SNP – the strongest eQTL SNP for a given probe.

		NSEA			*Best eQTL-SNP*					
SNP ID	Coded Allele	eQTL *p*-vaule	Zscore	FDR (5%)	SNP ID	eQTL *p*-vaule	Zscore	FDR (5%)	Gene name	ArrayID
rs7923609	a	3.4×10^{-5}	4.1	6.1×10^{-4}	rs10761725	4.1×10^{-7}	5.1	5.7×10^{-6}	*	1850242
rs2721173	t	2.1×10^{-27}	-24.0	$<<1.0\times10^{-7}$	rs6989368	7.2×10^{-132}	-24.4	$<<1.0\times10^{-7}$	*LRRC24*	2810687
		1.2×10^{-48}	-14.7	$<<1.0\times10^{-7}$	rs750472	1.6×10^{-56}	-15.8	$<<1.0\times10^{-7}$	*GPT/ PPP1R16A*	3140408
		3.4×10^{-27}	-10.8	$<<1.0\times10^{-7}$	rs3735840	9.8×10^{-198}	34.4	$<<1.0\times10^{-7}$	*VPS28*	1190110
		1.0×10^{-14}	7.7	$<<1.0\times10^{-7}$	rs3757966	7.5×10^{-15}	7.8	$<<1.0\times10^{-7}$	*MFSD3*	1510703
rs8049439	c	9.8×10^{-198}	57.7	$<<1.0\times10^{-7}$	rs8049439	9.8×10^{-198}	57.7	$<<1.0\times10^{-7}$	*TUFM*	6370097
		9.8×10^{-198}	35.6	$<<1.0\times10^{-7}$	rs8045689	$9.8^{-}\times10^{198}$	50.8	$<<1.0\times10^{-7}$	*SPNS1*	1230192
		2.1×10^{-49}	-14.8	$<<1.0\times10^{-7}$	rs480400	1.9×10^{-84}	19.5	$<<1.0\times10^{-7}$	*CCDC101*	1240113
		1.2×10^{-4}	3.8	2.0×10^{-3}	rs13331691	1.4×10^{-7}	5.3	2.5×10^{-6}	*SULT1A2/ SULT1A1*	7510711
		2.5×10^{-3}	3.0	0.03	rs4788115	1.6×10^{-5}	-4.3	2.8×10^{-4}	*LAT*	3610288
		2.9×10^{-3}	3.0	0.04	rs4788115	1.2×10^{-8}	-5.7	$<<1.0\times10^{-7}$	*LAT*	460259
rs4658552	c	3.1×10^{-17}	8.4	$<<1.0\times10^{-7}$	rs2275155	3.2×10^{-21}	9.5	$<<1.0\times10^{-7}$	*SDCCAG8*	460458
rs7980687	a	1.1×10^{-5}	-4.4	1.8×10^{-4}	rs1662	4.7×10^{-93}	20.5	$<<1.0\times10^{-7}$	*RILPL2*	1660286
		4.3×10^{-4}	3.2	6.5×10^{-3}	rs12366872	3.4×10^{-17}	8.4	$<<1.0\times10^{-7}$	*SETD8*	2350735
rs1892700	a	2.8×10^{-36}	12.4	$<<1.0\times10^{-7}$	rs2834217	9.8×10^{-198}	-34.8	$<<1.0\times10^{-7}$	*	4480647
		1.3×10^{-13}	-7.4	$<<1.0\times10^{-7}$	rs12626309	1.7×10^{-21}	-9.5	$<<1.0\times10^{-7}$	*GART*	20544
		4.8×10^{-10}	6.2	$<<1.0\times10^{-7}$	rs2251854	1.8×10^{-102}	-21.5	$<<1.0\times10^{-7}$	*ITSN1*	2507
		2.1×10^{-5}	4.3	3.7×10^{-4}	rs2834237	5.0×10^{-7}	5.0	6.5×10^{-6}	*GART*	3780435
rs3783006	c	6.0×10^{-6}	4.5	1.0×10^{-4}	rs4389009	$1.7^{-}\times10^{-40}$	-13.3	$<<1.0\times10^{-7}$	*STK24*	6180050
		1.4×10^{-3}	3.2	0.02	rs9513427	9.7×10^{-6}	4.4	1.7×10^{-4}	*STK24*	4480373
rs7309	a	5.8×10^{-10}	-6.2	$<<1.0\times10^{-7}$	rs1921310	1.8×10^{-13}	-7.4	$<<1.0\times10^{-7}$	*TANK*	2230113
		3.2×10^{-4}	-3.6	4.9×10^{-3}	rs11884495	2.0×10^{-4}	-3.7	0.003	*PSMD14*	2600025

Table S11. Results for the gene expression *cis*-eQTL analysis in brain tissues. SNP ID – nominally significant cognitive performance associated variant; FDR – false discovery rate; LD – linkage disequilibrium; DistanceArrayID – Affimetrix probe identifier; # – genes not considered as biological candidates in subsequent analysis due to distance > 250 kb from a *NSEA* SNP.

SNP ID	Proxy SNP	LD (r^2)	Distance (kb)	Brain tissue	eQTL *P*-vaule	Gene name	ArrayID
rs2721173	rs9071	1.00	6 077	Prefrontal cortex	1.3×10^{-89}	*LRRC14*	10025908411
	rs9071	1.00	6 077	Cerebellum	1.3×10^{-75}	*LRRC14*	10025908411
	rs9071	1.00	6 077	Visual cortex	1.5×10^{-62}	*LRRC14*	10025908411
	rs4532636	0.67	159 994	Prefrontal cortex	8.4×10^{-35}	*LRRC14*	10025908411
	rs4532636	0.67	159 994	Cerebellum	1.2×10^{-28}	*LRRC14*	10025908411
	rs4532636	0.67	159 994	Visual cortex	1.2×10^{-22}	*LRRC14*	10025908411
	rs748193	0.84	62 314	Cerebellum	4.3×10^{-7}	*LRRC24*	10023828992
	rs2721195	0.87	67 418	Cerebellum	4.8×10^{-6}	*LRRC24*	10031920304
	rs3757966	0.97	189	Prefrontal cortex	1.3×10^{-8}	*KIFC2*	10025905398
	rs3757936	0.67	159 994	Cerebellum	1.3×10^{-8}	*KIFC2*	10025905398
	rs2958492	0.65	174 698	Visual cortex	2.3×10^{-6}	*AF075035*	10025934744
rs8049439	rs4788102	0.97	35 883	Prefrontal cortex	1.7×10^{-13}	*EIF3C*	10025912109
	rs12928404	0.97	9 731	Prefrontal cortex	9.7×10^{-12}	*EIF3C*	10025912109
	rs4788102	0.97	35 883	Cerebellum	5.4×10^{-18}	*EIF3C*	10025912109
	rs12928404	0.97	9 731	Cerebellum	7.6×10^{-11}	*EIF3C*	10025912109
	rs4788102	0.97	35 883	Visual cortex	1.2×10^{-9}	*EIF3C*	10025912109
	rs12928404	0.97	9 731	Visual cortex	7.6×10^{-11}	*EIF3C*	10025912109
	rs6565259	0.68	61 278	Prefrontal cortex	8.0×10^{-10}	*LAT*	10023818276
	rs12928404	0.97	9 731	Prefrontal cortex	1.3×10^{-5}	*LAT*	10023818276
	rs1968752	0.80	205 930	Cerebellum	3.5×10^{-5}	*NUPR1*	10023813116
	rs12446550	0.76	294 134	Cerebellum	1.4×10^{-8}	*NFATC2IP*	10025913085
	rs8049439	–	–	Prefrontal cortex	2.3×10^{-5}	*TUFM*	10025905429
rs4658552	rs10926978	0.86	18 718	Prefrontal cortex	5.1×10^{-9}	*SDCCAG8*	10025912019
	rs2484639	0.54	49 431	Visual cortex	3.2×10^{-7}	*SDCCAG8*	10025912019
	rs10926975	0.56	15 154	Visual cortex	1.0×10^{-5}	*SDCCAG8*	10025912019
	rs10926975	0.56	15 154	Prefrontal cortex	1.0×10^{-5}	*SDCCAG8*	10025912019
rs7980687	rs7304782	0.57	103 267	Prefrontal cortex	1.1×10^{-8}	*SBNO1*	10025903955
	rs1727302	0.81	189 781	Prefrontal cortex	2.0×10^{-6}	*SBNO1*	10025903955

	rs655293	0.74	294 306	Cerebellum	5.6×10^{-10}	*C12ORF65*	10025904993
	rs1060105	0.94	164 920	Cerebellum	1.5×10^{-7}	*C12ORF65*	10025904993
	rs1060105	0.94	164 920	Visual cortex	5.8×10^{-7}	*C12ORF65*	10025904993
	rs7304782	0.69	103 267	Visual cortex	2.4×10^{-6}	*C12ORF65*	10025904993
	rs1790098	0.80	167 230	Prefrontal cortex	2.9×10^{-8}	*C12ORF65*	10025904993
	rs1060105	0.94	164 920	Prefrontal cortex	1.1×10^{-6}	*C12ORF65*	10025904993
	rs937564[#]	0.70	345 400	Cerebellum	1.5×10^{-7}	*MPHOSPH9*[#]	10025905642
rs1892700	rs9647066	0.84	13 801	Prefrontal cortex	1.3×10^{-6}	*TMEM50B*	10023807235
	rs8971	0.77	132 519	Cerebellum	7.7×10^{-5}	*GART*	10025903876
	rs2834213	0.66	223 227	Cerebellum	2.8×10^{-7}	*IFNGR2*	10025902355
rs3783006	rs9517337	0.59	70 438	Cerebellum	2.1×10^{-5}	*AK026896*	10025930847
	rs7338549	0.64	31 536	Visual cortex	2.6×10^{-5}	*AF339799*	10025928383

Table S12. Results of gene function prediction analysis in 80,000 gene expression profiles. Pathway terms originate from several databases: (1) Gene Ontology Biological Processes [GO-BioProc], (2) Gene Ontology Molecular Function [GO-MolFunc], (3) Gene Ontology Cellular Component [GO-CellComp], (4) REACTOME, and (5) KEGG. Table lists only genes with terms directly related to neuronal or central nervous system function – full predictions are available at – http://www.ssgac.org[3]. *P*-values refer to the correlation between the Gene principal component profile and the reconstituted Term principal component profile, uncorrected for multiple testing; all reported terms meet False Discovery Rate < 0.05. The Annotated column indicates if the gene has previously been listed as a member of that term (Y) or not (N). Results are sorted alphabetically by gene name.

Gene name	Database	Pathway term	Annotated	*P*-value
ATXN2L	GO-CellComp	npBAF complex	N	1.4×10^{-8}
ATXN2L	GO-CellComp	nBAF complex	N	3.0×10^{-7}
ATXN2L	GO-CellComp	chromatin remodeling complex	N	7.0×10^{-7}
ATXN2L	GO-CellComp	SWI/SNF-type complex	N	1.4×10^{-6}
ATXN2L	GO-CellComp	SWI/SNF complex	N	4.7×10^{-6}
CRYZL1	GO-BiolProc	synaptic vesicle endocytosis	N	9.1×10^{-9}
FARP1	GO-BiolProc	Axonogenesis	N	8.0×10^{-10}
FARP1	GO-BiolProc	axon guidance	N	2.0×10^{-9}
FARP1	GO-CellComp	Actomyosin	N	1.1×10^{-8}
FARP1	GO-CellComp	Synapse	N	2.0×10^{-8}
FARP1	KEGG	Axon guidance	N	5.6×10^{-4}
FARP1	REACTOME	Cell-extracellular matrix interactions	N	1.8×10^{-8}
FARP1	REACTOME	Axon guidance	N	5.9×10^{-8}
KCNMA1	GO-BiolProc	calcium ion transmembrane transport	N	2.8×10^{-12}
KCNMA1	GO-BiolProc	calcium ion transport	N	2.6×10^{-6}
KCNMA1	GO-BiolProc	synapse organization	N	3.9×10^{-6}
KCNMA1	GO-CellComp	Synapse	Y	1.4×10^{-6}
KCNMA1	GO-CellComp	synapse part	Y	2.8×10^{-6}
KCNMA1	GO-CellComp	Costamere	N	3.0×10^{-6}
KCNMA1	GO-CellComp	voltage-gated calcium channel complex	N	8.8×10^{-6}
KCNMA1	GO-CellComp	calcium channel complex	N	1.3×10^{-6}
KCNMA1	GO-CellComp	postsynaptic density	N	3.1×10^{-5}

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[3] The link will be activated on the day of publication of this article. The materials that will be posted online are included as a separate appendix to the submitted manuscript.

KCNMA1	GO-CellComp	dendritic spine head	N	3.1×10^{-5}
KCNMA1	GO-CellComp	Dendrite	N	4.0×10^{-5}
KCNMA1	GO-CellComp	neuron projection terminus	Y	4.7×10^{-5}
KCNMA1	GO-MolFunc	calcium channel activity	N	2.5×10^{-9}
KCNMA1	GO-MolFunc	voltage-gated calcium channel activity	N	1.1×10^{-8}
KCNMA1	GO-MolFunc	cation channel activity	Y	1.6×10^{-8}
KCNMA1	GO-MolFunc	voltage-gated cation channel activity	Y	5.6×10^{-8}
KCNMA1	GO-MolFunc	gated channel activity	Y	5.6×10^{-7}
KCNMA1	GO-MolFunc	solute:cation antiporter activity	N	7.4×10^{-7}
KCNMA1	GO-MolFunc	ion channel activity	Y	1.2×10^{-6}
KCNMA1	GO-MolFunc	substrate-specific channel activity	Y	1.6×10^{-6}
KCNMA1	GO-MolFunc	passive transmembrane transporter activity	Y	3.3×10^{-6}
KCNMA1	GO-MolFunc	channel activity	Y	3.3×10^{-6}
KCNMA1	GO-MolFunc	cation:cation antiporter activity	N	5.1×10^{-6}
KCNMA1	GO-MolFunc	glutamate receptor binding	N	9.1×10^{-6}
KCNMA1	GO-MolFunc	voltage-gated channel activity	Y	1.7×10^{-6}
KCNMA1	GO-MolFunc	voltage-gated ion channel activity	Y	1.7×10^{-6}
KCNMA1	GO-MolFunc	calmodulin binding	N	2.1×10^{-5}
KCNMA1	GO-MolFunc	ion gated channel activity	Y	2.3×10^{-5}
KCNMA1	KEGG	Calcium signaling pathway	N	3.4×10^{-9}
KCNMA1	KEGG	Long-term potentiation	N	1.9×10^{-7}
KCNMA1	KEGG	Vascular smooth muscle contraction	Y	1.0×10^{-4}
KCNMA1	REACTOME	Voltage gated Potassium channels	N	2.1×10^{-9}
KCNMA1	REACTOME	Neuronal System	Y	5.7×10^{-9}
KCNMA1	REACTOME	Unblocking of NMDA receptor, glutamate binding and activation	N	1.1×10^{-7}
KCNMA1	REACTOME	Potassium Channels	Y	5.2×10^{-7}
KCNMA1	REACTOME	Depolarization of the Presynaptic Terminal Triggers the Opening of Calcium Channels	N	2.6×10^{-6}
KCNMA1	REACTOME	Reduction of cytosolic Ca++ levels	N	5.0×10^{-6}
KCNMA1	REACTOME	Smooth Muscle Contraction	N	5.5×10^{-6}
KCNMA1	REACTOME	Platelet calcium homeostasis	N	7.5×10^{-6}

KCNMA1	REACTOME	CREB phosphorylation through the activation of CaMKII	N	7.7×10^{-6}
KCNMA1	REACTOME	Transmission across Chemical Synapses	N	1.0×10^{-5}
KCNMA1	REACTOME	Ras activation uopn Ca2+ infux through NMDA receptor	N	1.7×10^{-5}
KCNMA1	REACTOME	Activation of NMDA receptor upon glutamate binding and postsynaptic events	N	2.3×10^{-5}
KCNMA1	REACTOME	Glutamate Binding, Activation of AMPA Receptors and Synaptic Plasticity	N	4.3×10^{-5}
KCNMA1	REACTOME	Trafficking of AMPA receptors	N	4.3×10^{-5}
KIFC2	GO-BiolProc	neurotransmitter secretion	N	2.3×10^{-9}
KIFC2	GO-BiolProc	regulation of synaptic transmission	N	8.7×10^{-9}
KIFC2	GO-BiolProc	regulation of alpha-amino-3-hydroxy-5-methyl-4-isoxazole	N	3.9×10^{-8}
KIFC2	GO-BiolProc	regulation of transmission of nerve impulse	N	4.4×10^{-8}
KIFC2	GO-BiolProc	regulation of neurological system process	N	9.5×10^{-8}
KIFC2	GO-BiolProc	synaptic vesicle transport	N	3.3×10^{-7}
KIFC2	GO-BiolProc	regulation of neurotransmitter levels	N	6.2×10^{-7}
KIFC2	GO-BiolProc	regulation of synaptic plasticity	N	8.3×10^{-7}
KIFC2	GO-BiolProc	synaptic vesicle exocytosis	N	9.0×10^{-8}
KIFC2	GO-BiolProc	glutamate secretion	N	1.0×10^{-6}
KIFC2	GO-BiolProc	generation of a signal involved in cell-cell signaling	N	2.3×10^{-6}
KIFC2	GO-CellComp	Dendrite	N	1.3×10^{-7}
KIFC2	GO-CellComp	dendritic spine head	N	1.7×10^{-7}
KIFC2	GO-CellComp	postsynaptic density	N	1.7×10^{-7}
KIFC2	GO-CellComp	Synaptosome	N	1.8×10^{-7}
KIFC2	GO-CellComp	dendritic spine	N	2.8×10^{-7}
KIFC2	GO-CellComp	neuron spine	N	2.8×10^{-7}
KIFC2	GO-CellComp	voltage-gated calcium channel complex	N	3.0×10^{-7}
KIFC2	GO-CellComp	synapse part	N	1.1×10^{-6}
KIFC2	GO-CellComp	Synapse	N	1.1×10^{-6}
KIFC2	GO-CellComp	ciliary rootlet	N	2.3×10^{-6}
KIFC2	GO-CellComp	cell body	N	1.4×10^{-5}
KIFC2	GO-CellComp	synaptic membrane	N	2.2×10^{-5}

KIFC2	GO-CellComp	calcium channel complex	N	2.2×10^{-5}
KIFC2	GO-MolFunc	voltage-gated calcium channel activity	N	1.5×10^{-5}
KIFC2	REACTOME	Ras activation uopn Ca2+ infux through NMDA receptor	N	6.8×10^{-9}
KIFC2	REACTOME	Depolarization of the Presynaptic Terminal Triggers the Opening of Calcium Channels	N	1.2×10^{-8}
KIFC2	REACTOME	CREB phosphorylation through the activation of CaMKII	N	9.7×10^{-8}
KIFC2	REACTOME	Transmission across Chemical Synapses	N	3.4×10^{-7}
KIFC2	REACTOME	GABA synthesis, release, reuptake and degradation	N	4.2×10^{-6}
KIFC2	REACTOME	Neuronal System	N	1.1×10^{-5}
KIFC2	REACTOME	Dopamine Neurotransmitter Release Cycle	N	2.3×10^{-5}
KIFC2	REACTOME	Serotonin Neurotransmitter Release Cycle	N	2.3×10^{-5}
KIFC2	REACTOME	Trafficking of AMPA receptors	N	2.9×10^{-5}
KIFC2	REACTOME	Glutamate Binding, Activation of AMPA Receptors and Synaptic Plasticity	N	2.9×10^{-5}
KIFC2	REACTOME	Post NMDA receptor activation events	N	3.0×10^{-5}
KIFC2	REACTOME	NCAM signaling for neurite out-growth	N	3.1×10^{-5}
KIFC2	REACTOME	Neurotransmitter Release Cycle	N	3.4×10^{-5}
KIFC2	REACTOME	CREB phosphorylation through the activation of Ras	N	3.4×10^{-5}
KIFC2	REACTOME	Glutamate Neurotransmitter Release Cycle	N	3.7×10^{-5}
NRXN1	GO-BiolProc	glutamate signaling pathway	N	2.6×10^{-19}
NRXN1	GO-BiolProc	neurotransmitter secretion	N	1.5×10^{-16}
NRXN1	GO-BiolProc	gamma-aminobutyric acid signaling pathway	N	5.6×10^{-16}
NRXN1	GO-BiolProc	synaptic vesicle exocytosis	N	7.5×10^{-15}
NRXN1	GO-BiolProc	regulation of neurotransmitter levels	N	3.6×10^{-14}
NRXN1	GO-BiolProc	regulation of synaptic transmission	Y	8.4×10^{-14}
NRXN1	GO-BiolProc	neurotransmitter transport	N	8.7×10^{-14}
NRXN1	GO-BiolProc	regulation of neurological system process	Y	2.9×10^{-14}
NRXN1	GO-BiolProc	regulation of transmission of nerve impulse	Y	8.0×10^{-14}
NRXN1	GO-BiolProc	neuron-neuron synaptic transmission	Y	1.1×10^{-12}
NRXN1	GO-BiolProc	glutamate secretion	N	1.1×10^{-12}
NRXN1	GO-BiolProc	synaptic vesicle transport	N	5.8×10^{-12}

NRXN1	GO-BiolProc	synaptic transmission, glutamatergic	Y	2.1×10^{-11}
NRXN1	GO-BiolProc	signal release	N	6.7×10^{-11}
NRXN1	GO-BiolProc	generation of a signal involved in cell-cell signaling	N	6.7×10^{-11}
NRXN1	GO-BiolProc	learning or memory	Y	2.5×10^{-10}
NRXN1	GO-BiolProc	cellular potassium ion transport	N	2.7×10^{-10}
NRXN1	GO-BiolProc	potassium ion transmembrane transport	N	2.7×10^{-10}
NRXN1	GO-BiolProc	Axonogenesis	Y	3.0×10^{-10}
NRXN1	GO-BiolProc	regulation of excitatory postsynaptic membrane potential	Y	4.1×10^{-10}
NRXN1	GO-CellComp	presynaptic membrane	Y	1.7×10^{-26}
NRXN1	GO-CellComp	Synapse	Y	2.5×10^{-23}
NRXN1	GO-CellComp	Axon	Y	5.2×10^{-23}
NRXN1	GO-CellComp	axon part	Y	2.2×10^{-21}
NRXN1	GO-CellComp	synapse part	Y	4.2×10^{-21}
NRXN1	GO-CellComp	synaptic membrane	Y	2.5×10^{-19}
NRXN1	GO-CellComp	ion channel complex	N	1.3×10^{-16}
NRXN1	GO-CellComp	outer membrane-bounded periplasmic space	N	1.4×10^{-16}
NRXN1	GO-CellComp	periplasmic space	N	1.4×10^{-16}
NRXN1	GO-CellComp	cation channel complex	N	1.0×10^{-15}
NRXN1	GO-CellComp	main axon	N	1.1×10^{-15}
NRXN1	GO-CellComp	Dendrite	N	1.6×10^{-15}
NRXN1	GO-CellComp	external encapsulating structure part	N	2.2×10^{-15}
NRXN1	GO-CellComp	cell envelope	N	2.2×10^{-15}
NRXN1	GO-CellComp	postsynaptic membrane	N	2.3×10^{-14}
NRXN1	GO-CellComp	synaptic vesicle membrane	N	1.7×10^{-13}
NRXN1	GO-CellComp	Axolemma	N	2.8×10^{-13}
NRXN1	GO-CellComp	terminal button	N	3.1×10^{-13}
NRXN1	GO-CellComp	external encapsulating structure	N	4.3×10^{-13}
NRXN1	GO-CellComp	voltage-gated sodium channel complex	N	$5.\ \times10^{-13}$
NRXN1	GO-MolFunc	glutamate receptor activity	N	2.8×10^{-25}
NRXN1	GO-MolFunc	gated channel activity	N	2.2×10^{-21}

NRXN1	GO-MolFunc	substrate-specific channel activity	N	2.4×10^{-19}
NRXN1	GO-MolFunc	GABA receptor activity	N	7.7×10^{-19}
NRXN1	GO-MolFunc	passive transmembrane transporter activity	N	7.0×10^{-19}
NRXN1	GO-MolFunc	extracellular ligand-gated ion channel activity	N	1.1×10^{-17}
NRXN1	GO-MolFunc	GABA-A receptor activity	N	6.8×10^{-17}
NRXN1	GO-MolFunc	voltage-gated channel activity	N	7.9×10^{-17}
NRXN1	GO-MolFunc	voltage-gated ion channel activity	N	7.9×10^{-17}
NRXN1	GO-MolFunc	ionotropic glutamate receptor activity	N	1.5×10^{-16}
NRXN1	GO-MolFunc	extracellular-glutamate-gated ion channel activity	N	1.7×10^{-16}
NRXN1	GO-MolFunc	ligand-gated channel activity	N	4.7×10^{-16}
NRXN1	GO-MolFunc	ligand-gated ion channel activity	N	4.7×10^{-16}
NRXN1	GO-MolFunc	voltage-gated cation channel activity	N	3.5×10^{-15}
NRXN1	GO-MolFunc	cation channel activity	N	5.2×10^{-12}
NRXN1	GO-MolFunc	voltage-gated sodium channel activity	N	5.6×10^{-12}
NRXN1	KEGG	Neuroactive ligand-receptor interaction	N	9.5×10^{-6}
NRXN1	KEGG	Axon guidance	N	2.1×10^{-5}
NRXN1	KEGG	ErbB signaling pathway	N	2.7×10^{-5}
NRXN1	KEGG	Long-term potentiation	N	3.3×10^{-5}
NRXN1	KEGG	Amyotrophic lateral sclerosis (ALS)	N	2.9×10^{-4}
NRXN1	KEGG	Long-term depression	N	6.2×10^{-4}
NRXN1	KEGG	Cell adhesion molecules (CAMs)	Y	9.8×10^{-4}
NRXN1	REACTOME	GABA A receptor activation	N	7.0×10^{-23}
NRXN1	REACTOME	Neuronal System	N	2.6×10^{-22}
NRXN1	REACTOME	Ligand-gated ion channel transport	N	4.0×10^{-22}
NRXN1	REACTOME	Transmission across Chemical Synapses	N	6.4×10^{-20}
NRXN1	REACTOME	Interaction between L1 and Ankyrins	N	1.6×10^{-18}
NRXN1	REACTOME	Neurotransmitter Receptor Binding And Downstream Transmission In The Postsynaptic Cell	N	1.1×10^{-17}
NRXN1	REACTOME	GABA receptor activation	N	6.7×10^{-17}
NRXN1	REACTOME	Class C/3 (Metabotropic glutamate/pheromone receptors)	N	2.5×10^{-16}
NRXN1	REACTOME	Unblocking of NMDA receptor, glutamate binding and activation	N	1.4×10^{-14}

NRXN1	REACTOME	Potassium Channels	N	5.4×10^{-14}
NRXN1	REACTOME	Ion channel transport	N	3.9×10^{-13}
NRXN1	REACTOME	Serotonin Neurotransmitter Release Cycle	N	7.6×10^{-13}
NRXN1	REACTOME	Dopamine Neurotransmitter Release Cycle	N	7.6×10^{-13}
NRXN1	REACTOME	Voltage gated Potassium channels	N	1.7×10^{-11}
NRXN1	REACTOME	L1CAM interactions	N	5.0×10^{-11}
NRXN1	REACTOME	GABA synthesis, release, reuptake and degradation	N	8.5×10^{-10}
NRXN1	REACTOME	Norepinephrine Neurotransmitter Release Cycle	N	1.7×10^{-9}
NRXN1	REACTOME	Activation of NMDA receptor upon glutamate binding and postsynaptic events	N	2.2×10^{-9}
NRXN1	REACTOME	Glutamate Neurotransmitter Release Cycle	N	5.7×10^{-8}
NRXN1	REACTOME	Ionotropic activity of Kainate Receptors	N	5.9×10^{-8}
PITPNM2	GO-CellComp	cation channel complex	N	1.7×10^{-5}
PITPNM2	GO-CellComp	asymmetric synapse	N	2.3×10^{-5}
PITPNM2	GO-MolFunc	diacylglycerol kinase activity	N	7.03×10^{-7}
PITPNM2	GO-MolFunc	cation channel activity	N	5.7×10^{-6}
PITPNM2	GO-MolFunc	voltage-gated cation channel activity	N	2.5×10^{-5}
PITPNM2	GO-MolFunc	GTPase regulator activity	N	3.3×10^{-5}
PITPNM2	GO-MolFunc	nucleoside-triphosphatase regulator activity	N	4.3×10^{-5}
PITPNM2	GO-MolFunc	ion channel activity	N	5.0×10^{-5}
PITPNM2	GO-MolFunc	gated channel activity	N	6.0×10^{-5}
PITPNM2	GO-MolFunc	calmodulin-dependent protein kinase activity	N	6.1×10^{-5}
PITPNM2	GO-MolFunc	substrate-specific channel activity	N	6.6×10^{-5}
PITPNM2	GO-MolFunc	voltage-gated channel activity	N	1.0×10^{-4}
PITPNM2	GO-MolFunc	voltage-gated ion channel activity	N	1.0×10^{-4}
PITPNM2	KEGG	Calcium signaling pathway	N	1.4×10^{-4}
PITPNM2	REACTOME	Voltage gated Potassium channels	N	1.3×10^{-6}
PITPNM2	REACTOME	Potassium Channels	N	1.4×10^{-6}
PITPNM2	REACTOME	Effects of PIP2 hydrolysis	N	2.1×10^{-6}
PITPNM2	REACTOME	Ras activation uopn Ca2+ infux through NMDA receptor	N	1.5×10^{-5}

PITPNM2	REACTOME	Neuronal System	N	2.2×10^{-5}
PITPNM2	REACTOME	PLC-gamma1 signalling	N	6.6×10^{-5}
PITPNM2	REACTOME	DAG and IP3 signaling	N	8.2×10^{-5}
PITPNM2	REACTOME	Depolarization of the Presynaptic Terminal Triggers the Opening of Calcium Channels	N	9.9×10^{-5}
POU3F2	GO-BiolProc	central nervous system neuron differentiation	N	2.9×10^{-28}
POU3F2	GO-BiolProc	forebrain generation of neurons	N	4.1×10^{-22}
POU3F2	GO-BiolProc	forebrain neuron differentiation	N	3.1×10^{-21}
POU3F2	GO-BiolProc	telencephalon development	Y	5.8×10^{-19}
POU3F2	GO-BiolProc	forebrain development	Y	5.3×10^{-19}
POU3F2	GO-BiolProc	negative regulation of gliogenesis	N	9.1×10^{-18}
POU3F2	GO-BiolProc	astrocyte differentiation	Y	1.0×10^{-17}
POU3F2	GO-BiolProc	negative regulation of glial cell differentiation	N	2.9×10^{-17}
POU3F2	GO-BiolProc	brain development	Y	1.6×10^{-16}
POU3F2	GO-BiolProc	central nervous system neuron development	N	2.7×10^{-16}
POU3F2	GO-BiolProc	glial cell differentiation	Y	4.6×10^{-16}
POU3F2	GO-BiolProc	regulation of neuron differentiation	Y	1.6×10^{-15}
POU3F2	GO-BiolProc	pallium development	Y	2.8×10^{-15}
POU3F2	GO-BiolProc	cerebral cortex development	Y	4.7×10^{-15}
POU3F2	GO-BiolProc	neuron fate commitment	N	1.2×10^{-14}
POU3F2	GO-BiolProc	regulation of neurogenesis	Y	1.3×10^{-14}
POU3F2	GO-BiolProc	central nervous system projection neuron axonogenesis	N	1.5×10^{-14}
POU3F2	GO-BiolProc	positive regulation of neural precursor cell proliferation	N	2.2×10^{-14}
POU3F2	GO-BiolProc	Gliogenesis	Y	2.8×10^{-14}
POU3F2	GO-BiolProc	cerebral cortex neuron differentiation	N	3.0×10^{-14}
POU3F2	GO-CellComp	neuron projection membrane	N	2.8×10^{-7}
POU3F2	GO-CellComp	Axolemma	N	9.9×10^{-7}
POU3F2	GO-CellComp	Dendrite	N	1.2×10^{-6}
POU3F2	GO-CellComp	external encapsulating structure part	N	2.6×10^{-6}
POU3F2	GO-CellComp	cell envelope	N	2.6×10^{-6}

POU3F2	GO-CellComp	periplasmic space	N	7.5×10^{-6}
POU3F2	GO-CellComp	outer membrane-bounded periplasmic space	N	7.5×10^{-6}
POU3F2	GO-MolFunc	ionotropic glutamate receptor activity	N	3.7×10^{-6}
POU3F2	GO-MolFunc	ephrin receptor activity	N	5.0×10^{-6}
POU3F2	REACTOME	CRMPs in Sema3A signaling	N	1.1×10^{-5}
POU3F2	REACTOME	Unblocking of NMDA receptor, glutamate binding and activation	N	1.3×10^{-5}
SCRT1	GO-BiolProc	potassium ion transport	N	9.3×10^{-12}
SCRT1	GO-BiolProc	visual learning	N	2.5×10^{-11}
SCRT1	GO-BiolProc	locomotory behavior	N	3.2×10^{-11}
SCRT1	GO-BiolProc	mating behavior	N	2.5×10^{-10}
SCRT1	GO-BiolProc	visual behavior	N	7.0×10^{-10}
SCRT1	GO-BiolProc	associative learning	N	1.1×10^{-9}
SCRT1	GO-BiolProc	Learning	N	1.3×10^{-9}
SCRT1	GO-BiolProc	regulation of neurotransmitter levels	N	1.4×10^{-9}
SCRT1	GO-BiolProc	ionotropic glutamate receptor signaling pathway	N	2.7×10^{-9}
SCRT1	GO-BiolProc	neurotransmitter secretion	N	2.9×10^{-9}
SCRT1	GO-BiolProc	neurotransmitter transport	N	7.5×10^{-9}
SCRT1	GO-BiolProc	adult locomotory behavior	N	8.1×10^{-9}
SCRT1	GO-BiolProc	response to tropane	N	1.3×10^{-8}
SCRT1	GO-BiolProc	response to cocaine	N	1.3×10^{-8}
SCRT1	GO-BiolProc	neuron-neuron synaptic transmission	N	1.3×10^{-8}
SCRT1	GO-BiolProc	neuromuscular process	N	2.8×10^{-8}
SCRT1	GO-BiolProc	reproductive behavior	N	4.3×10^{-8}
SCRT1	GO-BiolProc	regulation of postsynaptic membrane potential	N	5.4×10^{-8}
SCRT1	GO-BiolProc	membrane hyperpolarization	N	6.4×10^{-8}
SCRT1	GO-BiolProc	synaptic transmission, glutamatergic	N	1.0×10^{-7}
SCRT1	GO-CellComp	axon part	N	2.2×10^{-12}
SCRT1	GO-CellComp	main axon	N	1.1×10^{-10}
SCRT1	GO-CellComp	synapse part	N	1.2×10^{-8}

SCRT1	GO-CellComp	Axon	N	1.2×10^{-8}
SCRT1	GO-CellComp	voltage-gated potassium channel complex	N	1.5×10^{-8}
SCRT1	GO-CellComp	potassium channel complex	N	1.5×10^{-8}
SCRT1	GO-CellComp	cation channel complex	N	3.0×10^{-8}
SCRT1	GO-CellComp	Synapse	N	1.2×10^{-7}
SCRT1	GO-CellComp	neuron projection terminus	N	2.9×10^{-7}
SCRT1	GO-CellComp	neuronal cell body	N	3.0×10^{-7}
SCRT1	GO-CellComp	cell body	N	7.0×10^{-7}
SCRT1	GO-CellComp	axon terminus	N	1.4×10^{-6}
SCRT1	GO-CellComp	terminal button	N	2.8×10^{-6}
SCRT1	GO-CellComp	dendritic spine head	N	5.8×10^{-6}
SCRT1	GO-CellComp	postsynaptic density	N	5.8×10^{-6}
SCRT1	GO-CellComp	ion channel complex	N	7.2×10^{-6}
SCRT1	GO-CellComp	synaptic membrane	N	8.8×10^{-6}
SCRT1	GO-CellComp	synaptic vesicle membrane	N	9.2×10^{-6}
SCRT1	GO-CellComp	ionotropic glutamate receptor complex	N	9.9×10^{-6}
SCRT1	GO-CellComp	periplasmic space	N	3.4×10^{-5}
SCRT1	GO-MolFunc	potassium ion transmembrane transporter activity	N	4.5×10^{-10}
SCRT1	GO-MolFunc	potassium channel activity	N	3.4×10^{-9}
SCRT1	GO-MolFunc	dopamine binding	N	4.5×10^{-9}
SCRT1	GO-MolFunc	voltage-gated potassium channel activity	N	7.4×10^{-9}
SCRT1	GO-MolFunc	voltage-gated cation channel activity	N	2.6×10^{-8}
SCRT1	GO-MolFunc	voltage-gated ion channel activity	N	2.4×10^{-7}
SCRT1	GO-MolFunc	voltage-gated channel activity	N	2.4×10^{-7}
SCRT1	GO-MolFunc	cation channel activity	N	9.1×10^{-7}
SCRT1	GO-MolFunc	gated channel activity	N	1.8×10^{-6}
SCRT1	GO-MolFunc	delayed rectifier potassium channel activity	N	2.3×10^{-6}
SCRT1	GO-MolFunc	extracellular-glutamate-gated ion channel activity	N	4.7×10^{-6}
SCRT1	GO-MolFunc	inorganic cation transmembrane transporter activity	N	6.2×10^{-6}
SCRT1	GO-MolFunc	ionotropic glutamate receptor activity	N	1.8×10^{-5}

SCRT1	KEGG	Neuroactive ligand-receptor interaction	N	2.92E-06
SCRT1	KEGG	Calcium signaling pathway	N	6.67E-04
SCRT1	REACTOME	Voltage gated Potassium channels	N	7.6×10^{-12}
SCRT1	REACTOME	Neuronal System	N	6.8×10^{-11}
SCRT1	REACTOME	Potassium Channels	N	2.1×10^{-10}
SCRT1	REACTOME	Unblocking of NMDA receptor, glutamate binding and activation	N	1.7×10^{-6}
SCRT1	REACTOME	Transmission across Chemical Synapses	N	7.6×10^{-6}
SCRT1	REACTOME	CREB phosphorylation through the activation of CaMKII	N	8.0×10^{-6}
SCRT1	REACTOME	GABA synthesis, release, reuptake and degradation	N	3.5×10^{-5}
SCRT1	REACTOME	Trafficking of AMPA receptors	N	3.8×10^{-5}
SCRT1	REACTOME	Glutamate Binding, Activation of AMPA Receptors and Synaptic Plasticity	N	3.8×10^{-5}
SCRT1	REACTOME	Amine ligand-binding receptors	N	4.0×10^{-5}
SCRT1	REACTOME	Neurotransmitter Release Cycle	N	4.6×10^{-5}
SCRT1	REACTOME	Ras activation uopn Ca2+ infux through NMDA receptor	N	5.7×10^{-5}
SCRT1	REACTOME	Dopamine Neurotransmitter Release Cycle	N	7.0×10^{-5}
SCRT1	REACTOME	Serotonin Neurotransmitter Release Cycle	N	7.0×10^{-5}
TBR1	GO-BiolProc	behavioral defense response	N	1.8×10^{-32}
TBR1	GO-BiolProc	behavioral fear response	N	3.5×10^{-27}
TBR1	GO-BiolProc	fear response	N	6.6×10^{-25}
TBR1	GO-BiolProc	hippocampus development	N	2.8×10^{-23}
TBR1	GO-BiolProc	pallium development	N	8.8×10^{-23}
TBR1	GO-BiolProc	G-protein coupled acetylcholine receptor signaling pathway	N	5.3×10^{-22}
TBR1	GO-BiolProc	axonal fasciculation	N	2.0×10^{-21}
TBR1	GO-BiolProc	limbic system development	N	9.4×10^{-18}
TBR1	GO-BiolProc	neuron recognition	N	3.5×10^{-17}
TBR1	GO-BiolProc	telencephalon development	N	2.1×10^{-16}
TBR1	GO-BiolProc	multicellular organismal response to stress	N	2.0×10^{-14}
TBR1	GO-BiolProc	forebrain development	N	4.9×10^{-14}
TBR1	GO-BiolProc	cerebral cortex neuron differentiation	N	1.2×10^{-13}

TBR1	GO-BiolProc	cerebral cortex radially oriented cell migration	N	1.5×10^{-13}
TBR1	GO-BiolProc	potassium ion transport	N	1.9×10^{-13}
TBR1	GO-BiolProc	synaptic transmission, glutamatergic	N	5.2×10^{-13}
TBR1	GO-BiolProc	ionotropic glutamate receptor signaling pathway	N	3.2×10^{-12}
TBR1	GO-BiolProc	neuron-neuron synaptic transmission	N	8.3×10^{-12}
TBR1	GO-BiolProc	learning or memory	N	1.6×10^{-11}
TBR1	GO-BiolProc	regulation of synaptic plasticity	N	2.4×10^{-11}
TBR1	GO-CellComp	synapse part	N	1.3×10^{-15}
TBR1	GO-CellComp	synaptic membrane	N	5.1×10^{-15}
TBR1	GO-CellComp	cation channel complex	N	5.4×10^{-15}
TBR1	GO-CellComp	potassium channel complex	N	6.5×10^{-15}
TBR1	GO-CellComp	voltage-gated potassium channel complex	N	6.5×10^{-15}
TBR1	GO-CellComp	ion channel complex	N	1.4×10^{-14}
TBR1	GO-CellComp	presynaptic membrane	N	4.7×10^{-13}
TBR1	GO-CellComp	Synapse	N	3.6×10^{-12}
TBR1	GO-CellComp	postsynaptic membrane	N	6.2×10^{-10}
TBR1	GO-CellComp	Dendrite	N	7.3×10^{-10}
TBR1	GO-CellComp	asymmetric synapse	N	5.6×10^{-9}
TBR1	GO-CellComp	site of polarized growth	N	3.0×10^{-8}
TBR1	GO-CellComp	growth cone	N	3.5×10^{-8}
TBR1	GO-CellComp	synaptic vesicle membrane	N	7.1×10^{-8}
TBR1	GO-MolFunc	voltage-gated potassium channel activity	N	2.3×10^{-17}
TBR1	GO-MolFunc	potassium channel activity	N	2.6×10^{-17}
TBR1	GO-MolFunc	voltage-gated cation channel activity	N	7.5×10^{-17}
TBR1	GO-MolFunc	voltage-gated channel activity	N	1.9×10^{-15}
TBR1	GO-MolFunc	voltage-gated ion channel activity	N	1.9×10^{-15}
TBR1	GO-MolFunc	acidic amino acid transmembrane transporter activity	N	2.3×10^{-15}
TBR1	GO-MolFunc	L-glutamate transmembrane transporter activity	N	1.0×10^{-14}
TBR1	GO-MolFunc	potassium ion transmembrane transporter activity	N	6.4×10^{-13}
TBR1	GO-MolFunc	gated channel activity	N	3.8×10^{-12}

TBR1	GO-MolFunc	ion channel activity	N	1.2×10^{-10}
TBR1	GO-MolFunc	substrate-specific channel activity	N	1.5×10^{-10}
TBR1	GO-MolFunc	G-protein coupled amine receptor activity	N	1.9×10^{-19}
TBR1	GO-MolFunc	metal ion transmembrane transporter activity	N	6.3×10^{-10}
TBR1	GO-MolFunc	cation channel activity	N	8.2×10^{-10}
TBR1	GO-MolFunc	GABA receptor activity	N	9.1×10^{-10}
TBR1	GO-MolFunc	passive transmembrane transporter activity	N	1.4×10^{-9}
TBR1	GO-MolFunc	channel activity	N	1.4×10^{-9}
TBR1	GO-MolFunc	GABA-A receptor activity	N	2.6×10^{-9}
TBR1	KEGG	Calcium signaling pathway	N	4.1×10^{-6}
TBR1	KEGG	Neuroactive ligand-receptor interaction	N	7.7×10^{-5}
TBR1	REACTOME	Voltage gated Potassium channels	N	2.4×10^{-15}
TBR1	REACTOME	GABA A receptor activation	N	4.2×10^{-14}
TBR1	REACTOME	Potassium Channels	N	4.4×10^{-14}
TBR1	REACTOME	Neuronal System	N	5.6×10^{-14}
TBR1	REACTOME	Amine ligand-binding receptors	N	4.4×10^{-13}
TBR1	REACTOME	Glutamate Neurotransmitter Release Cycle	N	2.4×10^{-11}
TBR1	REACTOME	Ligand-gated ion channel transport	N	3.8×10^{-11}
TBR1	REACTOME	Transmission across Chemical Synapses	N	5.7×10^{-9}
TBR1	REACTOME	Sema3A PAK dependent Axon repulsion	N	1.6×10^{-8}

Table S13. Results of mouse phenotype prediction analysis in 80,000 gene expression profiles. Phenotypic annotations are obtained from the Mouse Genetics Initiative database (www.informatics.jax.org). Table lists only genes and phenotypic annotations directly related to neuronal or central nervous system function or morphology (marked with an asterix) – full predictions are available at – http://www.ssgac.org[4]. *P*-values refer to the correlation between the Gene principal component profile and the reconstituted phenotypic annotation principal component profile, uncorrected for multiple testing; all reported terms meet False Discovery Rate < 0.05. The Annotated column indicates if the gene has previously been linked to a specific mouse phenotype (Y) or not (N). Results are sorted alphabetically by gene name.

Gene name	Predicted mouse knock-out/-in phenotype	Annotated	*P*-value
AKT3	abnormal hippocampus pyramidal cell layer	N	1.7×10^{-13}
AKT3	small hippocampus	N	1.8×10^{-8}
AKT3	abnormal neocortex morphology	N	5.6×10^{-6}
AKT3	decreased neuron number	N	6.5×10^{-6}
AKT3	placental labyrinth hypoplasia	N	1.1×10^{-5}
AKT3	abnormal brain ventricle morphology	N	1.7×10^{-5}
AKT3	abnormal sensory capabilities/reflexes/nociception	N	1.7×10^{-4}
AKT3	abnormal hippocampus morphology	N	1.9×10^{-4}
AKT3	abnormal cerebellar foliation	N	1.9×10^{-4}
AKT3	abnormal postnatal subventricular zone morphology	N	2.5×10^{-4}
ARHGAP39	dilated lateral ventricles	N	3.2×10^{-5}
ARHGAP39	abnormal ventral spinal root morphology	N	$9,0\times10^{-5}$
ARHGAP39	abnormal hippocampus layer morphology	N	1.6×10^{-4}
ARHGAP39	dilated third ventricle	N	2.9×10^{-4}
ARHGAP39	abnormal neural crest cell migration	N	7.9×10^{-4}
ARHGAP39	decreased motor neuron number	N	9.0×10^{-4}
ATXN2L	dilated lateral ventricles	N	4.5×10^{-8}
ATXN2L	increased brain size	N	2.9×10^{-7}
ATXN2L	abnormal dendritic cell morphology	N	4.8×10^{-4}
ATXN2L	dilated third ventricle	N	6.3×10^{-4}
C12orf65	impaired olfaction	N	6.0×10^{-3}
C12orf65	abnormal nervous system physiology	N	7.5×10^{-3}
C12orf65	abnormal medulla oblongata morphology	N	8.2×10^{-3}

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[4] The link will be activated on the day of publication of this article. The materials that will be posted online are included as a separate appendix to the submitted manuscript.

C12orf65	abnormal neural tube closure	N	1.4×10^{-2}
C12orf65	abnormal seizure response to electrical stimulation	N	1.6×10^{-2}
C12orf65	abnormal hippocampus CA1 region morphology	N	1.7×10^{-2}
C12orf65	absent distortion product otoacoustic emissions	N	1.8×10^{-2}
C12orf65	increased drinking behavior	N	1.8×10^{-2}
CELF4	abnormal CNS synaptic transmission	N	1.1×10^{-26}
CELF4	abnormal synaptic vesicle number	N	7.6×10^{-22}
CELF4	abnormal miniature excitatory postsynaptic currents	N	4.5×10^{-17}
CELF4	increased susceptibility to pharmacologically induced seizures	N	1.1×10^{-16}
CELF4	abnormal inhibitory postsynaptic currents	N	1.8×10^{-16}
CELF4	abnormal synaptic vesicle recycling	N	2.8×10^{-16}
CELF4	abnormal synaptic vesicle morphology	N	8.8×10^{-16}
CELF4	convulsive seizures	N	2.6×10^{-15}
CELF4	reduced long term potentiation	N	8.2×10^{-15}
CELF4	abnormal excitatory postsynaptic potential	N	2.2×10^{-14}
CELF4	increased synaptic depression	N	1.4×10^{-13}
CELF4	tonic-clonic seizures	Y	6.7×10^{-13}
CELF4	enhanced paired-pulse facilitation	N	7.8×10^{-13}
CELF4	abnormal excitatory postsynaptic currents	N	4.9×10^{-12}
CELF4	abnormal brain wave pattern	N	1.6×10^{-11}
CELF4	sporadic seizures	N	2.1×10^{-11}
CELF4	decreased paired-pulse facilitation	N	3.4×10^{-11}
CELF4	impaired coordination	N	5.7×10^{-11}
CELF4	abnormal conditioned taste aversion behaviour	N	9.7×10^{-11}
CRYZL1	abnormal synaptic vesicle recycling	N	2.1×10^{-4}
CYHR1	abnormal brain white matter morphology	N	4.7×10^{-8}
CYHR1	dilated third ventricle	N	5.1×10^{-5}
CYHR1	abnormal astrocyte morphology	N	1.5×10^{-4}
CYHR1	thick interventricular septum	N	6.7×10^{-4}

DEC1	hydroencephaly	N	3.2×10^{-3}
DEC1	abnormal startle reflex	N	5.6×10^{-3}
DEC1	impaired passive avoidance behavior	N	1.7×10^{-2}
DEC1	abnormal drinking behavior	N	2.2×10^{-2}
FOXH1	abnormal anterior visceral endoderm morphology	N	1.3×10^{-19}
FOXH1	abnormal neural fold formation	Y	1.4×10^{-14}
ITSN1	decreased brain size	N	2.8×10^{-7}
ITSN1	abnormal behavior	N	3.1×10^{-5}
ITSN1	microgliosis	N	4.1×10^{-5}
ITSN1	abnormal hippocampal commissure morphology	N	7.2×10^{-5}
ITSN1	ectopic Purkinje cell	N	1.3×10^{-4}
ITSN1	abnormal otic capsule morphology	N	1.5×10^{-4}
KCNMA1	decreased vasoconstriction	N	6.7×10^{-8}
KCNMA1	abnormal miniature excitatory postsynaptic currents	N	1.2×10^{-7}
KCNMA1	abnormal brain wave pattern	N	3.0×10^{-6}
KCNMA1	limb grasping	N	5.3×10^{-6}
KCNMA1	intracerebral hemorrhage	N	8.3×10^{-6}
KCNMA1	abnormal GABA-mediated receptor currents	N	9.2×10^{-6}
KCNMA1	abnormal synaptic plasticity	N	1.1×10^{-5}
KCNMA1	decreased aggression towards males	N	1.7×10^{-5}
KIFC2	abnormal miniature excitatory postsynaptic currents	N	6.4×10^{-7}
KIFC2	abnormal inhibitory postsynaptic currents	N	2.7×10^{-6}
KIFC2	abnormal spatial learning	N	3.8×10^{-6}
KIFC2	abnormal excitatory postsynaptic currents	N	5.5×10^{-6}
KIFC2	abnormal AMPA-mediated synaptic currents	N	5.6×10^{-6}
KIFC2	reduced long term depression	N	7.5×10^{-6}
KIFC2	abnormal hippocampal mossy fiber morphology	N	9.4×10^{-6}
KIFC2	abnormal long term depression	N	1.3×10^{-5}
KIFC2	enhanced long term potentiation	N	2.3×10^{-5}

KIFC2	enhanced paired-pulse facilitation	N	2.7×10^{-5}
KIFC2	abnormal synaptic vesicle morphology	N	4.5×10^{-5}
KIFC2	abnormal excitatory postsynaptic potential	N	5.2×10^{-5}
KIFC2	abnormal zygomatic bone morphology	N	8.3×10^{-5}
KIFC2	abnormal anxiety-related response	N	9.3×10^{-5}
KIFC2	abnormal synaptic vesicle recycling	N	9.9×10^{-5}
KIFC2	abnormal brain internal capsule morphology	N	1.7×10^{-4}
KIFC2	clonic seizures	N	2.0×10^{-4}
KIFC2	decreased susceptibility to pharmacologically induced seizures	N	2.1×10^{-4}
KIFC2	abnormal CNS synaptic transmission	N	2.1×10^{-4}
LRRC14	impaired coordination	N	2.6×10^{-5}
LRRC14	dilated third ventricle	N	1.2×10^{-3}
LRRC14	small cerebellum	N	1.3×10^{-3}
LRRC14	impaired contextual conditioning behavior	N	1.4×10^{-3}
LRRC14	impaired hearing	N	1.6×10^{-3}
LRRC14	abnormal axon outgrowth	N	1.7×10^{-3}
LRRC14	abnormal retinal apoptosis	N	2.3×10^{-3}
LRRC14	abnormal lateral ventricle morphology	N	3.2×10^{-3}
LRRC14	dilated lateral ventricles	N	3.5×10^{-3}
LRRC14	abnormal brain white matter morphology	N	4.1×10^{-3}
NRXN1	abnormal inhibitory postsynaptic currents	N	1.6×10^{-26}
NRXN1	abnormal CNS synaptic transmission	N	2.6×10^{-25}
NRXN1	abnormal GABA-mediated receptor currents	N	2.6×10^{-24}
NRXN1	abnormal excitatory postsynaptic currents	N	1.2×10^{-22}
NRXN1	hyperactivity	N	6.3×10^{-18}
NRXN1	abnormal synaptic transmission	N	1.4×10^{-17}
NRXN1	abnormal spatial learning	N	7.7×10^{-17}
NRXN1	abnormal synaptic vesicle number	N	3.6×10^{-16}
NRXN1	abnormal posture	N	6.4×10^{-16}
NRXN1	ataxia	N	1.4×10^{-14}

NRXN1	abnormal brain wave pattern	N	2.4×10^{-14}
NRXN1	seizures	N	6.8×10^{-14}
NRXN1	convulsive seizures	N	1.4×10^{-13}
NRXN1	abnormal nervous system electrophysiology	N	4.9×10^{-13}
NRXN1	abnormal spatial reference memory	N	4.9×10^{-13}
NRXN1	abnormal excitatory postsynaptic potential	N	8.1×10^{-13}
NRXN1	abnormal hippocampus morphology	N	1.2×10^{-12}
NRXN1	impaired coordination	N	1.4×10^{-12}
NRXN1	increased startle reflex	N	1.5×10^{-12}
NRXN1	abnormal social/conspecific interaction	N	3.9×10^{-12}
NUPR1	increased brain weight	N	1.7×10^{-7}
NUPR1	abnormal hippocampus layer morphology	N	6.7×10^{-6}
NUPR1	abnormal enteric neuron morphology	N	1.7×10^{-5}
PITPNM2	reduced long term depression	N	4.9×10^{-6}
PITPNM2	abnormal behavior	N	1.2×10^{-4}
PITPNM2	abnormal learning/ memory	N	2.3×10^{-4}
PITPNM2	impaired cued conditioning behavior	N	4.3×10^{-4}
PITPNM2	abnormal excitatory postsynaptic potential	N	5.2×10^{-4}
PITPNM2	impaired contextual conditioning behavior	N	6.6×10^{-4}
PITPNM2	abnormal calcium ion homeostasis	N	8.6×10^{-4}
POU3F2	abnormal brain commissure morphology	N	8.2×10^{-15}
POU3F2	enlarged third ventricle	N	1.2×10^{-14}
POU3F2	abnormal hippocampal mossy fiber morphology	N	2.2×10^{-13}
POU3F2	small olfactory bulb	N	7.7×10^{-12}
POU3F2	abnormal radial glial cell morphology	N	1.1×10^{-11}
POU3F2	abnormal cerebral cortex morphology	N	3.4×10^{-11}
POU3F2	abnormal axon guidance	N	3.5×10^{-10}
POU3F2	increased aggression towards mice	N	8.5×10^{-10}
POU3F2	abnormal corticospinal tract morphology	N	1.4×10^{-10}

POU3F2	decreased brain size	N	3.4×10^{-9}
POU3F2	abnormal hippocampus morphology	N	8.3×10^{-8}
POU3F2	abnormal embryonic/fetal subventricular zone morphology	N	1.0×10^{-8}
POU3F2	decreased corpus callosum size	N	1.6×10^{-8}
POU3F2	abnormal spinal cord interneuron morphology	N	1.8×10^{-8}
POU3F2	abnormal cerebellar foliation	N	1.9×10^{-8}
POU3F2	abnormal cerebrum morphology	N	3.7×10^{-8}
POU3F2	abnormal telencephalon development	N	4.2×10^{-8}
POU3F2	enlarged lateral ventricles	N	8.5×10^{-8}
REEP3	abnormal eating behavior	N	6.1×10^{-5}
REEP3	abnormal myelination	N	2.2×10^{-3}
REEP3	abnormal myelin sheath morphology	N	2.9×10^{-3}
REEP3	abnormal postural reflex	N	3.1×10^{-3}
REEP3	abnormal brain white matter morphology	N	3.2×10^{-3}
SCRT1	impaired conditioned place preference behavior	N	3.3×10^{-12}
SCRT1	abnormal spatial learning	N	8.6×10^{-12}
SCRT1	abnormal spike wave discharge	N	5.6×10^{-11}
SCRT1	impaired behavioral response to addictive substance	N	1.2×10^{-10}
SCRT1	increased exploration in new environment	N	1.6×10^{-10}
SCRT1	absence seizures	N	1.2×10^{-9}
SCRT1	abnormal nervous system electrophysiology	N	1.2×10^{-9}
SCRT1	enhanced coordination	N	1.8×10^{-9}
SCRT1	abnormal inhibitory postsynaptic currents	N	1.1×10^{-8}
SCRT1	decreased vertical activity	N	1.6×10^{-8}
SCRT1	abnormal behavioral response to xenobiotic	N	1.7×10^{-8}
SCRT1	sporadic seizures	N	2.1×10^{-8}
SCRT1	abnormal action potential	N	2.2×10^{-8}
SCRT1	abnormal excitatory postsynaptic currents	N	2.9×10^{-8}
SCRT1	decreased neurotransmitter release	N	2.9×10^{-8}
SCRT1	reduced long term depression	N	2.9×10^{-8}

SCRT1	ataxia	N	8.7×10^{-8}
SCRT1	abnormal brain wave pattern	N	2.3×10^{-7}
SCRT1	impaired swimming	N	3.2×10^{-7}
SCRT1	impaired coordination	N	4.0×10^{-7}
SNRNP35	abnormal brain morphology	N	7.1×10^{-4}
SNRNP35	abnormal action potential	N	1.5×10^{-4}
SNRNP35	astrocytosis	N	2.1×10^{-3}
SNRNP35	absent T cells	N	2.3×10^{-3}
SNRNP35	neurodegeneration	N	2.5×10^{-3}
SNRNP35	seminiferous tubule degeneration	N	2.8×10^{-3}
SNRNP35	abnormal miniature inhibitory postsynaptic currents	N	3.4×10^{-3}
SPNS1	astrocytosis	N	5.2×10^{-8}
SPNS1	Purkinje cell degeneration	N	7.8×10^{-6}
SPNS1	abnormal cued conditioning behavior	N	3.5×10^{-5}
SPNS1	abnormal Reichert's membrane morphology	N	2.2×10^{-4}
SPNS1	abnormal retinal ganglion layer morphology	N	2.8×10^{-4}
SPNS1	limb grasping	N	3.4×10^{-4}
SPNS1	myeloid hyperplasia	N	3.8×10^{-4}
SPNS1	gliosis	N	4.3×10^{-4}
SPNS1	abnormal anterior visceral endoderm morphology	N	9.2×10^{-4}
SPNS1	microgliosis	N	1.1×10^{-3}
TBR1	abnormal inhibitory postsynaptic currents	N	2.7×10^{-22}
TBR1	reduced long term depression	N	3.2×10^{-22}
TBR1	abnormal spatial learning	N	1.9×10^{-20}
TBR1	abnormal brain wave pattern	N	1.1×10^{-19}
TBR1	absent corpus callosum	N	4.7×10^{-18}
TBR1	sporadic seizures	N	4.7×10^{-16}
TBR1	increased startle reflex	N	4.8×10^{-16}
TBR1	abnormal cerebral cortex morphology	N	7.1×10^{-16}

TBR1	abnormal neocortex morphology	N	4.7×10^{-15}
TBR1	abnormal long term depression	N	7.9×10^{-15}
TBR1	hyperactivity	N	1.8×10^{-14}
TBR1	abnormal CNS synaptic transmission	N	4.3×10^{-14}
TBR1	increased anxiety-related response	N	4.4×10^{-13}
TBR1	abnormal GABA-mediated receptor currents	N	5.1×10^{-13}
TBR1	increased susceptibility to pharmacologically induced seizures	N	5.4×10^{-13}
TBR1	abnormal synaptic vesicle number	N	5.9×10^{-13}
TBR1	abnormal excitatory postsynaptic currents	N	2.2×10^{-12}
TBR1	abnormal thalamus morphology	N	3.2×10^{-12}
TBR1	abnormal telencephalon development	N	1.2×10^{-11}
TBR1	abnormal excitatory postsynaptic potential	N	1.7×10^{-8}

Table S14. Results of the tissue, organ and tissue type specific expression analysis in 80,000 gene expression profiles. The expression profiles were annotation into tissues, organs, or cell types using the MeSH database (http://www.nlm.nih.gov/mesh/). Table lists only genes in which show high expression in brain regions or specific nervous system cells – full predictions are available at http://www.ssgac.org[5]. Sample count specifies the number of expression profiles annotated with given annotation. AUC (*area under the curve*) gives the estimate how much of the variation on given gene expression profile is explained by a given tissue, organ or tissue type. *P*-values refer to enriched expression for a given gene in specific tissue, organ or tissue type compared to all other annotation terms. Results are sorted alphabetically by gene name.

Gene name	Tissue, organ or cell type	Sample count	AUC	*P*-value
AKT3	Prefrontal Cortex	46	0.98	6×10^{-30}
AKT3	Frontal Lobe	62	0.95	3×10^{-35}
AKT3	Visual Cortex	34	0.94	3×10^{-19}
AKT3	Occipital Lobe	42	0.94	5×10^{-23}
AKT3	Cerebral Cortex	276	0.94	3×10^{-14}
AKT3	Entorhinal Cortex	83	0.94	2×10^{-43}
AKT3	Temporal Lobe	91	0.94	5×10^{-47}
AKT3	Cerebellum	36	0.93	3×10^{-19}
AKT3	Hippocampus	55	0.93	7×10^{-28}
AKT3	Cerebrum	344	0.92	3×10^{-160}
AKT3	Parietal Lobe	17	0.91	5×10^{-9}
ARHGAP39	Hippocampus	55	0.88	5×10^{-22}
ARHGAP39	Visual Cortex	34	0.87	7×10^{-14}
ARHGAP39	Neural Stem Cells	11	0.87	3×10^{-5}
ARHGAP39	Occipital Lobe	42	0.86	5×10^{-16}
ARHGAP39	Parietal Lobe	17	0.86	3×10^{-7}
ARHGAP39	Hypothalamus	15	0.85	4×10^{-6}
ARHGAP39	Ganglia	11	0.83	2×10^{-4}
ARHGAP39	Cerebral Cortex	276	0.82	2×10^{-75}
ARHGAP39	Entorhinal Cortex	83	0.82	6×10^{-24}
ARHGAP39	Cerebrum	344	0.82	1×10^{-91}
ARHGAP39	Temporal Lobe	91	0.81	1×10^{-24}
ARHGAP39	Brain	1274	0.78	1×10^{-252}

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[5] The link will be activated on the day of publication of this article. The materials that will be posted online are included as a separate appendix to the submitted manuscript.

ARHGAP39	Central Nervous System	1302	0.78	2×10^{-251}
C12orf65	Hypothalamus	15	0.68	1×10^{-2}
CRYZL1	Prefrontal Cortex	46	0.95	6×10^{-26}
CRYZL1	Frontal Lobe	62	0.86	1×10^{-22}
CRYZL1	Cerebellum	36	0.86	9×10^{-14}
CRYZL1	Substantia Nigra	22	0.73	2×10^{-4}
CYHR1	Hypothalamus	15	0.82	1×10^{-5}
CYHR1	Putamen	16	0.78	1×10^{-4}
CYHR1	Parotid Gland	19	0.73	4×10^{-4}
CYHR1	Occipital Lobe	42	0.71	2×10^{-6}
CYHR1	Visual Cortex	34	0.71	2×10^{-5}
CYHR1	Cerebellum	36	0.7	3×10^{-5}
CYHR1	Thalamus	16	0.7	7×10^{-3}
CYHR1	Astrocytes	12	0.69	2×10^{-2}
CYHR1	Hippocampus	55	0.67	8×10^{-6}
DEC1	Substantia Nigra	22	0.78	6×10^{-6}
DEC1	Thalamus	16	0.75	5×10^{-4}
DEC1	Mesencephalon	41	0.74	7×10^{-8}
DEC1	Hypothalamus	15	0.73	2×10^{-3}
DEC1	Subthalamic Nucleus	12	0.68	3×10^{-2}
FARP1	Neural Stem Cells	11	0.96	1×10^{-7}
FARP1	Astrocytes	12	0.84	4×10^{-5}
FOXH1	Substantia Nigra	22	0.86	4×10^{-9}
FOXH1	Subthalamic Nucleus	12	0.84	5×10^{-5}
FOXH1	Thalamus	16	0.82	8×10^{-6}
FOXH1	Mesencephalon	41	0.8	4×10^{-11}
FOXH1	Parietal Lobe	17	0.77	9×10^{-5}
FOXH1	Occipital Lobe	42	0.75	4×10^{-8}
FOXH1	Visual Cortex	34	0.74	9×10^{-7}

FOXH1	Hypothalamus	15	0.74	2×10^{-3}
ITSN1	Abdominal Fat	69	0.99	2×10^{-44}
ITSN1	Visual Cortex	34	0.98	4×10^{-22}
ITSN1	Motor Neurons	12	0.98	1×10^{-8}
ITSN1	Occipital Lobe	42	0.97	4×10^{-26}
ITSN1	Prefrontal Cortex	46	0.97	8×10^{-26}
ITSN1	Frontal Lobe	62	0.96	1×10^{-35}
ITSN1	Entorhinal Cortex	83	0.96	4×10^{-47}
ITSN1	Cerebral Cortex	276	0.96	1×10^{-150}
ITSN1	Temporal Lobe	91	0.95	7×10^{-51}
ITSN1	Hippocampus	55	0.95	7×10^{-31}
ITSN1	Spinal Cord	19	0.94	2×10^{-11}
ITSN1	Cerebrum	344	0.94	5×10^{-175}
ITSN1	Cicatrix	19	0.94	3×10^{-11}
ITSN1	Parietal Lobe	17	0.94	4×10^{-10}
ITSN1	Cerebellum	36	0.92	1×10^{-18}
JMJD1C	Cerebellum	36	0.91	4×10^{-17}
JMJD1C	Prefrontal Cortex	46	0.66	2×10^{-4}
KCNMA1	Visual Cortex	34	0.95	7×10^{-20}
KCNMA1	Occipital Lobe	42	0.94	4×10^{-23}
KCNMA1	Prefrontal Cortex	46	0.93	2×10^{-24}
KCNMA1	Entorhinal Cortex	83	0.93	7×10^{-42}
KCNMA1	Aortic Valve	10	0.93	2×10^{-6}
KCNMA1	Muscle, Smooth	248	0.92	1×10^{-115}
KCNMA1	Cerebral Cortex	276	0.92	2×10^{-125}
KCNMA1	Frontal Lobe	62	0.91	10×10^{-29}
KCNMA1	Hippocampus	55	0.9	6×10^{-25}
KIFC2	Putamen	16	0.99	9×10^{-12}
KIFC2	Frontal Lobe	62	0.98	3×10^{-39}

KIFC2	Parietal Lobe	17	0.98	9×10^{-12}
KIFC2	Prefrontal Cortex	46	0.98	4×10^{-29}
KIFC2	Cerebral Cortex	276	0.97	6×10^{-162}
KIFC2	Entorhinal Cortex	83	0.97	7×10^{-50}
KIFC2	Temporal Lobe	91	0.97	3×10^{-54}
KIFC2	Occipital Lobe	42	0.97	9×10^{-26}
KIFC2	Visual Cortex	34	0.97	6×10^{-21}
KIFC2	Hippocampus	55	0.96	6×10^{-32}
KIFC2	Cerebrum	344	0.93	4×10^{-168}
KIFC2	Hypothalamus	15	0.92	2×10^{-8}
KIFC2	Thalamus	16	0.88	1×10^{-7}
KIFC2	Brain	1274	0.82	1×10^{-300}
KIFC2	Neural Stem Cells	11	0.81	3×10^{-4}
KIFC2	Central Nervous System	1302	0.81	1×10^{-300}
KIFC2	Nervous System	1358	0.81	7×10^{-300}
KIFC2	Substantia Nigra	22	0.8	7×10^{-7}
MPHOSPH9	Visual Cortex	34	0.82	5×10^{-11}
MPHOSPH9	Cerebellum	36	0.78	3×10^{-9}
MPHOSPH9	Neural Stem Cells	11	0.74	6×10^{-3}
MPHOSPH9	Occipital Lobe	42	0.74	1×10^{-7}
NPAS2	Prefrontal Cortex	46	0.93	3×10^{-24}
NPAS2	Frontal Lobe	62	0.91	1×10^{-28}
NPAS2	Putamen	16	0.9	3×10^{-8}
NPAS2	Entorhinal Cortex	83	0.85	5×10^{-28}
NPAS2	Hippocampus	55	0.85	6×10^{-19}
NPAS2	Cerebral Cortex	276	0.84	3×10^{-86}
NRXN1	Prefrontal Cortex	46	1	2×10^{-31}
NRXN1	Cerebellum	36	0.99	2×10^{-24}
NRXN1	Cerebral Cortex	276	0.99	5×10^{-47}

NRXN1	Temporal Lobe	91	0.99	5×10^{-58}
NRXN1	Entorhinal Cortex	83	0.99	5×10^{-53}
NRXN1	Occipital Lobe	42	0.99	1×10^{-27}
NRXN1	Visual Cortex	34	0.98	1×10^{-22}
NRXN1	Parietal Lobe	17	0.98	5×10^{-12}
NRXN1	Ganglia	11	0.98	4×10^{-8}
NRXN1	Thalamus	16	0.97	6×10^{-11}
NRXN1	Cerebrum	344	0.97	4×10^{-195}
NRXN1	Mesencephalon	41	0.97	6×10^{-25}
NRXN1	Putamen	16	0.96	1×10^{-11}
NRXN1	Substantia Nigra	22	0.96	6×10^{-14}
NRXN1	Hypothalamus	15	0.96	6×10^{-10}
NRXN1	Motor Neurons	12	0.95	5×10^{-8}
NRXN1	Subthalamic Nucleus	12	0.95	8×10^{-8}
PITPNM2	Frontal Lobe	62	0.88	1×10^{-24}
PITPNM2	Hippocampus	55	0.87	9×10^{-22}
PITPNM2	Prefrontal Cortex	46	0.87	7×10^{-18}
PITPNM2	Putamen	16	0.81	1×10^{-5}
PITPNM2	Temporal Lobe	91	0.8	1×10^{-23}
PITPNM2	Cerebral Cortex	276	0.8	8×10^{-67}
PITPNM2	Entorhinal Cortex	83	0.8	8×10^{-21}
PITPNM2	Heart Ventricles	124	0.79	1×10^{-28}
PITPNM2	Hypothalamus	15	0.78	2×10^{-4}
PITPNM2	Cerebrum	344	0.75	3×10^{-56}
POU3F2	Neural Stem Cells	11	0.98	4×10^{-8}
POU3F2	Spinal Cord	19	0.97	9×10^{-13}
POU3F2	Substantia Nigra	22	0.97	2×10^{-14}
POU3F2	Visual Cortex	34	0.97	5×10^{-21}
POU3F2	Prefrontal Cortex	46	0.97	6×10^{-28}
POU3F2	Occipital Lobe	42	0.97	1×10^{-25}

POU3F2	Retinal Pigment Epithelium	12	0.97	2×10^{-8}
POU3F2	Motor Neurons	12	0.97	2×10^{-8}
POU3F2	Mesencephalon	41	0.96	8×10^{-25}
POU3F2	Parietal Lobe	17	0.96	4×10^{-11}
POU3F2	Frontal Lobe	62	0.96	4×10^{-36}
POU3F2	Cerebral Cortex	276	0.96	5×10^{-151}
POU3F2	Putamen	16	0.95	3×10^{-10}
POU3F2	Cerebrum	344	0.95	2×10^{-180}
POU3F2	Temporal Lobe	91	0.95	2×10^{-49}
POU3F2	Entorhinal Cortex	83	0.95	4×10^{-45}
POU3F2	Subthalamic Nucleus	12	0.95	9×10^{-8}
POU3F2	Hippocampus	55	0.94	4×10^{-30}
REEP3	Retinal Pigment Epithelium	12	0.96	4×10^{-8}
REEP3	Neural Stem Cells	11	0.84	7×10^{-5}
RILPL1	Subthalamic Nucleus	12	0.97	2×10^{-8}
RILPL1	Substantia Nigra	22	0.96	7×10^{-14}
RILPL1	Mesencephalon	41	0.96	5×10^{-24}
RILPL1	Thalamus	16	0.95	4×10^{-10}
RILPL1	Putamen	16	0.94	8×10^{-10}
RILPL1	Parietal Lobe	17	0.94	4×10^{-10}
RILPL1	Temporal Lobe	91	0.93	1×10^{-45}
RILPL1	Spinal Cord	19	0.93	9×10^{-11}
RILPL1	Entorhinal Cortex	83	0.93	4×10^{-41}
RILPL1	Neural Stem Cells	11	0.92	1×10^{-6}
RILPL1	Cerebral Cortex	276	0.92	4×10^{-129}
SBNO1	Cerebellum	36	0.87	9×10^{-15}
SBNO1	Granulocyte Precursor Cells	30	0.86	5×10^{-12}
SBNO1	Prefrontal Cortex	46	0.82	4×10^{-14}
SBNO1	Visual Cortex	34	0.8	8×10^{-10}

SBNO1	Motor Neurons	12	0.76	2×10^{-3}
SBNO1	Frontal Lobe	62	0.76	9×10^{-13}
SBNO1	Occipital Lobe	42	0.76	7×10^{-9}
SLC15A1	Thalamus	16	0.85	2×10^{-6}
SLC15A1	Putamen	16	0.82	1×10^{-5}
SLC15A1	Ganglia	11	0.8	5×10^{-4}
SLC15A1	Subthalamic Nucleus	12	0.74	4×10^{-3}
SLC15A1	Mesencephalon	41	0.69	2×10^{-5}
SLC15A1	Substantia Nigra	22	0.69	2×10^{-3}
SLC15A1	Hypothalamus	15	0.68	2×10^{-2}
SNRNP35	Visual Cortex	34	0.83	2×10^{-11}
SNRNP35	Occipital Lobe	42	0.81	2×10^{-12}
SNRNP35	Subthalamic Nucleus	12	0.76	2×10^{-3}
SNRNP35	Hypothalamus	15	0.75	7×10^{-4}
SULT1A2	Hypothalamus	15	0.83	9×10^{-6}
SULT1A2	Substantia Nigra	22	0.76	3×10^{-5}
SULT1A2	Ganglia	11	0.75	4×10^{-3}
TBR1	Prefrontal Cortex	46	0.99	1×10^{-30}
TBR1	Frontal Lobe	62	0.99	2×10^{-40}
TBR1	Hippocampus	55	0.92	4×10^{-27}
TBR1	Parietal Lobe	17	0.89	3×10^{-8}
TBR1	Cerebral Cortex	276	0.88	2×10^{-104}
TBR1	Temporal Lobe	91	0.86	1×10^{-32}
TBR1	Entorhinal Cortex	83	0.85	4×10^{-28}
TBR1	Subthalamic Nucleus	12	0.81	2×10^{-4}
TBR1	Cerebrum	344	0.79	3×10^{-78}
TBR1	Thalamus	16	0.78	1×10^{-4}
TBR1	Brain	1274	0.75	2×10^{-206}
TBR1	Central Nervous System	1302	0.75	7×10^{-200}

TMEM50B	Motor Neurons	12	0.89	4×10^{-6}
TMEM50B	Thalamus	16	0.87	3×10^{-7}
TMEM50B	Cerebellum	36	0.87	2×10^{-14}
TMEM50B	Neural Stem Cells	11	0.84	8×10^{-5}
TMEM50B	Ganglia	11	0.81	4×10^{-4}
TMEM50B	Spinal Cord	19	0.78	2×10^{-5}
TMEM50B	Neurons	37	0.76	7×10^{-8}
TUFM	Neural Stem Cells	11	0.88	1×10^{-5}
TUFM	Astrocytes	12	0.71	1×10^{-2}
VPS28	Neural Stem Cells	11	0.72	1×10^{-2}

Table S15. Implicated candidate genes in cognitive performance associated genomic loci. Table outlines the levels of supportive biological evidence across several annotation analysis – 1) functional SNP annotation (Supplementary Table S9); 2) promising eQTLs in blood (Supplementary Table S10) and brain (Supplementary Table S11); 3) showing relevant coexpression prediction results for reconstituted pathway terms (Supplementary Table S12), mouse phenotypes (Supplementary Table S13) and high site specific expression profiles (Supplementary Table S14). Two last colums give another layer of supportive evidence from literature – A) clustering into modules related to neuronal or central nervous system function (neuronal function; synaptic transmission, neurogenesis, neuropeptide hormone, nerve myelination) constructed using brain derived gene expression profiles (reported in (28)) and B) isolated from the proteasome of human neocortex postsynaptic density [hPSD] (reported in (34)). SNPs rs1487441 and rs1487441 are located in gene deserts, thus the nearest gene is considered for analysis. Only genes with at least one relevant annotation are listed. SNP ID – nominally significant cognitive performance associated variant; * – denotes a gene not annotated within the co-expression database;

SNP ID	Genes names	nsSNPs	Blood eQTL	Brain eQTL (Prefrontal cortex)	Brain eQTL (Visual cortex)	Brain eQTL (Cerebellum)	Prediction (Brain related functions)	Prediction (Mouse phenotypes)	Region specific expression (Brain)	Modules of neuronal function (Zhang et al)	Postsynaptic density proteome (Bayés et al)	Levels of Evidence
rs1487441	*POU3F2*						Y	Y	Y	Y		4
rs7923609	*JMJD1C*	Y					Y	Y	Y			4
	REEP3							Y	Y			2
rs2721173	*LRRC14*	Y		Y	Y	Y		Y				5
	RECQL4	Y										1
	LRRC24		Y				*na*	*na*	*na*			1
	MFSD3		Y									1
	ARHGAP39							Y	Y			2
	GPT		Y									1
	PPP1R16A		Y									1
	FOXH1							Y	Y			2
	KIFC2			Y			Y	Y	Y	Y		5
	CYHR1							Y	Y			2
	VPS28		Y						Y			2
	CPSF1									Y		1
	SCRT1						Y	Y		Y		3

rs8049439	*ATXN2L*						Y	Y				2
	TUFM		Y	Y					Y		Y	4
	SH2B1	Y										1
	EIF3CL			Y	Y	Y	*na*	*na*	*na*			3
	NFATC2IP					Y			Y	Y		3
	NUPR1					Y		Y				2
	SPNS1		Y					Y				2
	LAT		Y	Y								2
	SULT1A1		Y									1
	SULT1A2		Y						Y			2
	CCDC101		Y									1
rs1606974	*NRXN1*						Y	Y	Y	Y	Y	5
rs2970992	*NPAS2*					Y			Y			2
	NMS						*na*	*na*	*na*	Y		1
rs3127447	*KCNMA1*						Y	Y	Y	Y		4
rs7847231	*DEC1*							Y	Y			2
rs4658552	*SDCCAG8*	Y	Y	Y	Y							4
	AKT3							Y	Y			2
rs1892700	*CRYZL1*						Y	Y	Y			3
	ITSN1		Y					Y	Y	Y	Y	5
	GART	Y	Y			Y						3
	DNAJC28	Y		Y								2
	TMEM50B			Y		Y	Y		Y	Y		5
	IFNGR2					Y	Y					2
rs7980687	*SBNO1*	Y		Y		Y			Y			4
	SETD8		Y				Y					2
	RILPL2		Y									1
	C12orf65			Y	Y	Y		Y	Y			5
	MPHOSPH9								Y			1

	SNRNP35				Y	Y			2
	RILPL1					Y			1
	PITPNM2			Y	Y	Y			3
	TMED2						Y		1
rs1187220	*CELF4*			Y	Y	Y			3
rs3783006	*STK24*	Y							1
	FARP1			Y		Y		Y	3
	SLC15A1					Y			1
rs7309	*TANK*	Y							1
	PSMD14	Y							1
	TBR1			Y	Y	Y	Y		4

Table S16. Regression of cognitive performance on a polygenic score (*PGS*) in the GS, MCTFR, QIMR, and STR cohorts (coefficients for constructing the *PGS* are from the meta-analysis of cognitive performance, with the meta-analysis sample excluding the respective validation sample). Analyses for GS are based on 1,081 siblings from 476 independent families, analyses for MCTFR are based on 1,346 siblings from 673 independent families, analyses for QIMR are based on 1,426 individuals from 628 independent families, and analyses for STR are based on 810 DZ twins from 405 independent families. ΔR^2 is the incremental R^2 of adding the *PGS* to the regression. The family dummies explain 64.3% of the variance for GS, 72.8% for MCTFR, 68.4% for QIMR, and 77.4% for STR. Standard errors are clustered at the family level. The pooled estimates of are calculated using inverse-variance weighting.

Analysis		GS	MCTFR	QIMR	STR	Pooled
Without family dummies	Beta	0.05	0.05	0.06	0.07	0.06
	S.E.	0.04	0.03	0.03	0.04	0.02
	p-value	0.19	0.11	0.03	0.10	8.17×10^{-4}
	ΔR^2	0.0023	0.0022	0.0041	0.0044	-
With family dummies	Beta	-0.05	0.05	0.03	0.08	0.03
	S.E.	0.07	0.06	0.06	0.07	0.03
	p-value	0.41	0.36	0.61	0.26	0.36
	ΔR^2	0.0007	0.0007	0.0002	0.0015	-

Table S17. Simulation Results for Power of Within-Family Analysis

β [R^2]	Model	Mean($\hat{\beta}$)	Mean(Standard Error)	Power
0.045 [0.20%]	Without family dummies	0.044	0.017	78.2%
	With family dummies	0.043	0.027	31.2%
0.065 [0.42%]	Without family dummies	0.065	0.017	96.8%
	With family dummies	0.063	0.027	64.2%

Table S18. Results from polygenic-score analysis in the Health and Retirement Study. TWR = Total Word Recall, TMS = Total Mental Score, TC = Total Cognition. Standard errors are clustered per individual in the regression and standard errors of the regression coefficients are given in square brackets below the regression coefficients. The regressions for ΔTMS and ΔTC have the knots of the age spline at 70 and 80 and do not include person-wave observations with age < 60. * $p < 0.05$; ** $p < 0.01$. ΔR^2 denotes the increase in R^2 of a model with the score, and score interactions if applicable, compared to a model with only the age spline and sex.

	(1)	(2)	(3)	(4)	(5)	(6)	(7)	(8)	(9)	(10)	(11)	(12)
	TWR	TWR	TMS	TMS	TC	TC	ΔTWR	ΔTWR	ΔTMS	ΔTMS	ΔTC	ΔTC
Score	0.040**	0.047**	0.062**	0.072**	0.057**	0.075**	-0.003	-0.005	-0.002	-0.008	-0.001	-0.006
	[0.007]	[0.010]	[0.010]	[0.012]	[0.009]	[0.012]	[0.002]	[0.004]	[0.004]	[0.006]	[0.004]	[0.007]
Age < 60	-0.006**	-0.006**	-0.006*	-0.006*	-0.007**	-0.007**	-0.002	-0.002				
	[0.002]	[0.002]	[0.003]	[0.003]	[0.002]	[0.002]	[0.001]	[0.001]				
Age 60-69	-0.037**	-0.037**	-0.004*	-0.004*	-0.031**	-0.031**	-0.006**	-0.006**	-0.013*	-0.013*	-0.023**	-0.023**
	[0.002]	[0.002]	[0.002]	[0.002]	[0.002]	[0.002]	[0.001]	[0.001]	[0.006]	[0.006]	[0.006]	[0.006]
Age 70-79	-0.051**	-0.051**	-0.018**	-0.018**	-0.047**	-0.047**	-0.005**	-0.005**	-0.007**	-0.007**	-0.006**	-0.006**
	[0.002]	[0.002]	[0.003]	[0.003]	[0.003]	[0.003]	[0.001]	[0.001]	[0.002]	[0.002]	[0.002]	[0.002]
Age ≥ 80	-0.056**	-0.056**	-0.053**	-0.053**	-0.066**	-0.067**	-0.006**	-0.006**	-0.019**	-0.019**	-0.015**	-0.015**
	[0.004]	[0.004]	[0.007]	[0.007]	[0.006]	[0.006]	[0.002]	[0.002]	[0.003]	[0.003]	[0.002]	[0.002]
Female	0.345**	0.344**	-0.169**	-0.169**	0.199**	0.198**	0.002	0.002	-0.018*	-0.018*	-0.011	-0.011
	[0.015]	[0.015]	[0.019]	[0.019]	[0.019]	[0.019]	[0.005]	[0.005]	[0.009]	[0.009]	[0.008]	[0.008]
Age 60-69 × score		0.000		-0.002		-0.002		0.000				
		[0.002]		[0.002]		[0.002]		[0.001]				
Age 70-79 × score		-0.001		0.002		0.000		0.001		0.002		0.002
		[0.003]		[0.003]		[0.003]		[0.001]		[0.001]		[0.001]
Age ≥ 80 × score		-0.008*		-0.004		-0.008		-0.004*		-0.003		-0.005*
		[0.004]		[0.006]		[0.005]		[0.002]		[0.002]		[0.002]
Constant	0.107	0.108	0.764**	0.764**	0.533**	0.534**	0.154*	0.155*	1.008**	1.006**	1.620**	1.619**
	[0.124]	[0.124]	[0.151]	[0.151]	[0.143]	[0.143]	[0.072]	[0.071]	[0.381]	[0.381]	[0.395]	[0.395]
N, person-wave	49,988	49,988	32,289	32,289	32,289	32,289	40,744	40,744	20,781	20,781	20,781	20,781
N, persons	8,652	8,652	8,539	8,539	8,539	8,539	8,543	8,543	5,248	5,248	5,248	5,248
R^2	0.164	0.164	0.038	0.038	0.135	0.135	0.002	0.002	0.005	0.005	0.000	0.000
ΔR^2	0.002	0.002	0.004	0.004	0.003	0.004	0.000	0.000	0.000	0.000	0.000	0.000

Table S19. Results from polygenic-score analysis in the Health and Retirement Study with years of education added as a control variable. TWR = Total Word Recall, TMS = Total Mental Score, TC = Total Cognition. Standard errors are clustered per individual in the regression and standard errors of the regression coefficients are given in square brackets below the regression coefficients. The regressions for ΔTMS and ΔTC have the knots of the age spline at 70 and 80 and do not include person-wave observations with age < 60. * $p < 0.05$; ** $p < 0.01$. ΔR^2 denotes the increase in R^2 of a model with the score, and score interactions if applicable, compared to a model with only the age spline and sex.

	(1)	(2)	(3)	(4)	(5)	(6)	(7)	(8)	(9)	(10)	(11)	(12)
	TWR	TWR	TMS	TMS	TC	TC	ΔTWR	ΔTWR	ΔTMS	ΔTMS	ΔTC	ΔTC
Score	0.014*	0.022*	0.031**	0.043**	0.024**	0.045**	-0.002	-0.005	-0.003	-0.010	-0.002	-0.007
	[0.007]	[0.009]	[0.009]	[0.012]	[0.008]	[0.011]	[0.002]	[0.004]	[0.004]	[0.006]	[0.004]	[0.007]
Age < 60	-0.003	-0.003	-0.000	-0.000	-0.001	-0.001	-0.002	-0.002				
	[0.002]	[0.002]	[0.003]	[0.002]	[0.002]	[0.002]	[0.001]	[0.001]				
Age 60-69	-0.032**	-0.032**	-0.002	-0.002	-0.029**	-0.029**	-0.006**	-0.006**	-0.013*	-0.013*	-0.023**	-0.023**
	[0.002]	[0.002]	[0.002]	[0.002]	[0.002]	[0.002]	[0.001]	[0.001]	[0.006]	[0.006]	[0.006]	[0.006]
Age 70-79	-0.050**	-0.050**	-0.016**	-0.016**	-0.045**	-0.045**	-0.005**	-0.005**	-0.007**	-0.007**	-0.006**	-0.006**
	[0.002]	[0.002]	[0.003]	[0.003]	[0.003]	[0.003]	[0.001]	[0.001]	[0.002]	[0.002]	[0.002]	[0.002]
Age ≥ 80	-0.054**	-0.054**	-0.051**	-0.051**	-0.064**	-0.064**	-0.006**	-0.006**	-0.019**	-0.019**	-0.015**	-0.015**
	[0.004]	[0.004]	[0.007]	[0.006]	[0.006]	[0.005]	[0.002]	[0.002]	[0.003]	[0.003]	[0.002]	[0.002]
Female	0.392**	0.391**	-0.109**	-0.109**	0.261**	0.261**	0.002	0.002	-0.015	-0.015	-0.010	-0.010
	[0.014]	[0.014]	[0.018]	[0.018]	[0.017]	[0.017]	[0.005]	[0.005]	[0.009]	[0.009]	[0.008]	[0.008]
Years of education	0.101**	0.101**	0.120**	0.120**	0.127**	0.127**	0.000	0.000	0.004*	0.004*	0.001	0.001
	[0.003]	[0.003]	[0.004]	[0.004]	[0.004]	[0.004]	[0.001]	[0.001]	[0.002]	[0.002]	[0.002]	[0.002]
Age 60-69 × score		-0.000		-0.002		-0.002		0.000				
		[0.002]		[0.002]		[0.002]		[0.001]				
Age 70-79 × score		-0.002		0.002		-0.000		0.001		0.002		0.002
		[0.002]		[0.003]		[0.003]		[0.001]		[0.001]		[0.001]
Age ≥ 80 × score		-0.007		-0.004		-0.007		-0.004*		-0.003		-0.005*
		[0.004]		[0.006]		[0.005]		[0.002]		[0.002]		[0.002]
Constant	-1.513**	-1.512**	-1.270**	-1.270**	-1.622**	-1.621**	0.149*	0.149*	0.950*	0.948*	1.637**	1.636**
	[0.124]	[0.124]	[0.158]	[0.158]	[0.146]	[0.146]	[0.074]	[0.074]	[0.386]	[0.386]	[0.399]	[0.399]
N, person-wave	49,827	49,827	32,204	32,204	32,204	32,204	40,622	40,622	20,737	20,737	20,737	20,737
N, persons	8,615	8,615	8,504	8,504	8,504	8,504	8,506	8,506	5,235	5,235	5,235	5,235
R^2	0.225	0.225	0.128	0.128	0.236	0.236	0.002	0.002	0.005	0.005	0.005	0.005
ΔR^2	0.000	0.000	0.001	0.001	0.001	0.001	0.000	0.000	0.000	0.000	0.000	0.000

Table S20. Power of GWAS on cognitive performance vs. candidate-SNP method in our Cognitive Performance Sample (*N* = 24,189)

	Effect size of SNP on cognitive performance (in R^2)			
	0.02%	0.04%	0.06%	0.08%
GWAS ($\alpha = 5\times10^{-8}$)	0.06%	1%	5%	15%
Candidate-SNP ($\alpha = .00072$)	12%	39%	67%	85%

Source: Authors' calculations using (22).

Table S21. Ex ante calculations of the expected number of true positive results, given alternative thresholds of including SNPs associated with educational attainment (EA) in the second stage on cognitive performance. Calculations are based on the actual sample sizes for EA in stage 1 (N = 106,703) and for cognitive performance in stage 2 (N = 24,189). The calculations assume that the effect of a SNP that is truly associated with EA only operates through cognitive performance and no other mediating factor. Under this assumption, the effect size of an EA-associated SNP would be attenuated by the imperfect correlation between EA and cognitive performance (see SI Appendix section 15). (1) and (2) are based on actual results of the stage 1 GWAS, after pruning SNPs for LD (the HapMap 2 CEU genotypes were used as reference panel; the physical threshold for clumping was 1000 kB, and the R^2 threshold for clumping was 0.01). Power in (3) and (7) was calculated using G*Power 3.1 (48, 49). Posterior beliefs in row (4) are calculated using Bayes' formula (21), with prior beliefs equal to 0.01%, power equal to (3), and α equal to the respective p-value threshold of the column. (5) results from dividing the family-wide significance level of 0.05 by (1). (6) results from dividing (2) by the assumed phenotypic correlation between EA and cognitive performance (0.6). (8) reports the expected number of true positives in the second stage by multiplying (1) × (4) × (7). (9) is calculated using Bayes' formula (21), with prior beliefs equal to (4), power equal to (7), and α equal to (5). Note that the available sample size for stage 2 and the assumed correlation between EA and cognitive performance only affect the absolute values in (8), whereas the p-value threshold that maximizes (8) depends only on the results of the first-stage GWAS.

		p-value threshold for including EA-associated SNPs in the second stage analyses on cognitive performance							
		5×10^{-8}	1×10^{-7}	1×10^{-6}	1×10^{-5}	1×10^{-4}	1×10^{-3}	1×10^{-2}	5×10^{-2}
Results of stage 1									
(1)	Number of EA-associated candidate SNPs	3	4	15	69	198	891	3,013	5,720
(2)	Avg R^2 of SNPs with EA	2.80×10^{-4}	2.73×10^{-4}	2.33×10^{-4}	1.98×10^{-4}	1.65×10^{-4}	1.25×10^{-4}	9.11×10^{-5}	7.05×10^{-5}
(3)	Ex-post power (two-sided) in first stage	55%	52%	52%	57%	62%	64%	71%	78%
(4)	Posterior belief that a candidate SNP from (1) is truly associated with EA	99.9%	99.8%	98.1%	85.1%	38.3%	6.0%	0.7%	0.2%
Ex-ante expectations for stage 2									
(5)	Bonferroni-adjusted *p*-value for second stage	1.67×10^{-2}	1.25×10^{-2}	3.33×10^{-3}	7.25×10^{-4}	2.53×10^{-4}	5.61×10^{-5}	1.66×10^{-5}	8.74×10^{-6}
(6)	Expected avg R^2 of SNPs in second stage given (2)	7.77×10^{-4}	7.59×10^{-4}	6.46×10^{-4}	5.51×10^{-4}	4.57×10^{-4}	3.47×10^{-4}	2.53×10^{-4}	1.96×10^{-4}
(7)	Expected power (two-sided) in second stage given (5) and (6)	97.4%	96.3%	84.6%	60.7%	36.9%	12.9%	3.3%	1.2%
(8)	Expected true positives second stage	3	4	12	36	28	7	7	0
(9)	Posterior belief (true|significant), using the *p*-value threshold of (5)	100%	100%	100%	100%	99.9%	99.5%	99.5%	75.8%

Additional Notes

1. Author contributions

Daniel Benjamin, David Cesarini, and Philipp Koellinger conceived and designed the study and organized the SSGAC consortium. Cornelius Rietveld performed the selection of education-associated SNPs and together with Gail Davies he also performed the quality control and meta-analyses of cohort-specific GWAS results. Anna Vinkhuyzen contributed to the interpretation of the meta-analysis results. The CHIC consortium was organized by George Davey Smith, Ian Deary, Robert Plomin and Peter Visscher. Beben Benyamin and Peter Visscher provided the CHIC meta-analysis results. Patrick Turley developed the correction of effect sizes for the winner's curse and the power calculations for the HRS polygenic score analyses. Christopher Chabris and Olga Rostapshova performed the selection of theory-based candidate SNPs. Daniel Benjamin conducted the Bayesian analysis of the credibility of the SNP associations. Cornelius Rietveld performed the polygenic score analyses in the HRS. Riccardo Marioni, Sarah Medland, Michael Miller, and Cornelius Rietveld performed the polygenic score analyses in the family samples. Tõnu Esko, Valur Emilsson, Rudolf Fehrmann, Lude Franke, Andrew Johnson, Juha Karjalainen and Tune Pers conducted the biological annotation. Daniel Benjamin, David Cesarini, Philipp Koellinger and Cornelius Rietveld wrote the first draft of the manuscript. Daniel Benjamin, David Cesarini, Tõnu Esko, Philipp Koellinger, Cornelius Rietveld and Patrick Turley all wrote substantial portions of the supplementary materials. Cornelius Rietveld prepared most of the tables and figures in the main text and supplementary materials. Christopher Chabris, Ian Deary, Robert Plomin, Vincent Jaddoe, Magnus Johannesson, David Laibson, Steven Pinker, Henning Tiemeier, Nicholas Timpson, Peter Visscher and Mary Ward critically reviewed and edited the manuscript.

2. Cohort-specific contributions

Cohort	Author	Overseeing (PI)	Genotyping	Phenotyping	Data analysis
ALSPAC	George Davey Smith	X			
	Nicholas Timpson		X	X	
	George McMahon				X
	Mary Ward				X
ERF	Sven van der Lee				X
	Carla Ibrahim-Verbaas				X
	Najaf Amin				X
	André Uitterlinden		X		
	Cornelia van Duijn	X	X	X	
GenR	Henning Tiemeier	X		X	
	Vincent Jaddoe	X	X		
	Christiaan De Leeuw				X
	Danielle Posthuma	X			X
	Frank Verhulst	X			
	Fernando Rivadeneira		X		
GS	Blair Smith			X	
	David Porteous		X	X	
	Caroline Hayward		X		
	Riccardo Marioni				X
HU	James Lee		X	X	X
	Steven Pinker	X			
	Christopher Chabris	X			
	David Laibson	X			
	Edward Glaeser	X			
LBC	Gail Davies		X		X
	David Liewald		X		X

	John Starr	X		X	
	Ian Deary	X		X	
MCTFR	Michael B. Miller		X	X	X
	Matt McGue	X			
	William G. Iacono	X			
	Jaime Derringer				X
QIMR	Sarah Medland				X
	Margaret Wright	X		X	
	Narelle Hansell			X	X
	Nicholas Martin	X	X		
STR	Patrik Magnusson		X	X	X
	Nancy Pedersen	X			
	Paul Lichtenstein	X			
	Magnus Johannesson	X		X	X
	Cornelius Rietveld				X
	David Cesarini				X
TEDS	Robert Plomin	X			
	Maciej Trzaskowski				X

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POU3F2

Term	P-value	Annotated
central nervous system neuron differentiation	2,91E-28	N
forebrain generation of neurons	4,05E-22	N
forebrain neuron differentiation	3,08E-21	N
telencephalon development	5,79E-19	Y
forebrain development	5,25E-18	Y
negative regulation of gliogenesis	9,08E-18	N
astrocyte differentiation	1,02E-17	Y
negative regulation of glial cell differentiation	2,91E-17	N
brain development	1,57E-16	Y
central nervous system neuron development	2,67E-16	N
glial cell differentiation	4,58E-16	Y
regulation of neuron differentiation	1,59E-15	Y
pallium development	2,79E-15	Y
cerebral cortex development	4,66E-15	Y
neuron fate commitment	1,18E-14	N
regulation of neurogenesis	1,25E-14	Y
central nervous system projection neuron axonogenesis	1,46E-14	N
positive regulation of neural precursor cell proliferation	2,15E-14	N
gliogenesis	2,79E-14	Y
cerebral cortex neuron differentiation	3,02E-14	N

JMJD1C

Term	P-value	Annotated
regulation of protein import into nucleus, translocation	1,87E-08	N

REEP3

Term	P-value	Annotated
lysosomal transport	1,08E-06	N
vacuolar transport	1,11E-06	N
sphingolipid metabolic process	1,40E-05	N

LRRC14

Term	P-value	Annotated
Endocytosis	5,72E-04	N
Tight junction	1,22E-03	N

ARHGAP39
FOXH1

Term	P-value	Annotated
cell migration involved in gastrulation	5,39E-34	Y
primitive streak formation	5,82E-28	N
anterior/posterior axis specification	1,08E-22	N
gastrulation with mouth forming second	3,62E-21	N
gastrulation	1,15E-20	Y
endoderm development	9,78E-19	N
signal transduction involved in regulation of gene expression	3,08E-14	N
axis specification	5,11E-13	N
formation of primary germ layer	7,73E-12	N
mesoderm development	1,09E-10	Y
somitogenesis	1,38E-10	N
endoderm formation	2,31E-10	N
cell fate commitment involved in formation of primary germ layers	8,47E-10	N

blastocyst formation	1,35E-09	N
heart looping	2,63E-09	Y
determination of heart left/right asymmetry	2,63E-09	Y
somite development	6,65E-09	N
embryonic axis specification	1,61E-08	N
ncRNA catabolic process	3,65E-08	N
trophectodermal cell differentiation	3,73E-08	N

KIFC2

Term	P-value	Annotated
regulation of receptor activity	2,06E-09	N
neurotransmitter secretion	2,31E-09	N
regulation of synaptic transmission	8,68E-09	N
regulation of alpha-amino-3-hydroxy-5-methyl-4-isoxazole propionate selective glutama...	3,93E-08	N
regulation of transmission of nerve impulse	4,39E-08	N
regulation of neurological system process	9,50E-08	N
synaptic vesicle transport	3,34E-07	N
regulation of neurotransmitter levels	6,16E-07	N
regulation of synaptic plasticity	8,28E-07	N
synaptic vesicle exocytosis	8,98E-07	N
glutamate secretion	1,01E-06	N
generation of a signal involved in cell-cell signaling	2,27E-06	N
signal release	2,27E-06	N

CYHR1
VPS28

Term	P-value	Annotated
mannose metabolic process	2,58E-12	N

SCRT1

Term	P-value	Annotated
potassium ion transport	9,34E-12	N
visual learning	2,46E-11	N
locomotory behavior	3,15E-11	N
mating behavior	2,53E-10	N
visual behavior	7,01E-10	N
associative learning	1,07E-09	N
learning	1,29E-09	N
regulation of neurotransmitter levels	1,39E-09	N
ionotropic glutamate receptor signaling pathway	2,68E-09	N
neurotransmitter secretion	2,90E-09	N
neurotransmitter transport	7,48E-09	N
adult locomotory behavior	8,13E-09	N
response to tropane	1,28E-08	N
response to cocaine	1,28E-08	N
neuron-neuron synaptic transmission	1,33E-08	N
neuromuscular process	2,84E-08	N
reproductive behavior	4,27E-08	N
regulation of postsynaptic membrane potential	5,42E-08	N
membrane hyperpolarization	6,39E-08	N
synaptic transmission, glutamatergic	1,04E-07	N

ATXN2L

Term	P-value	Annotated

positive regulation of gene expression, epigenetic	9,87E-13	N
protein-DNA complex disassembly	3,07E-09	N
nucleosome disassembly	3,07E-09	N
chromatin disassembly	3,07E-09	N

TUFM

Term	P-value	Annotated
mitochondrion organization	2,55E-17	N
aerobic respiration	3,38E-15	N
cellular respiration	7,45E-14	N
oxidative phosphorylation	4,70E-13	N
respiratory electron transport chain	6,50E-13	N
quinone cofactor metabolic process	1,10E-12	N
mitochondrial translation	1,54E-11	N
cofactor metabolic process	1,59E-11	N
electron transport chain	2,15E-11	N
ATP synthesis coupled electron transport	3,01E-11	N
mitochondrial ATP synthesis coupled electron transport	3,01E-11	N
energy derivation by oxidation of organic compounds	6,05E-11	N
mitochondrial RNA metabolic process	1,69E-10	N
generation of precursor metabolites and energy	1,76E-10	N
branched chain family amino acid catabolic process	1,76E-10	N
tRNA metabolic process	2,52E-10	N
cofactor biosynthetic process	3,48E-10	N
tricarboxylic acid cycle	4,25E-10	N
coenzyme metabolic process	7,42E-10	N
acetyl-CoA catabolic process	7,63E-10	N

SH2B1
NFATC2IP

Term	P-value	Annotated
recombinational repair	3,39E-11	N
double-strand break repair via homologous recombination	4,67E-11	N
DNA replication	1,06E-07	N
double-strand break repair	1,44E-07	N
DNA recombination	2,29E-07	N
DNA repair	4,74E-07	N

SPNS1

Term	P-value	Annotated
lysosome organization	1,04E-20	N
vacuole organization	1,45E-18	N
organophosphate metabolic process	3,04E-13	N
phospholipid metabolic process	1,15E-12	N
phospholipid biosynthetic process	1,71E-12	N
ferric iron transport	1,64E-10	N
transferrin transport	1,64E-10	N
sphingolipid metabolic process	1,65E-10	N
sphingoid metabolic process	3,78E-10	N
ceramide metabolic process	4,28E-10	N
transition metal ion transport	4,29E-10	N
membrane lipid metabolic process	5,92E-10	N
glycosphingolipid metabolic process	2,51E-08	N
glycolipid metabolic process	2,94E-08	N

iron ion transport	7,12E-08	N

LAT

Term	P-value	Annotated
T cell receptor signaling pathway	2,02E-78	Y
antigen receptor-mediated signaling pathway	1,35E-71	Y
immune response-activating cell surface receptor signaling pathway	2,30E-71	Y
immune response-regulating cell surface receptor signaling pathway	4,87E-71	Y
T cell activation	5,29E-62	Y
lymphocyte costimulation	1,12E-56	N
T cell costimulation	1,12E-56	N
regulation of T cell activation	4,83E-52	Y
lymphocyte activation	3,24E-50	Y
T cell selection	6,20E-50	N
positive regulation of T cell activation	1,34E-48	N
regulation of cell activation	3,90E-46	Y
regulation of lymphocyte activation	1,26E-45	Y
regulation of leukocyte activation	1,43E-45	Y
leukocyte activation	1,21E-44	Y
positive regulation of leukocyte activation	1,01E-43	N
T cell differentiation	1,14E-43	N
positive T cell selection	2,71E-43	N
positive regulation of lymphocyte activation	4,01E-43	N
positive regulation of cell activation	2,35E-42	N

SULT1A1
SULT1A2

Term	P-value	Annotated
response to xenobiotic stimulus	3,47E-08	Y
cellular response to xenobiotic stimulus	3,47E-08	Y
triglyceride homeostasis	4,24E-08	N
xenobiotic metabolic process	5,58E-08	Y
complement activation, alternative pathway	3,81E-07	N

CCDC101

Term	P-value	Annotated
N-acetyltransferase activity	3,25E-06	N
acetyltransferase activity	3,81E-06	N
N-acyltransferase activity	6,12E-06	N

NRXN1

Term	P-value	Annotated
glutamate signaling pathway	2,62E-19	N
neurotransmitter secretion	1,58E-16	N
gamma-aminobutyric acid signaling pathway	5,57E-16	N
synaptic vesicle exocytosis	7,47E-15	N
regulation of neurotransmitter levels	3,56E-14	N
regulation of synaptic transmission	8,38E-14	Y
neurotransmitter transport	8,67E-14	N
regulation of neurological system process	2,88E-13	Y
regulation of transmission of nerve impulse	7,94E-13	Y
neuron-neuron synaptic transmission	1,06E-12	Y
glutamate secretion	1,09E-12	N
synaptic vesicle transport	5,79E-12	N

synaptic transmission, glutamatergic	2,06E-11	Y
signal release	6,74E-11	N
generation of a signal involved in cell-cell signaling	6,74E-11	N
learning or memory	2,45E-10	Y
cellular potassium ion transport	2,70E-10	N
potassium ion transmembrane transport	2,70E-10	N
axonogenesis	3,02E-10	Y
regulation of excitatory postsynaptic membrane potential	4,07E-10	Y

NUPR1

Term	P-value	Annotated
serine family amino acid biosynthetic process	7,90E-12	N
regulation of fatty acid biosynthetic process	4,66E-10	N
response to acid	1,16E-09	N
response to amino acid stimulus	2,68E-09	N
response to hypoxia	3,34E-09	N
response to oxygen levels	4,73E-09	N

NPAS2
KCNMA1

Term	P-value	Annotated
calcium ion transmembrane transport	2,84E-12	N
lymphoid progenitor cell differentiation	3,54E-07	N
calcium ion transport	2,61E-06	N
divalent inorganic cation transport	3,40E-06	N
synapse organization	3,92E-06	N

DEC1
SDCCAG8

Term	P-value	Annotated
negative regulation of JNK cascade	1,96E-05	N

AKT3
CRYZL1

Term	P-value	Annotated
synaptic vesicle endocytosis	9,05E-09	N

ITSN1
SON

Term	P-value	Annotated
RNA splicing, via transesterification reactions	4,37E-17	N
RNA splicing, via transesterification reactions with bulged adenosine as nucleophile	7,22E-17	N
nuclear mRNA splicing, via spliceosome	7,22E-17	N
RNA splicing	2,18E-14	N
mRNA processing	4,98E-14	N
mRNA 3'-end processing	1,72E-11	N
spliceosome assembly	3,90E-11	N
histone H3-K4 methylation	6,12E-11	N
intracellular steroid hormone receptor signaling pathway	7,67E-11	N
alternative nuclear mRNA splicing, via spliceosome	1,67E-10	N
RNA 3'-end processing	1,97E-10	N
RNA localization	2,59E-10	N
androgen receptor signaling pathway	2,61E-10	N
mRNA transport	3,31E-10	N

RNA export from nucleus	3,64E-10	N
chromatin modification	4,23E-10	N
mRNA export from nucleus	8,08E-10	N
RNA transport	9,30E-10	N
establishment of RNA localization	9,30E-10	N
nucleic acid transport	9,30E-10	N

GART

Term	P-value	Annotated
ncRNA metabolic process	3,42E-26	N
ncRNA processing	3,69E-24	N
rRNA processing	3,54E-22	N
ribosome biogenesis	7,22E-22	N
rRNA metabolic process	2,36E-21	N
cellular component biogenesis at cellular level	5,23E-21	N
ribonucleoprotein complex biogenesis	5,51E-21	N
tRNA metabolic process	3,14E-20	N
RNA modification	1,36E-17	N
tRNA processing	1,04E-15	N
rRNA transcription	3,86E-15	N
tRNA aminoacylation for protein translation	1,06E-14	N
ribonucleoside monophosphate biosynthetic process	2,81E-14	Y
amino acid activation	1,23E-13	N
tRNA aminoacylation	1,23E-13	N
nucleobase biosynthetic process	2,69E-13	Y
spliceosomal snRNP assembly	6,31E-13	N
nucleobase metabolic process	1,23E-12	Y
tRNA modification	2,21E-12	N
ribonucleoside monophosphate metabolic process	2,27E-12	Y

DNAJC28
TMEM50B

Term	P-value	Annotated
ER-associated protein catabolic process	1,78E-09	N
protein N-linked glycosylation via asparagine	3,33E-09	N
peptidyl-asparagine modification	3,33E-09	N
protein N-linked glycosylation	7,26E-09	N
protein folding	7,82E-09	N
response to unfolded protein	8,72E-09	N
response to topologically incorrect protein	1,72E-08	N
protein glycosylation	2,67E-08	N
macromolecule glycosylation	2,67E-08	N
cell redox homeostasis	5,55E-08	N
phospholipid biosynthetic process	6,59E-08	N
glycosylation	8,77E-08	N

IFNGR2

Term	P-value	Annotated
innate immune response-activating signal transduction	3,69E-22	N
pattern recognition receptor signaling pathway	9,49E-22	N
I-kappaB kinase/NF-kappaB cascade	1,95E-21	N
activation of innate immune response	2,00E-21	N
toll-like receptor signaling pathway	3,17E-20	N
Toll signaling pathway	1,29E-17	N

positive regulation of NF-kappaB transcription factor activity	1,41E-17	N
toll-like receptor 4 signaling pathway	5,07E-16	N
toll-like receptor 2 signaling pathway	1,52E-15	N
positive regulation of I-kappaB kinase/NF-kappaB cascade	1,55E-15	N
regulation of I-kappaB kinase/NF-kappaB cascade	1,68E-15	N
MyD88-dependent toll-like receptor signaling pathway	2,37E-15	N
positive regulation of innate immune response	1,12E-14	N
toll-like receptor 1 signaling pathway	1,19E-14	N
toll-like receptor 3 signaling pathway	1,43E-14	N
cellular response to mechanical stimulus	1,93E-14	N
cytoplasmic pattern recognition receptor signaling pathway	2,06E-14	N
nucleotide-binding domain, leucine rich repeat containing receptor signaling pathway	2,06E-14	N
nucleotide-binding oligomerization domain containing signaling pathway	2,06E-14	N
MyD88-independent toll-like receptor signaling pathway	3,36E-14	N

SBNO1

Term	P-value	Annotated
protein deubiquitination	7,80E-07	N
protein ubiquitination involved in ubiquitin-dependent protein catabolic process	1,08E-06	N
histone lysine methylation	3,64E-06	N

SETD8
RILPL2

Term	P-value	Annotated
regulation of T cell activation	2,55E-08	N
negative regulation of lymphocyte activation	2,67E-08	N
regulation of lymphocyte activation	2,84E-08	N
negative regulation of leukocyte activation	7,22E-08	N
regulation of interleukin-2 biosynthetic process	8,30E-08	N
regulation of interleukin-2 production	1,88E-07	N
regulation of leukocyte activation	2,48E-07	N
negative regulation of leukocyte proliferation	2,87E-07	N
interleukin-2 production	3,78E-07	N
regulation of cell activation	4,14E-07	N
negative regulation of immune system process	5,04E-07	N
leukocyte apoptosis	6,10E-07	N
regulation of B cell activation	8,94E-07	N
negative regulation of cell activation	9,69E-07	N
positive regulation of interleukin-2 biosynthetic process	1,11E-06	N
immune response-activating signal transduction	1,98E-06	N
T cell proliferation	2,02E-06	N
negative regulation of B cell activation	2,02E-06	N
immune response-regulating signaling pathway	2,19E-06	N
negative regulation of T cell activation	2,52E-06	N

C12orf65
MPHOSPH9

Term	P-value	Annotated
M phase of mitotic cell cycle	5,68E-09	Y
organelle fission	5,85E-09	N
mitosis	6,40E-09	N
nuclear division	6,40E-09	N
microtubule anchoring	1,45E-08	N
mitotic prometaphase	2,11E-08	N

cell division	5,89E-08	N
M phase	1,67E-07	N
attachment of spindle microtubules to chromosome	2,10E-07	N
spindle organization	2,50E-07	N
mitotic sister chromatid segregation	5,09E-07	N
chromosome segregation	5,75E-07	N
microtubule cytoskeleton organization	6,25E-07	N
mitotic spindle organization	6,91E-07	N
cell cycle arrest	8,48E-07	N
G2/M transition of mitotic cell cycle	9,45E-07	N
mitotic metaphase/anaphase transition	1,28E-06	N
attachment of spindle microtubules to kinetochore	1,38E-06	N
sister chromatid segregation	1,51E-06	N
regulation of cell cycle process	1,65E-06	N

SNRNP35
RILPL1

Term	P-value	Annotated
nuclear-transcribed mRNA catabolic process	6,13E-08	N
nuclear-transcribed mRNA catabolic process, deadenylation-dependent decay	1,51E-06	N
mRNA catabolic process	4,59E-06	N
RNA catabolic process	7,44E-06	N

PITPNM2

Term	P-value	Annotated
platelet activation	6,48E-06	
blood coagulation	1,34E-05	
hemostasis	1,47E-05	
G-protein coupled acetylcholine receptor signaling pathway	1,89E-05	
regulation of cAMP metabolic process	1,94E-05	
regulation of metal ion transport	2,01E-05	
coagulation	2,04E-05	
regulation of ion transport	2,06E-05	

STK24
FARP1

Term	P-value	Annotated
regulation of cell morphogenesis	2,78E-10	N
axonogenesis	8,03E-10	N
axon guidance	2,02E-09	N
regulation of mesenchymal cell proliferation	4,54E-09	N
epithelial to mesenchymal transition	1,07E-08	N
artery development	1,07E-08	N
regulation of epithelial to mesenchymal transition	1,47E-08	N
regulation of cell morphogenesis involved in differentiation	2,21E-08	N
positive regulation of mesenchymal cell proliferation	4,54E-08	N
regulation of cell development	5,43E-08	N
ureteric bud development	6,35E-08	N
embryonic digit morphogenesis	6,98E-08	N
epithelial tube formation	9,10E-08	N
positive regulation of epithelial to mesenchymal transition	9,10E-08	N
positive regulation of cell morphogenesis involved in differentiation	1,13E-07	N
embryonic cranial skeleton morphogenesis	1,18E-07	N
embryonic appendage morphogenesis	1,31E-07	N

embryonic limb morphogenesis	1,31E-07	N
SMAD protein import into nucleus	1,32E-07	N
mammary gland epithelial cell proliferation	1,38E-07	N

SLC15A1
TANK

Term	P-value	Annotated
pattern recognition receptor signaling pathway	8,19E-13	N
toll-like receptor signaling pathway	8,92E-13	N
positive regulation of T cell mediated immunity	9,75E-13	N
innate immune response-activating signal transduction	1,29E-12	N
positive regulation of innate immune response	4,22E-12	N
positive regulation of lymphocyte mediated immunity	6,58E-12	N
positive regulation of leukocyte mediated immunity	6,58E-12	N
positive regulation of NF-kappaB transcription factor activity	7,52E-12	N
positive regulation of adaptive immune response based on somatic recombination of imm...	1,28E-11	N
activation of innate immune response	1,38E-11	N
toll-like receptor 4 signaling pathway	1,47E-11	N
alpha-beta T cell proliferation	1,73E-11	N
positive regulation of adaptive immune response	2,22E-11	N
positive regulation of interleukin-10 production	2,68E-11	N
positive regulation of defense response	6,57E-11	N
toll-like receptor 3 signaling pathway	7,23E-11	N
Toll signaling pathway	1,04E-10	N
MyD88-independent toll-like receptor signaling pathway	1,29E-10	N
regulation of innate immune response	1,90E-10	N
positive regulation of leukocyte proliferation	2,03E-10	N

PSMD14

Term	P-value	Annotated
negative regulation of ubiquitin-protein ligase activity involved in mitotic cell cycle	1,29E-48	Y
negative regulation of ligase activity	5,60E-47	Y
negative regulation of ubiquitin-protein ligase activity	5,60E-47	Y
positive regulation of ligase activity	8,59E-47	Y
regulation of cellular amino acid metabolic process	9,36E-47	Y
positive regulation of ubiquitin-protein ligase activity	1,13E-46	Y
positive regulation of ubiquitin-protein ligase activity involved in mitotic cell cycle	2,13E-46	Y
regulation of ubiquitin-protein ligase activity involved in mitotic cell cycle	1,30E-44	Y
M/G1 transition of mitotic cell cycle	1,92E-44	Y
regulation of ligase activity	5,58E-44	Y
signal transduction involved in mitotic cell cycle checkpoint	1,01E-43	Y
signal transduction involved in mitotic cell cycle G1/S checkpoint	1,01E-43	Y
signal transduction involved in mitotic cell cycle G1/S transition DNA damage checkpo...	1,01E-43	Y
signal transduction involved in DNA integrity checkpoint	1,01E-43	Y
DNA damage response, signal transduction by p53 class mediator resulting in cell cycl...	1,01E-43	Y
signal transduction involved in DNA damage checkpoint	1,01E-43	Y
regulation of ubiquitin-protein ligase activity	1,25E-43	Y
signal transduction involved in cell cycle checkpoint	1,72E-43	Y
signal transduction involved in G1/S transition checkpoint	1,72E-43	Y
negative regulation of protein ubiquitination	4,02E-42	Y

TBR1

Term	P-value	Annotated
behavioral defense response	1,76E-32	N

behavioral fear response	3,51E-27	N
fear response	6,58E-25	N
hippocampus development	2,81E-23	N
pallium development	8,84E-23	N
G-protein coupled acetylcholine receptor signaling pathway	5,31E-22	N
axonal fasciculation	2,02E-21	N
limbic system development	9,43E-18	N
neuron recognition	3,49E-17	N
telencephalon development	2,07E-16	N
multicellular organismal response to stress	2,03E-14	N
forebrain development	4,94E-14	N
cerebral cortex neuron differentiation	1,15E-13	N
cerebral cortex radially oriented cell migration	1,48E-13	N
potassium ion transport	1,94E-13	N
synaptic transmission, glutamatergic	5,15E-13	N
ionotropic glutamate receptor signaling pathway	3,21E-12	N
neuron-neuron synaptic transmission	8,34E-12	N
learning or memory	1,63E-11	N
regulation of synaptic plasticity	2,39E-11	N

POU3F2

Term	P-value	Annotated
neuron projection membrane	2,77E-07	N
axolemma	9,98E-07	N
dendrite	1,20E-06	N
external encapsulating structure part	2,58E-06	N
cell envelope	2,58E-06	N
periplasmic space	7,53E-06	N
outer membrane-bounded periplasmic space	7,53E-06	N

REEP3

Term	P-value	Annotated
early endosome	7,45E-05	N

LRRC14
ARHGAP39
FOXH1

Term	P-value	Annotated
translation initiation factor binding	6,07E-09	N

KIFC2

Term	P-value	Annotated
dendrite	1,26E-07	N
dendritic spine head	1,74E-07	N
postsynaptic density	1,74E-07	N
synaptosome	1,77E-07	N
dendritic spine	2,77E-07	N
neuron spine	2,77E-07	N
voltage-gated calcium channel complex	3,03E-07	N
synapse part	1,10E-06	N
synapse	1,14E-06	N
ciliary rootlet	2,33E-06	N
cell body	1,44E-05	N
synaptic membrane	2,15E-05	N
calcium channel complex	2,16E-05	N

CYHR1
VPS28

Term	P-value	Annotated
respiratory chain	1,30E-09	N
eukaryotic translation initiation factor 3 complex	1,45E-09	N
mitochondrial respiratory chain	1,19E-08	N

SCRT1

Term	P-value	Annotated
axon part	2,20E-12	N
main axon	1,07E-10	N
synapse part	1,18E-08	N
axon	1,21E-08	N
voltage-gated potassium channel complex	1,48E-08	N
potassium channel complex	1,48E-08	N
cation channel complex	2,97E-08	N
synapse	1,22E-07	N
neuron projection terminus	2,92E-07	N
neuronal cell body	3,00E-07	N
cell body	6,98E-07	N
axon terminus	1,35E-06	N
terminal button	2,84E-06	N
dendritic spine head	5,76E-06	N
postsynaptic density	5,76E-06	N
ion channel complex	7,17E-06	N
synaptic membrane	8,81E-06	N
synaptic vesicle membrane	9,15E-06	N
ionotropic glutamate receptor complex	9,98E-06	N
periplasmic space	3,43E-05	N

ATXN2L

Term	P-value	Annotated
npBAF complex	1,43E-08	N
nuclear chromatin	4,86E-08	N
nBAF complex	3,05E-07	N
chromatin remodeling complex	7,03E-07	N
SWI/SNF-type complex	1,36E-06	N
PRC1 complex	1,77E-06	N
SWI/SNF complex	4,69E-06	N
sex chromosome	5,76E-06	N
methyltransferase complex	5,86E-06	N
histone methyltransferase complex	5,86E-06	N

TUFM

Term	P-value	Annotated
mitochondrial matrix	9,13E-34	Y
mitochondrial inner membrane	2,48E-23	N
organelle inner membrane	4,09E-23	N
mitochondrial membrane	9,90E-23	N
mitochondrial envelope	1,04E-22	N
mitochondrial nucleoid	1,33E-22	Y
nucleoid	2,31E-21	Y

mitochondrial membrane part	4,74E-15	N
respiratory chain	1,17E-12	N
mitochondrial respiratory chain	2,93E-12	N
organellar ribosome	8,49E-12	N
mitochondrial ribosome	8,49E-12	N
ribosome	1,72E-10	N
small ribosomal subunit	4,90E-10	N
organellar small ribosomal subunit	4,97E-10	N
mitochondrial small ribosomal subunit	4,97E-10	N
integral to mitochondrial membrane	5,96E-10	N
respiratory chain complex I	1,87E-08	N
mitochondrial respiratory chain complex I	1,87E-08	N
NADH dehydrogenase complex	1,87E-08	N

SH2B1
NFATC2IP

Term	P-value	Annotated
PML body	2,87E-09	N
nuclear body	1,08E-06	N
methyltransferase complex	1,64E-06	N
histone methyltransferase complex	1,64E-06	N
chromosomal part	1,20E-05	N

SPNS1

Term	P-value	Annotated
vacuolar part	1,17E-22	N
vacuolar membrane	3,96E-22	N
lysosomal membrane	2,64E-21	N
vacuole	1,52E-18	N
lysosome	5,29E-17	N
lytic vacuole	5,29E-17	N
late endosome	1,83E-09	N
lysosomal lumen	7,86E-09	N
vacuolar lumen	7,88E-09	N
proton-transporting V-type ATPase complex	2,87E-07	N
intrinsic to endoplasmic reticulum membrane	5,76E-07	N
integral to endoplasmic reticulum membrane	1,26E-06	N
endosome membrane	3,09E-06	N
late endosome membrane	3,21E-06	N
autophagic vacuole	3,45E-06	N
endosomal part	3,76E-06	N
endosome	7,38E-06	N

LAT

Term	P-value	Annotated
T cell receptor complex	5,18E-103	N
external side of plasma membrane	5,22E-45	N
immunological synapse	2,02E-32	Y
receptor complex	3,12E-32	N
cell surface	6,99E-24	N
integrin complex	3,24E-14	N

SULT1A1
SULT1A2

Term	P-value	Annotated
high-density lipoprotein particle	2,84E-07	N

CCDC101

Term	P-value	Annotated
Base excision repair	1,29E-04	N

NRXN1

Term	P-value	Annotated
presynaptic membrane	1,71E-26	Y
synapse	2,47E-23	Y
axon	5,24E-23	Y
axon part	2,21E-21	Y
synapse part	4,15E-21	Y
synaptic membrane	2,50E-19	Y
ion channel complex	1,25E-16	N
outer membrane-bounded periplasmic space	1,42E-16	N
periplasmic space	1,42E-16	N
cation channel complex	1,02E-15	N
main axon	1,05E-15	N
dendrite	1,59E-15	N
external encapsulating structure part	2,24E-15	N
cell envelope	2,24E-15	N
postsynaptic membrane	2,28E-14	N
synaptic vesicle membrane	1,74E-13	N
axolemma	2,80E-13	N
terminal button	3,10E-13	N
external encapsulating structure	4,32E-13	N
voltage-gated sodium channel complex	5,32E-13	N

NUPR1
NPAS2
KCNMA1

Term	P-value	Annotated

synapse	1,35E-08	Y
synapse part	2,81E-06	Y
costamere	2,95E-06	N
voltage-gated calcium channel complex	8,84E-06	N
calcium channel complex	1,25E-05	N
postsynaptic density	3,06E-05	N
dendritic spine head	3,06E-05	N
dendrite	4,01E-05	N
neuron projection terminus	4,66E-05	Y

DEC1
SDCCAG8

Term	P-value	Annotated
microtubule organizing center	2,39E-05	Y
centrosome	1,14E-04	Y

AKT3

Term	P-value	Annotated
intrinsic to Golgi membrane	1,12E-05	N

CRYZL1

Term	P-value	Annotated
aggresome	2,87E-06	N

ITSN1
SON

Term	P-value	Annotated
nuclear speck	2,67E-18	Y
nuclear body	5,80E-18	Y
catalytic step 2 spliceosome	1,43E-14	N
spliceosomal complex	3,92E-13	N
Cajal body	1,35E-08	N
aggresome	1,54E-08	N
chromatin remodeling complex	2,49E-08	N
cytoplasmic stress granule	5,84E-08	N
histone acetyltransferase complex	9,44E-08	N
inclusion body	2,36E-06	N
heterogeneous nuclear ribonucleoprotein complex	3,29E-06	N

GART

Term	P-value	Annotated
preribosome	5,23E-22	N
nucleolus	7,58E-22	N
Cajal body	9,44E-15	N

nucleolar part	7,14E-14	N
nuclear pore	7,16E-13	N
pore complex	9,51E-11	N
mitochondrial nucleoid	1,66E-08	N
nuclear DNA-directed RNA polymerase complex	2,49E-08	N
DNA-directed RNA polymerase complex	2,49E-08	N
RNA polymerase complex	3,28E-08	N
MLL1 complex	4,72E-08	N
small nucleolar ribonucleoprotein complex	1,96E-07	N
ribonucleoprotein complex	2,54E-07	N
nuclear envelope	2,81E-07	N
nucleoid	3,18E-07	N
Nup107-160 complex	1,19E-06	N
nuclear matrix	2,08E-06	N
histone methyltransferase complex	3,86E-06	N
methyltransferase complex	3,86E-06	N
mitochondrial matrix	8,86E-06	N

DNAJC28
TMEM50B

Term	P-value	Annotated
dendrite cytoplasm	1,00E-10	N
endoplasmic reticulum lumen	1,33E-07	N
endoplasmic reticulum-Golgi intermediate compartm	1,80E-07	N
cell projection cytoplasm	4,00E-07	N
integral to endoplasmic reticulum membrane	6,78E-07	N
oligosaccharyltransferase complex	1,82E-06	N

IFNGR2

Term	P-value	Annotated
receptor complex	1,25E-06	N
endosome	6,73E-06	N

SBNO1

Term	P-value	Annotated
histone methyltransferase complex	5,62E-07	N
methyltransferase complex	5,62E-07	N
nuclear body	1,12E-05	N
polysome	1,65E-05	N
nuclear speck	4,07E-05	N
PcG protein complex	6,96E-05	N

SETD8
RILPL2

Term	P-value	Annotated
anchored to external side of plasma membrane	2,67E-05	N

C12orf65
MPHOSPH9

Term	P-value	Annotated
centrosome	1,67E-10	Y
microtubule organizing center part	3,26E-09	Y
centriole	3,60E-09	Y
nuclear ubiquitin ligase complex	5,66E-09	N
spindle pole	1,40E-08	N
kinetochore	6,33E-08	N
microtubule organizing center	9,13E-08	N
condensed chromosome kinetochore	1,48E-07	N
anaphase-promoting complex	1,68E-07	N
spindle	3,50E-07	N
condensed chromosome, centromeric region	8,20E-07	N
condensed chromosome	1,14E-06	N
chromosome, centromeric region	1,90E-06	N
spindle microtubule	1,18E-05	N

SNRNP35
RILPL1

Term	P-value	Annotated
sarcoplasm	1,75E-05	N
I band	9,08E-05	N

PITPNM2

Term	P-value	Annotated
cation channel complex	1,65E-05	N
asymmetric synapse	2,15E-05	N

STK24
FARP1

Term	P-value	Annotated
cell leading edge	6,05E-12	N
adherens junction	2,92E-11	N
anchoring junction	1,98E-10	N
lamellipodium	3,22E-10	N
leading edge membrane	8,05E-10	N
septin complex	8,18E-09	N
septin cytoskeleton	8,18E-09	N
stress fiber	1,09E-08	N
actomyosin	1,14E-08	N

cell projection membrane	2,55E-08	N
actin filament bundle	5,01E-08	N
focal adhesion	9,15E-08	N
cell-substrate adherens junction	3,98E-07	N
cell cortex	9,40E-07	N
cell-substrate junction	1,11E-06	N
actin cytoskeleton	9,10E-06	N
synapse	1,98E-05	N

SLC15A1
TANK
PSMD14

Term	P-value	Annotated
proteasome complex	1,36E-54	y
proteasome accessory complex	1,49E-42	N
proteasome core complex	2,62E-26	N
mitochondrial ribosome	2,35E-11	N
organellar ribosome	2,35E-11	N
ribonucleoprotein complex	1,83E-10	N
ribosome	3,69E-09	N
nuclear envelope	9,72E-09	N
signalosome	1,88E-08	N
nuclear pore	2,33E-08	N
pore complex	6,28E-08	N
integrator complex	5,12E-07	N
organellar large ribosomal subunit	2,06E-06	N
mitochondrial large ribosomal subunit	2,06E-06	N

TBR1

Term	P-value	Annotated
synapse part	1,33E-15	N
synaptic membrane	5,07E-15	N
cation channel complex	5,37E-15	N
potassium channel complex	6,51E-15	N
voltage-gated potassium channel complex	6,51E-15	N
ion channel complex	1,40E-13	N
presynaptic membrane	4,68E-13	N
synapse	3,59E-12	N
postsynaptic membrane	6,20E-10	N
dendrite	7,25E-10	N
asymmetric synapse	5,60E-09	N
site of polarized growth	2,96E-08	N
growth cone	3,54E-08	N
synaptic vesicle membrane	7,08E-08	N

POU3F2

Term	P-value	Annotated
HMG box domain binding	7,52E-07	N
ionotropic glutamate receptor activity	3,68E-06	N
ephrin receptor activity	4,97E-06	N

JMJD1C

Term	P-value	Annotated
mitogen-activated protein kinase binding	1,12E-08	N
nuclear hormone receptor binding	1,15E-06	Y
histone acetyltransferase activity	2,63E-06	N
hormone receptor binding	4,18E-06	Y
protein kinase binding	5,80E-06	N
thyroid hormone receptor binding	7,04E-06	Y
helicase activity	1,11E-05	N
purine NTP-dependent helicase activity	1,42E-05	N
ATP-dependent helicase activity	1,42E-05	N
histone deacetylase binding	2,02E-05	N

REEP3
LRRC14
ARHGAP39

Term	P-value	Annotated
microtubule motor activity	5,17E-05	N
Rho GTPase binding	9,71E-05	N

FOXH1
KIFC2

Term	P-value	Annotated
voltage-gated calcium channel activity	1,56E-05	N

CYHR1
VPS28
SCRT1

Term	P-value	Annotated
potassium ion transmembrane transporter activity	4,45E-10	N
potassium channel activity	3,44E-09	N
dopamine binding	4,48E-09	N
voltage-gated potassium channel activity	7,42E-09	N
voltage-gated cation channel activity	2,60E-08	N
voltage-gated ion channel activity	2,35E-07	N
voltage-gated channel activity	2,35E-07	N
tau-protein kinase activity	2,91E-07	N
monovalent inorganic cation transmembrane transporter activity	4,64E-07	N

cation channel activity	9,05E-07	N
metal ion transmembrane transporter activity	1,06E-06	N
gated channel activity	1,77E-06	N
delayed rectifier potassium channel activity	2,29E-06	N
extracellular-glutamate-gated ion channel activity	4,72E-06	N
inorganic cation transmembrane transporter activity	6,20E-06	N
ionotropic glutamate receptor activity	1,78E-05	N

ATXN2L

Term	P-value	Annotated
transcription cofactor activity	6,47E-11	N
transcription factor binding transcription factor activity	8,61E-11	N
protein binding transcription factor activity	2,03E-10	N
tau-protein kinase activity	7,03E-10	N
transcription corepressor activity	1,47E-09	N

TUFM

Term	P-value	Annotated
4 iron, 4 sulfur cluster binding	5,57E-23	N
iron-sulfur cluster binding	8,95E-15	N
metal cluster binding	8,95E-15	N
unfolded protein binding	2,23E-09	N
hydrogen ion transporting ATP synthase activity, rotational mechan	5,37E-09	N
cofactor binding	1,02E-08	N
oxidoreductase activity, acting on NADH or NADPH	1,93E-08	N
ligase activity, forming aminoacyl-tRNA and related compounds	2,48E-08	N
aminoacyl-tRNA ligase activity	2,48E-08	N
ligase activity, forming carbon-oxygen bonds	2,48E-08	N
NADH dehydrogenase (ubiquinone) activity	2,69E-08	N
NADH dehydrogenase (quinone) activity	2,69E-08	N
NADH dehydrogenase activity	2,69E-08	N
oxidoreductase activity, acting on the CH-CH group of donors	3,94E-08	N
structural constituent of ribosome	6,53E-08	N
NAD binding	4,32E-07	N
coenzyme binding	5,03E-07	N
modified amino acid binding	6,67E-07	N
oxidoreductase activity, acting on NADH or NADPH, quinone or simi	7,42E-07	N
translation factor activity, nucleic acid binding	9,90E-07	Y

SH2B1
NFATC2IP

Term	P-value	Annotated
deoxyribonuclease activity	9,14E-07	N
methylated histone residue binding	3,30E-06	N

SPNS1

Term	P-value	Annotated
hexosaminidase activity	4,20E-14	N
active transmembrane transporter activity	2,63E-08	N
ATPase activity, coupled to transmembrane movement of ions	1,47E-07	N
cation-transporting ATPase activity	2,47E-07	N
primary active transmembrane transporter activity	2,94E-07	N
P-P-bond-hydrolysis-driven transmembrane transporter activity	2,94E-07	N

LAT

Term	P-value	Annotated
receptor signaling complex scaffold activity	2,00E-26	N
G-protein coupled chemoattractant receptor activity	2,26E-22	N
chemokine receptor activity	2,26E-22	N
C-C chemokine receptor activity	1,58E-17	N
antigen binding	1,00E-16	N
tumor necrosis factor receptor binding	1,12E-16	N
signaling adaptor activity	3,30E-16	Y
SH2 domain binding	4,18E-16	N
cytokine receptor activity	3,47E-15	N
MHC protein binding	2,15E-14	N
MHC class I protein binding	2,17E-14	N
tumor necrosis factor receptor superfamily binding	2,60E-14	N
coreceptor activity	7,84E-14	N
SH3/SH2 adaptor activity	1,76E-12	Y

SULT1A1
SULT1A2

Term	P-value	Annotated
cargo receptor activity	4,59E-09	N
lipid binding	6,00E-09	N
monocarboxylic acid binding	7,17E-09	N
retinol binding	1,89E-08	N
retinal binding	3,60E-08	N
scavenger receptor activity	4,79E-08	N
bacterial cell surface binding	7,69E-08	N
isoprenoid binding	7,82E-08	N
vitamin binding	8,73E-08	N
retinoid binding	1,12E-07	N
fatty acid binding	1,74E-07	N
carboxylic acid binding	1,10E-06	N
oxidoreductase activity, acting on the CH-CH group of donors, NAD	1,60E-06	N
calmodulin-dependent protein kinase activity	2,66E-06	N

CCDC101
NRXN1

Term	P-value	Annotated
glutamate receptor activity	2,79E-25	N
gated channel activity	2,16E-21	N
ion channel activity	2,04E-19	N
substrate-specific channel activity	2,42E-19	N
GABA receptor activity	7,65E-19	N
passive transmembrane transporter activity	6,99E-18	N
channel activity	6,99E-18	N
extracellular ligand-gated ion channel activity	1,12E-17	N
GABA-A receptor activity	6,77E-17	N
voltage-gated channel activity	7,92E-17	N
voltage-gated ion channel activity	7,92E-17	N
ionotropic glutamate receptor activity	1,51E-16	N
extracellular-glutamate-gated ion channel activity	1,71E-16	N
ligand-gated channel activity	4,65E-16	N
ligand-gated ion channel activity	4,65E-16	N
voltage-gated cation channel activity	3,54E-15	N
cation channel activity	5,15E-12	N
voltage-gated sodium channel activity	5,62E-12	N
chloride channel activity	3,10E-11	N
anion channel activity	4,03E-11	N
		N

NUPR1

Term	P-value	Annotated
insulin-like growth factor binding	1,54E-09	N
ligase activity, forming carbon-oxygen bonds	6,15E-07	N
aminoacyl-tRNA ligase activity	6,15E-07	N
ligase activity, forming aminoacyl-tRNA and related compounds	6,15E-07	N

NPAS2

Term	P-value	Annotated
Hsp90 protein binding	8,78E-11	N

KCNMA1

Term	P-value	Annotated
calcium channel activity	2,51E-09	N
voltage-gated calcium channel activity	1,10E-08	N
cation channel activity	1,56E-08	Y
voltage-gated cation channel activity	5,63E-08	Y
gated channel activity	5,58E-07	Y
solute:cation antiporter activity	7,43E-07	N

ion channel activity	1,21E-06	Y
substrate-specific channel activity	1,60E-06	Y
passive transmembrane transporter activity	3,28E-06	Y
channel activity	3,28E-06	Y
cation:cation antiporter activity	5,08E-06	N
glutamate receptor binding	9,05E-06	N
voltage-gated channel activity	1,66E-05	Y
voltage-gated ion channel activity	1,66E-05	Y
calmodulin binding	2,09E-05	N
ion gated channel activity	2,28E-05	Y

DEC1
SDCCAG8
AKT3

Term	P-value	Annotated
Rho GTPase binding	1,68E-06	N

CRYZL1
ITSN1
SON

Term	P-value	Annotated
RNA-dependent ATPase activity	6,35E-13	N
ATP-dependent RNA helicase activity	2,04E-12	N
thyroid hormone receptor binding	5,69E-12	N
RNA helicase activity	1,18E-11	N
transcription coactivator activity	7,30E-11	N
nuclear hormone receptor binding	9,59E-11	N
hormone receptor binding	4,08E-09	N
ubiquitin thiolesterase activity	6,96E-09	N
ATP-dependent helicase activity	2,22E-08	N
purine NTP-dependent helicase activity	2,22E-08	N
vitamin D receptor binding	2,42E-08	N
transcription cofactor activity	4,47E-08	N
transcription factor binding transcription factor activity	1,32E-07	N
histone methyltransferase activity (H3-K4 specific)	1,42E-07	N
protein binding transcription factor activity	1,46E-07	N
androgen receptor binding	6,52E-07	N

GART

Term	P-value	Annotated
transferase activity, transferring one-carbon groups	7,96E-17	Y
methyltransferase activity	4,15E-15	Y
RNA polymerase activity	5,15E-14	N
DNA-directed RNA polymerase activity	5,15E-14	N

RNA methyltransferase activity	2,04E-13	N
ligase activity, forming aminoacyl-tRNA and related compounds	1,00E-12	N
aminoacyl-tRNA ligase activity	1,00E-12	N
ligase activity, forming carbon-oxygen bonds	1,00E-12	N
S-adenosylmethionine-dependent methyltransferase activity	4,46E-12	N
tRNA methyltransferase activity	1,82E-11	N
RNA helicase activity	6,73E-11	N
DNA helicase activity	9,00E-11	N
tRNA binding	6,65E-10	N
helicase activity	8,93E-10	N
nucleotidyltransferase activity	2,51E-09	N
ATP-dependent DNA helicase activity	4,19E-09	N
N-methyltransferase activity	5,73E-09	N
ATP-dependent helicase activity	8,06E-09	N
purine NTP-dependent helicase activity	8,06E-09	N
ATP-dependent RNA helicase activity	1,71E-08	N

DNAJC28
TMEM50B

Term	P-value	Annotated
intramolecular oxidoreductase activity, interconverting keto- and e	1,66E-14	N
unfolded protein binding	3,35E-07	N
oligosaccharyl transferase activity	6,88E-07	N
oxidoreductase activity, acting on a sulfur group of donors	1,14E-06	N
cysteine-type endopeptidase activity	1,58E-06	N

IFNGR2
SBNO1

Term	P-value	Annotated
N-methyltransferase activity	5,41E-09	N
histone methyltransferase activity	1,32E-08	N
histone methyltransferase activity (H3-K4 specific)	1,66E-08	N
small conjugating protein-specific protease activity	2,36E-08	N
histone-lysine N-methyltransferase activity	3,53E-08	N
ubiquitin-specific protease activity	4,07E-08	N
ubiquitin thiolesterase activity	4,27E-08	N
lysine N-methyltransferase activity	1,09E-07	N
protein-lysine N-methyltransferase activity	1,09E-07	N
cysteine-type peptidase activity	2,20E-06	N

SETD8
RILPL2
C12orf65
MPHOSPH9

SNRNP35

Term	P-value	Annotated
Rho GTPase binding	3,36E-05	N
insulin receptor substrate binding	5,66E-05	N

RILPL1
PITPNM2

Term	P-value	Annotated
diacylglycerol kinase activity	7,03E-07	N
cation channel activity	5,66E-06	N
voltage-gated cation channel activity	2,49E-05	N
GTPase regulator activity	3,34E-05	N
nucleoside-triphosphatase regulator activity	4,33E-05	N
ion channel activity	5,03E-05	N
gated channel activity	5,99E-05	N
calmodulin-dependent protein kinase activity	6,09E-05	N
substrate-specific channel activity	6,59E-05	N
voltage-gated channel activity	1,02E-04	N
voltage-gated ion channel activity	1,02E-04	N

STK24

Term	P-value	Annotated
Rho guanyl-nucleotide exchange factor activity	2,63E-08	N
receptor signaling protein activity	2,27E-06	N

FARP1

Term	P-value	Annotated
beta-catenin binding	1,82E-11	N

SLC15A1
TANK

Term	P-value	Annotated
tumor necrosis factor receptor binding	1,76E-09	N
tumor necrosis factor receptor superfamily binding	3,26E-08	N

PSMD14

Term	P-value	Annotated
threonine-type endopeptidase activity	3,22E-26	N
threonine-type peptidase activity	3,22E-26	N
unfolded protein binding	1,52E-15	N
chaperone binding	4,97E-11	N
RNA polymerase II carboxy-terminal domain kinase activity	1,27E-10	N
small conjugating protein binding	3,87E-08	N
ATPase activity	5,86E-08	N

TBR1		
Term	P-value	Annotated
voltage-gated potassium channel activity	2,38E-17	N
potassium channel activity	2,60E-17	N
voltage-gated cation channel activity	7,53E-17	N
voltage-gated channel activity	1,91E-15	N
voltage-gated ion channel activity	1,91E-15	N
acidic amino acid transmembrane transporter activity	2,28E-15	N
L-glutamate transmembrane transporter activity	1,04E-14	N
potassium ion transmembrane transporter activity	6,42E-13	N
gated channel activity	3,80E-12	N
ion channel activity	1,20E-10	N
substrate-specific channel activity	1,51E-10	N
G-protein coupled amine receptor activity	1,86E-10	N
metal ion transmembrane transporter activity	6,28E-10	N
cation channel activity	8,22E-10	N
GABA receptor activity	9,07E-10	N
passive transmembrane transporter activity	1,39E-09	N
channel activity	1,39E-09	N
GABA-A receptor activity	2,63E-09	N

POU3F2

Term	P-value	Annotated
Glycosaminoglycan biosynthesis - heparan sulfate	2,28E-04	N
Notch signaling pathway	3,65E-04	N

JMJD1C

Term	P-value	Annotated
Circadian rhythm - mammal	4,58E-06	N
Notch signaling pathway	1,80E-05	N

REEP3

Term	P-value	Annotated
Sphingolipid metabolism	5,92E-05	N

LRRC14
ARHGAP39
FOXH1

Term	P-value	Annotated
Nitrogen metabolism	4,31E-05	N
Wnt signaling pathway	7,31E-04	N

KIFC2

Term	P-value	Annotated
Ubiquitin mediated proteolysis	3,85E-05	N
Phosphatidylinositol signaling system	5,19E-04	N

CYHR1

Term	P-value	Annotated
Glycerophospholipid metabolism	2,13E-05	N
Spliceosome	3,41E-04	N
Adherens junction	5,89E-04	N
Regulation of actin cytoskeleton	5,94E-04	N

VPS28

Term	P-value	Annotated
Huntington's disease	1,55E-10	N
Parkinson's disease	2,02E-10	N
Oxidative phosphorylation	2,63E-09	N
Alzheimer's disease	5,63E-09	N
Proteasome	6,05E-06	N
Endocytosis	4,83E-05	Y
Amino sugar and nucleotide sugar metabolism	4,09E-04	N
Glyoxylate and dicarboxylate metabolism	8,00E-04	N

SCRT1

Term	P-value	Annotated
Neuroactive ligand-receptor interaction	2,92E-06	N
Calcium signaling pathway	6,67E-04	N

ATXN2L

Term	P-value	Annotated
Valine, leucine and isoleucine biosynthesis	1,89E-06	N
Aminoacyl-tRNA biosynthesis	9,56E-06	N
Vasopressin-regulated water reabsorption	2,36E-05	N

TUFM

Term	P-value	Annotated
Parkinson's disease	7,63E-12	N
Huntington's disease	1,02E-10	N
Valine, leucine and isoleucine degradation	2,12E-10	N
Oxidative phosphorylation	3,66E-10	N
Citrate cycle (TCA cycle)	2,96E-09	N
Alzheimer's disease	1,27E-08	N
Aminoacyl-tRNA biosynthesis	2,94E-08	N
Propanoate metabolism	1,66E-07	N
Butanoate metabolism	6,01E-07	N
beta-Alanine metabolism	1,05E-06	N
Selenoamino acid metabolism	1,38E-06	N
Fatty acid metabolism	3,30E-06	N
Pyruvate metabolism	3,97E-06	N
RNA polymerase	1,67E-05	N
Valine, leucine and isoleucine biosynthesis	1,75E-05	N
Glycolysis / Gluconeogenesis	9,40E-05	N
Cardiac muscle contraction	1,02E-04	N
Lysine degradation	1,67E-04	N
Oocyte meiosis	3,69E-04	N
Glyoxylate and dicarboxylate metabolism	3,84E-04	N

SH2B1
NFATC2IP

Term	P-value	Annotated
DNA replication	2,30E-06	N
Base excision repair	8,74E-06	N
Homologous recombination	4,15E-05	N
Mismatch repair	1,07E-03	N

SPNS1

Term	P-value	Annotated

Lysosome	6,30E-25	N
Glycerophospholipid metabolism	1,42E-06	N
Glycosylphosphatidylinositol(GPI)-anchor biosynthesis	4,33E-06	N
Sphingolipid metabolism	1,25E-05	N
Other glycan degradation	2,61E-05	N
Glycosphingolipid biosynthesis - ganglio series	9,58E-05	N
Glycosaminoglycan degradation	1,52E-04	N
Glycosphingolipid biosynthesis - globo series	1,56E-04	N
Glycosaminoglycan biosynthesis - heparan sulfate	3,16E-04	N
Vibrio cholerae infection	7,40E-04	N

LAT

Term	P-value	Annotated
T cell receptor signaling pathway	1,57E-59	Y
Primary immunodeficiency	1,44E-58	N
Hematopoietic cell lineage	2,86E-53	N
Natural killer cell mediated cytotoxicity	3,03E-17	Y
Cytokine-cytokine receptor interaction	4,37E-17	N
Chemokine signaling pathway	3,87E-14	N
Cell adhesion molecules (CAMs)	2,33E-09	N
Jak-STAT signaling pathway	1,05E-08	N
Autoimmune thyroid disease	1,89E-05	N
Fc epsilon RI signaling pathway	4,98E-05	Y
Allograft rejection	9,15E-05	N
Regulation of actin cytoskeleton	2,55E-04	N
Intestinal immune network for IgA production	3,51E-04	N
Thyroid cancer	5,67E-04	N

SULT1A1
SULT1A2

Term	P-value	Annotated
Drug metabolism - cytochrome P450	2,47E-10	N
Retinol metabolism	1,22E-08	N
Metabolism of xenobiotics by cytochrome P450	1,48E-08	N
Tyrosine metabolism	4,36E-08	N
Complement and coagulation cascades	3,47E-06	N
Histidine metabolism	7,83E-06	N
Phenylalanine metabolism	2,76E-05	N
Primary bile acid biosynthesis	1,11E-04	N
Ascorbate and aldarate metabolism	1,64E-04	N
Valine, leucine and isoleucine degradation	3,51E-04	N
Arachidonic acid metabolism	3,97E-04	N
Selenoamino acid metabolism	5,02E-04	N
Steroid hormone biosynthesis	5,21E-04	N

Fatty acid metabolism	5,39E-04	N
Drug metabolism - other enzymes	8,03E-04	N

CCDC101
NRXN1

Term	P-value	Annotated
Neuroactive ligand-receptor interaction	9,49E-06	N
Axon guidance	2,06E-05	N
ErbB signaling pathway	2,72E-05	N
Long-term potentiation	3,34E-05	N
Type II diabetes mellitus	6,29E-05	N
Amyotrophic lateral sclerosis (ALS)	2,89E-04	N
Long-term depression	6,16E-04	N
Cell adhesion molecules (CAMs)	9,76E-04	Y

NUPR1

Term	P-value	Annotated
Aminoacyl-tRNA biosynthesis	4,03E-09	N
Nitrogen metabolism	7,81E-05	N
Glycine, serine and threonine metabolism	5,54E-04	N

NPAS2
KCNMA1

Term	P-value	Annotated
Calcium signaling pathway	3,43E-09	N
Long-term potentiation	1,93E-07	N
Phosphatidylinositol signaling system	3,38E-05	N
Vascular smooth muscle contraction	1,02E-04	Y

DEC1
SDCCAG8
AKT3

Term	P-value	Annotated
Glycosphingolipid biosynthesis - lacto and neolacto serie	9,78E-06	N
Glutathione metabolism	3,43E-04	N
Oxidative phosphorylation	6,42E-04	N
Tight junction	6,53E-04	Y

CRYZL1

Term	P-value	Annotated
SNARE interactions in vesicular transport	7,49E-06	N
One carbon pool by folate	7,05E-04	N

ITSN1

Term	P-value	Annotated
VEGF signaling pathway	4,49E-04	N
Notch signaling pathway	1,58E-03	N

SON

Term	P-value	Annotated
Spliceosome	4,09E-11	N
Folate biosynthesis	2,30E-04	N

GART

Term	P-value	Annotated
Aminoacyl-tRNA biosynthesis	1,46E-13	N
Valine, leucine and isoleucine biosynthesis	1,69E-11	N
Pyrimidine metabolism	5,39E-11	N
RNA polymerase	1,74E-09	N
Purine metabolism	4,68E-07	Y
One carbon pool by folate	8,15E-07	Y
Cysteine and methionine metabolism	6,73E-06	N
Gap junction	3,02E-05	N
Long-term potentiation	3,49E-05	N
Mismatch repair	4,86E-05	N
Selenoamino acid metabolism	5,95E-05	N
Non-homologous end-joining	8,52E-05	N
Alanine, aspartate and glutamate metabolism	1,69E-04	N
DNA replication	1,76E-04	N
Nucleotide excision repair	2,80E-04	N
Spliceosome	2,87E-04	N
Melanogenesis	3,06E-04	N
Glycine, serine and threonine metabolism	9,34E-04	N
Homologous recombination	9,53E-04	N
Valine, leucine and isoleucine degradation	1,28E-03	N

DNAJC28
TMEM50B

Term	P-value	Annotated
Protein export	9,82E-08	N
Glycerophospholipid metabolism	5,80E-06	N
N-Glycan biosynthesis	5,88E-06	N
Non-homologous end-joining	2,24E-05	N
Riboflavin metabolism	4,11E-05	N
Glycosylphosphatidylinositol(GPI)-anchor biosynthesis	7,31E-05	N
Nitrogen metabolism	1,17E-04	N
Antigen processing and presentation	1,33E-04	N
Mismatch repair	5,97E-04	N

Gap junction	6,98E-04	N
Nucleotide excision repair	8,24E-04	N
DNA replication	1,08E-03	N

IFNGR2

Term	P-value	Annotated
Toll-like receptor signaling pathway	2,92E-14	N
NOD-like receptor signaling pathway	4,87E-13	N
B cell receptor signaling pathway	1,34E-09	N
Apoptosis	3,70E-09	N
Neurotrophin signaling pathway	7,43E-09	N
Leishmania infection	4,46E-08	Y
Small cell lung cancer	3,86E-07	N
Chemokine signaling pathway	4,94E-07	N
Epithelial cell signaling in Helicobacter pylori infection	2,96E-05	N
Ubiquitin mediated proteolysis	7,87E-05	N
Glycosphingolipid biosynthesis - lacto and neolacto serie	8,19E-05	N
Fc gamma R-mediated phagocytosis	1,43E-04	N
Acute myeloid leukemia	1,87E-04	N
Chronic myeloid leukemia	2,36E-04	N
Pancreatic cancer	2,38E-04	N
Colorectal cancer	7,69E-04	N

SBNO1

Term	P-value	Annotated
Basal transcription factors	1,75E-05	N
Ubiquitin mediated proteolysis	7,79E-04	N

SETD8

Term	P-value	Annotated
Prostate cancer	2,02E-04	N
Renal cell carcinoma	2,21E-04	N
Progesterone-mediated oocyte maturation	4,65E-04	N
Neurotrophin signaling pathway	4,70E-04	N
Chronic myeloid leukemia	7,29E-04	N

RILPL2

Term	P-value	Annotated
T cell receptor signaling pathway	3,26E-04	N
B cell receptor signaling pathway	9,22E-04	N

C12orf65
MPHOSPH9

Term	P-value	Annotated

Thyroid cancer	5,76E-07	N
Cell cycle	9,10E-06	N
Oocyte meiosis	5,66E-04	N
Mismatch repair	6,38E-04	N
DNA replication	6,44E-04	N

SNRNP35
RILPL1

Term	P-value	Annotated
Drug metabolism - other enzymes	9,98E-07	N

PITPNM2

Term	P-value	Annotated
Calcium signaling pathway	1,35E-04	N

STK24

Term	P-value	Annotated
Adherens junction	1,79E-07	N
Thyroid cancer	2,22E-04	N
Regulation of actin cytoskeleton	4,22E-04	N
Renal cell carcinoma	5,80E-04	N
ErbB signaling pathway	7,67E-04	N

FARP1

Term	P-value	Annotated
Adherens junction	4,25E-08	N
Melanogenesis	7,86E-08	N
Tight junction	8,09E-05	N
Basal cell carcinoma	1,73E-04	N
Axon guidance	5,55E-04	N

SLC15A1
TANK

Term	P-value	Annotated
Apoptosis	3,27E-11	N
Toll-like receptor signaling pathway	1,14E-09	N
RIG-I-like receptor signaling pathway	1,27E-09	N
NOD-like receptor signaling pathway	2,93E-09	N
Cytokine-cytokine receptor interaction	9,29E-07	N
Leishmania infection	3,34E-06	N
T cell receptor signaling pathway	4,71E-06	N
Jak-STAT signaling pathway	6,56E-06	N
Amyotrophic lateral sclerosis (ALS)	1,41E-05	N
Pancreatic cancer	1,73E-04	N

Small cell lung cancer	4,54E-04	N
Epithelial cell signaling in Helicobacter pylori infection	1,01E-03	N

PSMD14

Term	P-value	Annotated
Proteasome	1,89E-45	Y
Ubiquitin mediated proteolysis	1,34E-07	N
Aminoacyl-tRNA biosynthesis	9,39E-07	N
RNA degradation	1,35E-06	N
Spliceosome	5,67E-06	N
Phosphatidylinositol signaling system	1,75E-05	N
Inositol phosphate metabolism	2,80E-05	N
Nucleotide excision repair	3,11E-05	N
Pathogenic Escherichia coli infection	5,93E-05	N
Cell cycle	8,70E-05	N
Valine, leucine and isoleucine biosynthesis	1,95E-04	N
Vascular smooth muscle contraction	3,81E-04	N
Lysine degradation	5,22E-04	N

TBR1

Term	P-value	Annotated
Calcium signaling pathway	4,10E-06	N
Neuroactive ligand-receptor interaction	7,65E-05	N

POU3F2

Term	P-value	Annotated
CRMPs in Sema3A signaling	1,05E-05	N
Unblocking of NMDA receptor, glutamate binding and activation	1,28E-05	N

JMJD1C

Term	P-value	Annotated
Circadian Clock	2,67E-09	N
BMAL1:CLOCK/NPAS2 Activates Gene Expression	2,57E-08	N
Myogenesis	7,03E-08	N
CDO in myogenesis	7,03E-08	N

REEP3

Term	P-value	Annotated
Sphingolipid metabolism	4,17E-05	N
Sphingolipid de novo biosynthesis	6,48E-05	N

LRRC14
ARHGAP39
FOXH1

Term	P-value	Annotated
Signaling by NODAL	1,44E-17	Y
FGFR ligand binding and activation	5,01E-07	N
SHC-mediated cascade	1,48E-06	N
Negative regulation of FGFR signaling	1,56E-06	N
FGFR1 ligand binding and activation	2,93E-06	N
Signaling by BMP	5,62E-06	N
FRS2-mediated cascade	6,49E-06	N

KIFC2

Term	P-value	Annotated
Ras activation uopn Ca2+ infux through NMDA receptor	6,84E-09	N
Depolarization of the Presynaptic Terminal Triggers the Opening of Calcium Channels	1,19E-08	N
CREB phosphorylation through the activation of CaMKII	9,65E-08	N
Transmission across Chemical Synapses	3,39E-07	N
GABA synthesis, release, reuptake and degradation	4,23E-06	N
Neuronal System	1,10E-05	N
Dopamine Neurotransmitter Release Cycle	2,28E-05	N
Serotonin Neurotransmitter Release Cycle	2,28E-05	N
Trafficking of AMPA receptors	2,92E-05	N
Glutamate Binding, Activation of AMPA Receptors and Synaptic Plasticity	2,92E-05	N
Post NMDA receptor activation events	3,02E-05	N
NCAM signaling for neurite out-growth	3,07E-05	N
Neurotransmitter Release Cycle	3,36E-05	N
CREB phosphorylation through the activation of Ras	3,37E-05	N
Glutamate Neurotransmitter Release Cycle	3,72E-05	N

CYHR1

Term	P-value	Annotated
Assembly of HIV virion	3,26E-09	N
Membrane binding and targetting of GAG proteins	3,14E-08	N

VPS28

Term	P-value	Annotated
Respiratory electron transport, ATP synthesis by chemiosmotic coupling, and heat prod...	3,99E-10	N

Respiratory electron transport	5,73E-10	N
Endosomal Sorting Complex Required For Transport (ESCRT)	6,29E-09	Y
The citric acid (TCA) cycle and respiratory electron transport	4,51E-08	N
Regulation of mRNA Stability by Proteins that Bind AU-rich Elements	1,25E-07	N

SCRT1

Term	P-value	Annotated
Voltage gated Potassium channels	7,55E-12	N
Neuronal System	6,75E-11	N
Potassium Channels	2,11E-10	N
Unblocking of NMDA receptor, glutamate binding and activation	1,65E-06	N
Transmission across Chemical Synapses	7,56E-06	N
CREB phosphorylation through the activation of CaMKII	7,96E-06	N
GABA synthesis, release, reuptake and degradation	3,55E-05	N
Trafficking of AMPA receptors	3,81E-05	N
Glutamate Binding, Activation of AMPA Receptors and Synaptic Plasticity	3,81E-05	N
Amine ligand-binding receptors	3,98E-05	N
Neurotransmitter Release Cycle	4,57E-05	N
Ras activation uopn Ca2+ infux through NMDA receptor	5,68E-05	N
Dopamine Neurotransmitter Release Cycle	7,01E-05	N
Serotonin Neurotransmitter Release Cycle	7,01E-05	N

ATXN2L

Term	P-value	Annotated
EGFR downregulation	4,94E-08	N

TUFM

Term	P-value	Annotated
Mitochondrial tRNA aminoacylation	1,54E-16	N
Citric acid cycle (TCA cycle)	7,05E-14	N
The citric acid (TCA) cycle and respiratory electron transport	9,77E-14	N
Pyruvate metabolism and Citric Acid (TCA) cycle	2,63E-12	N
Respiratory electron transport	3,35E-11	N
Respiratory electron transport, ATP synthesis by chemiosmotic coupling, and heat prod...	5,84E-11	N
Mitochondrial Fatty Acid Beta-Oxidation	4,42E-10	N
tRNA Aminoacylation	7,33E-08	N
Gluconeogenesis	7,47E-08	N
RNA Polymerase III Transcription Initiation From Type 1 Promoter	1,58E-07	N
RNA Polymerase III Transcription Initiation From Type 2 Promoter	2,09E-07	N
Formation of ATP by chemiosmotic coupling	3,76E-07	N
RNA Polymerase III Chain Elongation	4,27E-07	N
Branched-chain amino acid catabolism	1,76E-06	N

SH2B1
NFATC2IP

Term	P-value	Annotated
G0 and Early G1	2,58E-08	N
Activation of ATR in response to replication stress	1,14E-07	N
G2/M Checkpoints	1,16E-07	N
Processive synthesis on the C-strand of the telomere	1,36E-07	N
Fanconi Anemia pathway	3,92E-07	N
Activation of the pre-replicative complex	9,49E-07	N
Processive synthesis on the lagging strand	1,77E-06	N
DNA strand elongation	2,61E-06	N
Removal of the Flap Intermediate	3,31E-06	N

Telomere C-strand (Lagging Strand) Synthesis	1,05E-05	N
Unwinding of DNA	1,17E-05	N
Gap-filling DNA repair synthesis and ligation in TC-NER	1,76E-05	N
Gap-filling DNA repair synthesis and ligation in GG-NER	1,76E-05	N
Resolution of Abasic Sites (AP sites)	1,92E-05	N
Base Excision Repair	1,92E-05	N

SPNS1

Term	P-value	Annotated
Glycosphingolipid metabolism	3,03E-12	N
Sphingolipid metabolism	2,69E-10	N
Transferrin endocytosis and recycling	1,11E-09	N
Iron uptake and transport	1,67E-06	N
Insulin receptor recycling	1,84E-06	N
Transmembrane transport of small molecules	4,07E-06	N

LAT

Term	P-value	Annotated
Generation of second messenger molecules	4,46E-56	Y
TCR signaling	9,03E-44	Y
Immunoregulatory interactions between a Lymphoid and a non-Lymphoid cell	9,44E-42	N
Translocation of ZAP-70 to Immunological synapse	8,42E-37	N
PD-1 signaling	1,71E-34	N
Phosphorylation of CD3 and TCR zeta chains	4,19E-30	N
Costimulation by the CD28 family	2,58E-27	N
PECAM1 interactions	1,64E-26	N
Downstream TCR signaling	4,80E-22	N
The role of Nef in HIV-1 replication and disease pathogenesis	3,27E-21	N
Adaptive Immune System	5,70E-19	Y
Chemokine receptors bind chemokines	2,18E-18	N
Cell surface interactions at the vascular wall	3,78E-18	N
Regulation of KIT signaling	4,26E-16	N
CD28 dependent Vav1 pathway	4,30E-16	N
Hemostasis	6,10E-16	Y
Platelet activation, signaling and aggregation	7,32E-16	Y
Platelet Adhesion to exposed collagen	7,71E-16	Y
Interleukin-2 signaling	5,08E-13	N
Platelet Aggregation (Plug Formation)	9,80E-13	N

SULT1A1
SULT1A2

Term	P-value	Annotated
Biological oxidations	5,08E-09	N
Phase 1 - Functionalization of compounds	7,59E-08	N
Ethanol oxidation	2,11E-07	N
Formation of Fibrin Clot (Clotting Cascade)	1,25E-05	N

CCDC101
NRXN1

Term	P-value	Annotated
GABA A receptor activation	7,01E-23	N
Neuronal System	2,61E-22	N
Ligand-gated ion channel transport	4,00E-22	N
Transmission across Chemical Synapses	6,35E-20	N
Interaction between L1 and Ankyrins	1,62E-18	N

Neurotransmitter Receptor Binding And Downstream Transmission In The Postsynaptic Cell	1,12E-17	N
GABA receptor activation	6,71E-17	N
Class C/3 (Metabotropic glutamate/pheromone receptors)	2,53E-16	N
Unblocking of NMDA receptor, glutamate binding and activation	1,43E-14	N
Potassium Channels	5,40E-14	N
Ion channel transport	3,86E-13	N
Serotonin Neurotransmitter Release Cycle	7,57E-13	N
Dopamine Neurotransmitter Release Cycle	7,57E-13	N
Voltage gated Potassium channels	1,73E-11	N
L1CAM interactions	4,99E-11	N
GABA synthesis, release, reuptake and degradation	8,50E-10	N
Norepinephrine Neurotransmitter Release Cycle	1,73E-09	N
Activation of NMDA receptor upon glutamate binding and postsynaptic events	2,16E-09	N
Glutamate Neurotransmitter Release Cycle	5,65E-08	N
Ionotropic activity of Kainate Receptors	5,90E-08	N

NUPR1

Term	P-value	Annotated
Cytosolic tRNA aminoacylation	8,79E-14	N
Amino acid synthesis and interconversion (transamination)	4,98E-13	N
Activation of Genes by ATF4	2,08E-10	N
tRNA Aminoacylation	1,19E-08	N
PERK regulated gene expression	1,72E-08	N

NPAS2
KCNMA1

Term	P-value	Annotated
Voltage gated Potassium channels	2,12E-09	N
Neuronal System	5,68E-09	Y
Unblocking of NMDA receptor, glutamate binding and activation	1,14E-07	N
Potassium Channels	5,22E-07	Y
Depolarization of the Presynaptic Terminal Triggers the Opening of Calcium Channels	2,58E-06	N
Reduction of cytosolic Ca++ levels	4,96E-06	N
Smooth Muscle Contraction	5,48E-06	N
Platelet calcium homeostasis	7,49E-06	N
CREB phosphorylation through the activation of CaMKII	7,74E-06	N
Transmission across Chemical Synapses	1,01E-05	N
Ras activation uopn Ca2+ infux through NMDA receptor	1,66E-05	N
Activation of NMDA receptor upon glutamate binding and postsynaptic events	2,29E-05	N
Glutamate Binding, Activation of AMPA Receptors and Synaptic Plasticity	4,28E-05	N
Trafficking of AMPA receptors	4,28E-05	N

DEC1
SDCCAG8
AKT3

Term	P-value	Annotated
Thrombin signalling through proteinase activated receptors (PARs)	1,24E-05	N

CRYZL1
ITSN1
SON

Term	P-value	Annotated
Processing of Capped Intron-Containing Pre-mRNA	5,67E-18	N
mRNA Splicing - Major Pathway	2,32E-16	N
mRNA Splicing	2,32E-16	N

mRNA Processing	5,21E-16	N
mRNA 3'-end processing	1,07E-12	N
Post-Elongation Processing of Intron-Containing pre-mRNA	1,07E-12	N
Transport of Mature mRNA derived from an Intron-Containing Transcript	1,44E-12	N
Transport of Mature Transcript to Cytoplasm	2,99E-12	N
Cleavage of Growing Transcript in the Termination Region	1,65E-10	N
RNA Polymerase II Transcription Termination	1,65E-10	N
Post-Elongation Processing of the Transcript	1,65E-10	N
mRNA Splicing - Minor Pathway	2,48E-10	N
Transport of Ribonucleoproteins into the Host Nucleus	1,90E-08	N
Vpr-mediated nuclear import of PICs	9,63E-08	N
Transport of the SLBP independent Mature mRNA	3,02E-07	N
Transport of Mature mRNA Derived from an Intronless Transcript	3,08E-07	N
Transport of Mature mRNAs Derived from Intronless Transcripts	4,71E-07	N
RNA Polymerase II Transcription	4,92E-07	N
NEP/NS2 Interacts with the Cellular Export Machinery	4,92E-07	N
Transport of the SLBP Dependant Mature mRNA	5,39E-07	N

GART

Term	P-value	Annotated
Metabolism of non-coding RNA	1,16E-19	N
snRNP Assembly	1,16E-19	N
tRNA Aminoacylation	5,57E-15	N
Transport of Mature mRNA Derived from an Intronless Transcript	6,41E-15	N
Transport of Mature mRNAs Derived from Intronless Transcripts	9,25E-15	N
Purine ribonucleoside monophosphate biosynthesis	3,91E-14	N
Rev-mediated nuclear export of HIV-1 RNA	1,97E-13	N
Transport of Ribonucleoproteins into the Host Nucleus	2,81E-13	N
Interactions of Rev with host cellular proteins	3,79E-13	N
Export of Viral Ribonucleoproteins from Nucleus	4,79E-13	N
NEP/NS2 Interacts with the Cellular Export Machinery	6,37E-13	N
Transport of the SLBP independent Mature mRNA	1,14E-12	N
Transport of Mature Transcript to Cytoplasm	1,18E-12	N
Transport of the SLBP Dependant Mature mRNA	1,52E-12	N
Nuclear import of Rev protein	2,39E-12	N
Vpr-mediated nuclear import of PICs	3,39E-12	N
Glucose transport	7,76E-12	N
Interactions of Vpr with host cellular proteins	1,98E-11	N
Regulation of Glucokinase by Glucokinase Regulatory Protein	2,71E-11	N
Metabolism of nucleotides	3,07E-11	N

DNAJC28
TMEM50B

Term	P-value	Annotated
Activation of Chaperones by IRE1alpha	2,11E-09	N
Activation of Chaperones by ATF6-alpha	4,50E-09	N
Asparagine N-linked glycosylation	1,90E-08	N
Antigen Presentation: Folding, assembly and peptide loading of class I MHC	4,37E-08	N
Activation of Chaperone Genes by XBP1(S)	1,34E-07	N
Early Phase of HIV Life Cycle	2,62E-07	N
Calnexin/calreticulin cycle	2,77E-07	N
N-glycan trimming in the ER and Calnexin/Calreticulin cycle	5,86E-07	N
Unfolded Protein Response	1,19E-06	N

IFNGR2

Term	P-value	Annotated
Toll Like Receptor 4 (TLR4) Cascade	6,51E-20	N
Toll Receptor Cascades	4,47E-19	N
TAK1 activates NFkB by phosphorylation and activation of IKKs complex	1,98E-18	N
Activated TLR4 signalling	2,71E-18	N
Viral dsRNA:TLR3:TRIF Complex Activates RIP1	3,04E-17	N
Toll Like Receptor TLR6:TLR2 Cascade	1,27E-16	N
MyD88:Mal cascade initiated on plasma membrane	1,27E-16	N
Toll Like Receptor TLR1:TLR2 Cascade	1,27E-16	N
Toll Like Receptor 2 (TLR2) Cascade	1,27E-16	N
MyD88-independent cascade initiated on plasma membrane	4,44E-16	N
NFkB and MAP kinases activation mediated by TLR4 signaling repertoire	1,03E-14	N
MyD88 cascade initiated on plasma membrane	2,51E-14	N
Toll Like Receptor 10 (TLR10) Cascade	2,51E-14	N
Toll Like Receptor 5 (TLR5) Cascade	2,51E-14	N
TRAF6 mediated NF-kB activation	3,33E-14	N
TRIF mediated TLR3 signaling	4,28E-14	N
Toll Like Receptor 3 (TLR3) Cascade	4,28E-14	N
MyD88 dependent cascade initiated on endosome	7,79E-14	N
Toll Like Receptor 7/8 (TLR7/8) Cascade	7,79E-14	N
TRAF6 mediated induction of NFkB and MAP kinases upon TLR7/8 or 9 activation	1,30E-13	N

SBNO1

Term	P-value	Annotated
Late Phase of HIV Life Cycle	7,26E-06	N
Transcription of the HIV genome	1,32E-05	N

SETD8

Term	P-value	Annotated
Purine salvage	1,55E-04	N

RILPL2

Term	P-value	Annotated
Regulation of IFNG signaling	3,41E-05	N

C12orf65
MPHOSPH9

Term	P-value	Annotated
Cell Cycle, Mitotic	4,72E-09	N
Cell Cycle	9,45E-09	N
M Phase	2,38E-08	N
Mitotic Prometaphase	2,67E-08	N
Centrosome maturation	1,88E-07	N
Recruitment of mitotic centrosome proteins and complexes	1,88E-07	N
Loss of Nlp from mitotic centrosomes	3,06E-07	N
Loss of proteins required for interphase microtubule organization from the centrosome	3,06E-07	N
G2/M Transition	5,87E-07	N
Mitotic G2-G2/M phases	7,71E-07	N
Mitotic M-M/G1 phases	1,17E-06	N
DNA Replication	2,26E-06	N
Telomere C-strand (Lagging Strand) Synthesis	1,77E-05	N
G2/M Checkpoints	1,93E-05	N
Repair synthesis of patch ~27-30 bases long by DNA polymerase	2,04E-05	N
Repair synthesis for gap-filling by DNA polymerase in TC-NER	2,04E-05	N
Extension of Telomeres	2,80E-05	N

APC-Cdc20 mediated degradation of Nek2A	3,27E-05	N

SNRNP35
RILPL1

Term	P-value	Annotated
Deadenylation-dependent mRNA decay	9,03E-07	N
mRNA Processing	6,52E-06	N
Processing of Capped Intron-Containing Pre-mRNA	8,99E-06	N
mRNA Splicing - Major Pathway	1,02E-05	N
mRNA Splicing	1,02E-05	N

PITPNM2

Term	P-value	Annotated
Voltage gated Potassium channels	1,29E-06	N
Potassium Channels	1,41E-06	N
Effects of PIP2 hydrolysis	2,09E-06	N
Ras activation uopn Ca2+ infux through NMDA receptor	1,48E-05	N
Neuronal System	2,17E-05	N
PLC-gamma1 signalling	6,59E-05	N
DAG and IP3 signaling	8,21E-05	N
Hemostasis	8,24E-05	N
Depolarization of the Presynaptic Terminal Triggers the Opening of Calcium Channels	9,90E-05	N
Platelet activation, signaling and aggregation	1,05E-04	N

STK24

Term	P-value	Annotated
G alpha (12/13) signalling events	1,78E-07	N
NRAGE signals death through JNK	8,67E-07	N

FARP1

Term	P-value	Annotated
Cell-extracellular matrix interactions	1,78E-08	N
Axon guidance	5,91E-08	N
Semaphorin interactions	5,68E-07	N
Rho GTPase cycle	3,73E-06	N
Signaling by Rho GTPases	3,73E-06	N

SLC15A1
TANK

Term	P-value	Annotated
NOD1/2 Signaling Pathway	1,31E-14	N
Death Receptor Signalling	3,09E-14	N
Extrinsic Pathway for Apoptosis	3,09E-14	N
Regulation of IFNG signaling	9,47E-11	N
Nucleotide-binding domain, leucine rich repeat containing receptor (NLR) signaling pa...	8,32E-10	N
MyD88-independent cascade initiated on plasma membrane	1,10E-09	N
TRIF mediated TLR3 signaling	1,20E-09	N
Toll Like Receptor 3 (TLR3) Cascade	1,20E-09	N
Innate Immune System	3,76E-09	Y
Activated TLR4 signalling	6,59E-09	N
TAK1 activates NFkB by phosphorylation and activation of IKKs complex	9,55E-09	N
Toll Like Receptor 4 (TLR4) Cascade	1,37E-08	N
Toll Receptor Cascades	1,46E-08	N
TRAF6 mediated NF-kB activation	1,56E-08	N
NFkB and MAP kinases activation mediated by TLR4 signaling repertoire	4,16E-08	N

Interleukin-1 signaling	5,64E-08	N
TRAF6 Mediated Induction of proinflammatory cytokines	1,37E-07	N
MyD88 cascade initiated on plasma membrane	2,36E-07	N
Toll Like Receptor 10 (TLR10) Cascade	2,36E-07	N
Toll Like Receptor 5 (TLR5) Cascade	2,36E-07	N

PSMD14

Term	P-value	Annotated
CDT1 association with the CDC6:ORC:origin complex	1,10E-55	Y
Assembly of the pre-replicative complex	9,20E-53	Y
Cross-presentation of soluble exogenous antigens (endosomes)	1,81E-51	Y
Regulation of ornithine decarboxylase (ODC)	1,95E-49	Y
Destabilization of mRNA by AUF1 (hnRNP D0)	2,58E-49	Y
Orc1 removal from chromatin	4,06E-49	Y
Switching of origins to a post-replicative state	4,06E-49	Y
Removal of licensing factors from origins	6,34E-49	Y
Autodegradation of Cdh1 by Cdh1:APC/C	7,83E-49	Y
Regulation of activated PAK-2p34 by proteasome mediated degradation	9,21E-49	Y
Autodegradation of the E3 ubiquitin ligase COP1	1,00E-48	Y
SCF-beta-TrCP mediated degradation of Emi1	1,05E-48	Y
Stabilization of p53	1,08E-48	Y
Vpu mediated degradation of CD4	1,54E-48	Y
Vif-mediated degradation of APOBEC3G	3,90E-48	Y
Ubiquitin-dependent degradation of Cyclin D	6,57E-48	Y
Ubiquitin-dependent degradation of Cyclin D1	6,57E-48	Y
Regulation of DNA replication	1,27E-47	Y
p53-Independent DNA Damage Response	1,63E-47	Y
p53-Independent G1/S DNA damage checkpoint	1,63E-47	Y

TBR1

Term	P-value	Annotated
Voltage gated Potassium channels	2,35E-15	N
GABA A receptor activation	4,18E-14	N
Potassium Channels	4,41E-14	N
Neuronal System	5,60E-14	N
Amine ligand-binding receptors	4,44E-13	N
Glutamate Neurotransmitter Release Cycle	2,41E-11	N
Ligand-gated ion channel transport	3,77E-11	N
Transmission across Chemical Synapses	5,70E-09	N
Sema3A PAK dependent Axon repulsion	1,62E-08	N

POU3F2

Term	P-value	Annotated
abnormal brain commissure morphology	8,24E-15	N
enlarged third ventricle	1,17E-14	N
abnormal hippocampal mossy fiber morphology	2,26E-14	N
small olfactory bulb	7,66E-12	N
abnormal radial glial cell morphology	1,07E-11	N
abnormal cerebral cortex morphology	3,42E-11	N
abnormal axon guidance	3,50E-10	N
increased aggression towards mice	8,47E-10	N
abnormal corticospinal tract morphology	1,38E-09	N
decreased brain size	3,43E-09	N
abnormal hippocampus morphology	8,28E-09	N
abnormal embryonic/fetal subventricular zone morphology	1,02E-08	N
decreased corpus callosum size	1,61E-08	N
abnormal spinal cord interneuron morphology	1,79E-08	N
abnormal cerebellar foliation	1,85E-08	N
disorganized pancreatic islets	2,16E-08	N
abnormal cerebrum morphology	3,66E-08	N
abnormal telencephalon development	4,19E-08	N
enlarged lateral ventricles	8,50E-08	N
abnormal pancreas development	9,41E-08	N

JMJD1C

Term	P-value	Annotated
increased cellular sensitivity to ultraviolet irradiation	8,76E-09	N
abnormal somite development	5,00E-07	N
kidney inflammation	6,90E-07	N
thin cerebellar molecular layer	7,08E-07	N
decreased Purkinje cell number	7,47E-06	N
abnormal renal glomerulus morphology	8,38E-06	N
partial postnatal lethality	1,59E-05	N
increased platelet cell number	2,03E-05	N
asymmetric rib-sternum attachment	2,67E-05	N
complete embryonic lethality during organogenesis	3,20E-05	N
delayed embryo turning	3,42E-05	N
postnatal lethality	3,51E-05	N
abnormal spermatid morphology	7,24E-05	N
abnormal circulating protein level	8,88E-05	N
globozoospermia	1,13E-04	N
abnormal cell death	1,31E-04	N
embryonic growth retardation	1,33E-04	N
decreased survivor rate	1,38E-04	N
failure of eyelid fusion	1,43E-04	N

increased single-positive T cell number	1,62E-04	N

REEP3

Term	P-value	Annotated
abnormal lysosome morphology	1,90E-06	N
globozoospermia	2,36E-05	N
abnormal eating behavior	6,12E-05	N
cachexia	7,92E-04	N
decreased trabecular bone volume	9,63E-04	N
absent vibrissae	1,08E-03	N
abnormal hair follicle morphology	1,27E-03	N
thin epidermis	1,36E-03	N
blepharitis	2,02E-03	N
abnormal myelination	2,20E-03	N
increased single-positive T cell number	2,22E-03	N
complete preweaning lethality	2,42E-03	N
enlarged sebaceous gland	2,84E-03	N
abnormal myelin sheath morphology	2,89E-03	N
induced chromosome breakage	2,98E-03	N
abnormal postural reflex	3,07E-03	N
abnormal brain white matter morphology	3,15E-03	N
postnatal growth retardation	3,20E-03	N
increased lung adenoma incidence	3,27E-03	N
intraventricular hemorrhage	3,31E-03	

LRRC14

Term	P-value	Annotated
impaired coordination	2,56E-05	N
premature hair loss	2,09E-04	N
abnormal thymus corticomedullary boundary morphology	3,03E-04	N
decreased embryo weight	3,27E-04	N
dilated third ventricle	1,20E-03	N
increased keratinocyte proliferation	1,23E-03	N
small cerebellum	1,29E-03	N
impaired contextual conditioning behavior	1,41E-03	N
impaired hearing	1,58E-03	N
abnormal axon outgrowth	1,65E-03	N
abnormal retinal apoptosis	2,30E-03	N
abnormal female meiosis	2,75E-03	N
abnormal vascular branching morphogenesis	2,75E-03	N
abnormal lateral ventricle morphology	3,18E-03	N
mixed cellular infiltration to dermis	3,43E-03	N
dilated lateral ventricles	3,46E-03	N
increased circulating alanine transaminase level	3,81E-03	N

decreased prepulse inhibition	3,92E-03	N
abnormal brain white matter morphology	4,05E-03	N
increased circulating aspartate transaminase level	4,34E-03	N

ARHGAP39

Term	P-value	Annotated
abnormal embryonic cilium morphology	2,26E-05	N
dilated lateral ventricles	3,21E-05	N
abnormal ventral spinal root morphology	8,98E-05	N
abnormal cochlear outer hair cell morphology	9,02E-05	N
abnormal hippocampus layer morphology	1,62E-04	N
decreased lymphocyte cell number	1,83E-04	N
decreased immature B cell number	2,81E-04	N
polydactyly	2,85E-04	N
dilated third ventricle	2,91E-04	N
abnormal organ of Corti morphology	4,17E-04	N
polycystic kidney	4,83E-04	N
decreased neutrophil cell number	4,88E-04	N
herniated diaphragm	4,92E-04	N
hypotonia	5,17E-04	N
increased monocyte cell number	6,57E-04	N
abnormal neural crest cell migration	7,92E-04	N
decreased motor neuron number	9,00E-04	N
cochlear hair cell degeneration	1,09E-03	N
abnormal lymphocyte physiology	1,21E-03	N
belly spot	1,24E-03	N

FOXH1

Term	P-value	Annotated
abnormal primitive streak morphology	2,96E-31	Y
abnormal primitive streak formation	3,05E-23	N
abnormal mesoderm development	1,28E-22	Y
abnormal embryonic-extraembryonic boundary morphology	4,79E-21	Y
abnormal developmental patterning	2,50E-20	N
abnormal anterior visceral endoderm morphology	1,29E-19	N
abnormal rostral-caudal axis patterning	2,11E-19	N
absent primitive node	2,13E-18	Y
abnormal ectoderm development	2,22E-18	N
transposition of great arteries	5,89E-18	N
abnormal somite development	7,86E-18	Y
abnormal neural fold formation	1,36E-15	Y
abnormal axial mesoderm	2,48E-15	N
abnormal heart looping	3,51E-14	Y
abnormal embryogenesis/ development	6,31E-13	N

absent mesoderm	1,17E-12	N
right pulmonary isomerism	7,26E-12	N
abnormal heart development	9,15E-12	Y
decreased caudal vertebrae number	1,77E-11	N
abnormal gastrulation	1,82E-11	N

KIFC2

Term	P-value	Annotated
abnormal miniature excitatory postsynaptic currents	6,38E-07	N
abnormal inhibitory postsynaptic currents	2,73E-06	N
abnormal spatial learning	3,81E-06	N
abnormal excitatory postsynaptic currents	5,50E-06	N
abnormal AMPA-mediated synaptic currents	5,60E-06	N
reduced long term depression	7,45E-06	N
abnormal hippocampal mossy fiber morphology	9,40E-06	N
abnormal long term depression	1,30E-05	N
enhanced long term potentiation	2,29E-05	N
enhanced paired-pulse facilitation	2,72E-05	N
abnormal synaptic vesicle morphology	4,49E-05	N
abnormal excitatory postsynaptic potential	5,23E-05	N
abnormal zygomatic bone morphology	8,26E-05	N
abnormal anxiety-related response	9,26E-05	N
skin lesions	9,54E-05	N
abnormal synaptic vesicle recycling	9,97E-05	N
abnormal brain internal capsule morphology	1,68E-04	N
clonic seizures	2,03E-04	N
decreased susceptibility to pharmacologically induced seizures	2,11E-04	N
abnormal CNS synaptic transmission	2,11E-04	N

CYHR1

Term	P-value	Annotated
abnormal brain white matter morphology	4,74E-08	N
decreased embryo weight	5,75E-08	N
abnormal lung interstitium morphology	1,87E-06	N
abnormal reproductive system development	1,68E-05	N
decreased liver cholesterol level	2,66E-05	N
abnormal digestion	4,27E-05	N
dilated third ventricle	5,09E-05	N
reddish skin	6,08E-05	N
abnormal astrocyte morphology	1,54E-04	N
abnormal hematopoietic system physiology	1,60E-04	N
herniated abdominal wall	1,63E-04	N
abnormal cell adhesion	1,64E-04	N
increased keratinocyte proliferation	2,70E-04	N

abnormal epididymal fat pad morphology	4,92E-04	N
skin lesions	5,36E-04	N
increased susceptibility to endotoxin shock	5,73E-04	N
abnormal stomach epithelium morphology	5,81E-04	N
thick interventricular septum	6,66E-04	N
decreased circulating insulin level	7,29E-04	N
abnormal cell migration	8,07E-04	N

VPS28

Term	P-value	Annotated
reddish skin	1,16E-06	N
skin lesions	2,10E-06	N
large intestinal inflammation	1,72E-05	N
aneuploidy	2,85E-05	N
premature hair loss	2,89E-05	N
alopecia	1,60E-04	N
increased skin tumor incidence	2,09E-04	N
increased cellular sensitivity to oxidative stress	2,27E-04	N
epidermal hyperplasia	4,84E-04	N
abnormal brain white matter morphology	5,72E-04	N
abnormal coat appearance	5,82E-04	N
lung carcinoma	7,44E-04	N
absent Peyer's patches	7,58E-04	N
herniated abdominal wall	7,89E-04	N
diarrhea	8,46E-04	N
abnormal large intestine crypts of Lieberkuhn morphology	8,60E-04	N
dilated third ventricle	1,04E-03	N
abnormal small intestine crypts of Lieberkuhn morphology	1,15E-03	N
decreased germ cell number	1,24E-03	N
mixed cellular infiltration to dermis	1,40E-03	N

SCRT1

Term	P-value	Annotated
impaired conditioned place preference behavior	3,30E-12	N
abnormal spatial learning	8,64E-12	N
abnormal spike wave discharge	5,55E-11	N
impaired behavioral response to addictive substance	1,17E-10	N
increased exploration in new environment	1,60E-10	N
absence seizures	1,17E-09	N
abnormal nervous system electrophysiology	1,18E-09	N
enhanced coordination	1,76E-09	N
abnormal inhibitory postsynaptic currents	1,13E-08	N
decreased vertical activity	1,64E-08	N
abnormal behavioral response to xenobiotic	1,69E-08	N

sporadic seizures	2,07E-08	N
abnormal action potential	2,15E-08	N
abnormal excitatory postsynaptic currents	2,89E-08	N
decreased neurotransmitter release	2,91E-08	N
reduced long term depression	2,92E-08	N
ataxia	8,70E-08	N
abnormal brain wave pattern	2,28E-07	N
impaired swimming	3,23E-07	N
impaired coordination	4,00E-07	N

ATXN2L

Term	P-value	Annotated
dilated lateral ventricles	4,53E-08	N
decreased susceptibility to viral infection	1,36E-07	N
increased brain size	2,85E-07	N
cardia bifida	7,70E-07	N
abnormal inner cell mass morphology	1,08E-06	N
abnormal cell death	1,54E-06	N
small testis	6,04E-05	N
trabecula carnea hypoplasia	1,32E-04	N
abnormal gastrulation	1,95E-04	N
decreased birth body size	2,03E-04	N
mesangial cell hyperplasia	3,13E-04	N
thin myocardium compact layer	3,82E-04	N
abnormal dendritic cell morphology	4,78E-04	N
abnormal reproductive system physiology	4,94E-04	N
increased cellular sensitivity to ionizing radiation	5,19E-04	N
partial postnatal lethality	5,56E-04	N
dilated kidney collecting duct	5,90E-04	N
abnormal proerythroblast morphology	6,08E-04	N
abnormal extraembryonic tissue morphology	6,16E-04	N
dilated third ventricle	6,30E-04	N

TUFM

Term	P-value	Annotated
abnormal mitochondrial morphology	5,93E-06	N
extended life span	4,15E-05	N
abnormal mitochondrial physiology	5,23E-05	N
abnormal aerobic energy metabolism	7,23E-05	N
astrocytosis	9,35E-04	N
abnormal mitosis	1,03E-03	N
abnormal channel response	1,05E-03	N
reduced male fertility	1,60E-03	N
decreased erythroid progenitor cell number	1,90E-03	N

abnormal cerebellar cortex morphology	2,27E-03	N
abnormal cell cycle checkpoint function	2,35E-03	N
abnormal mechanical nociception	2,55E-03	N
cryptorchism	2,86E-03	N
complete embryonic lethality between implantation and placent	3,22E-03	N
partial lethality at weaning	3,82E-03	N
abnormal embryonic neuroepithelial layer differentiation	3,83E-03	N
abnormal tail bud morphology	4,69E-03	N
hydroureter	4,83E-03	N
abnormal mitotic spindle morphology	5,06E-03	N
vertebral transformation	5,11E-03	N

SH2B1

Term	P-value	Annotated
microgliosis	4,98E-04	N
complete embryonic lethality before implantation	9,28E-04	N
partial lethality at weaning	9,61E-04	N
spongiform encephalopathy	1,16E-03	N
abnormal trophoblast layer morphology	1,51E-03	N
Leydig cell hyperplasia	2,19E-03	N
abnormal embryonic neuroepithelial layer differentiation	2,39E-03	N
absent common myeloid progenitor cells	3,65E-03	N
failure to form blastocele	4,20E-03	N
abnormal oligodendrocyte morphology	4,45E-03	N
abnormal glycogen homeostasis	4,51E-03	N
abnormal aorta elastic tissue morphology	4,67E-03	N
renal tubule atrophy	5,59E-03	N
hunched posture	5,60E-03	N
decreased susceptibility to diet-induced obesity	5,82E-03	N
astrocytosis	6,01E-03	N
thin ventricular wall	6,18E-03	N
paraparesis	6,23E-03	N
inner cell mass degeneration	6,30E-03	N
incomplete cephalic closure	6,41E-03	N

NFATC2IP

Term	P-value	Annotated
abnormal chromosome morphology	1,07E-09	N
partial embryonic lethality before implantation	2,09E-05	N
absent somites	2,61E-05	N
abnormal inner cell mass proliferation	4,01E-05	N
polyploidy	1,11E-04	N
abnormal inner cell mass morphology	1,13E-04	N
abnormal blastocyst morphology	1,38E-04	N

complete embryonic lethality before somite formation	1,58E-04	N
abnormal outflow tract development	2,15E-04	N
abnormal cell cycle	2,91E-04	N
chromosome breakage	3,22E-04	N
decreased cell proliferation	4,74E-04	N
decreased ovary weight	5,98E-04	N
ectopic cerebellar granule cells	7,51E-04	N
progressive muscle weakness	7,72E-04	N
absent ovarian follicles	9,30E-04	N
increased drinking behavior	1,58E-03	N
chromosomal instability	1,75E-03	N
abnormal cell nucleus morphology	2,28E-03	N
increased histiocytic sarcoma incidence	2,35E-03	N

SPNS1

Term	P-value	Annotated
abnormal lysosome morphology	9,16E-10	N
astrocytosis	5,15E-08	N
Purkinje cell degeneration	7,77E-06	N
short stride length	1,22E-05	N
abnormal lysosome physiology	3,05E-05	N
abnormal cued conditioning behavior	3,54E-05	N
increased interleukin-2 secretion	4,94E-05	N
muscular atrophy	1,64E-04	N
hindlimb paralysis	1,82E-04	N
abnormal Reichert's membrane morphology	2,18E-04	N
epidermal hyperplasia	2,71E-04	N
abnormal retinal ganglion layer morphology	2,76E-04	N
limb grasping	3,39E-04	N
myeloid hyperplasia	3,83E-04	N
absent kidney	4,07E-04	N
gliosis	4,30E-04	N
abnormal chromosome morphology	5,28E-04	N
abnormal anterior visceral endoderm morphology	9,22E-04	N
microgliosis	1,07E-03	N
single kidney	1,07E-03	N

LAT

Term	P-value	Annotated
arrested T cell differentiation	1,13E-75	Y
abnormal T cell differentiation	3,52E-71	Y
decreased CD4-positive T cell number	5,23E-70	N
abnormal CD8-positive T cell differentiation	1,67E-67	N
abnormal double-negative T cell morphology	8,78E-66	Y

decreased CD8-positive T cell number	1,03E-65	N
abnormal positive T cell selection	1,66E-62	N
abnormal thymocyte activation	5,83E-62	Y
thymus hypoplasia	2,43E-55	Y
decreased interleukin-2 secretion	3,13E-53	N
decreased double-positive T cell number	2,02E-51	Y
increased T cell apoptosis	1,83E-49	N
abnormal T cell morphology	5,46E-48	Y
abnormal T cell activation	9,40E-48	Y
abnormal T cell subpopulation ratio	5,31E-47	Y
decreased T cell proliferation	8,76E-47	Y
absent T cells	2,29E-46	Y
abnormal CD8-positive T cell morphology	2,10E-45	Y
decreased T cell number	2,63E-44	Y
decreased thymocyte number	2,90E-44	Y

SULT1A1
SULT1A2

Term	P-value	Annotated
increased sensitivity to induced morbidity/mortality	1,68E-09	
abnormal pregnancy	1,69E-08	
abnormal blood coagulation	1,03E-07	
abnormal circulating amino acid level	2,18E-07	
abnormal liver physiology	2,43E-07	
abnormal homeostasis	9,13E-07	
hepatic steatosis	9,29E-07	
increased circulating cholesterol level	2,41E-06	
abnormal lipid homeostasis	3,78E-06	
abnormal iron level	3,78E-06	
expanded mesangial matrix	5,89E-06	
abnormal amino acid level	8,28E-06	
abnormal enterocyte proliferation	9,84E-06	
gastrointestinal hemorrhage	1,04E-05	
increased circulating aldosterone level	1,27E-05	
increased circulating triglyceride level	2,83E-05	
abnormal leukocyte morphology	3,01E-05	
increased circulating ammonia level	3,47E-05	
abnormal bile salt level	3,59E-05	
other aberrant phenotype	4,63E-05	

CCDC101

Term	P-value	Annotated
absent somites	3,92E-06	N
abnormal chromosome morphology	2,29E-05	N

small Peyer's patches	2,90E-05	N
decreased immunoglobulin level	3,17E-04	N
decreased Peyer's patch number	3,34E-04	N
abnormal cytokine level	6,78E-04	N
increased hematopoietic stem cell number	6,90E-04	N
decreased IgM level	8,30E-04	N
abnormal extraembryonic endoderm formation	9,16E-04	N
complete embryonic lethality before implantation	9,18E-04	N
liver hemorrhage	1,15E-03	N
increased leukocyte cell number	1,16E-03	N
abnormal enteric nervous system morphology	1,34E-03	N
abnormal lymphocyte cell number	1,49E-03	N
abnormal Peyer's patch morphology	1,52E-03	N
abnormal molar morphology	1,77E-03	N
abnormal Peyer's patch germinal center morphology	2,05E-03	N
increased IgG1 level	2,09E-03	N
decreased IgG level	2,11E-03	N
abnormal spleen marginal zone morphology	2,54E-03	N

NRXN1

Term	P-value	Annotated
abnormal inhibitory postsynaptic currents	1,60E-26	N
abnormal CNS synaptic transmission	2,60E-25	N
abnormal GABA-mediated receptor currents	2,63E-24	N
abnormal excitatory postsynaptic currents	1,21E-22	N
hyperactivity	6,32E-18	N
abnormal synaptic transmission	1,36E-17	N
abnormal spatial learning	7,66E-17	N
abnormal synaptic vesicle number	3,62E-16	N
abnormal posture	6,36E-16	N
ataxia	1,43E-14	N
abnormal brain wave pattern	2,38E-14	N
seizures	6,80E-14	N
convulsive seizures	1,40E-13	N
abnormal nervous system electrophysiology	4,86E-13	N
abnormal spatial reference memory	4,89E-13	N
abnormal excitatory postsynaptic potential	8,07E-13	N
abnormal hippocampus morphology	1,16E-12	N
impaired coordination	1,37E-12	N
increased startle reflex	1,52E-12	N
abnormal social/conspecific interaction	3,89E-12	N

NUPR1

Term	P-value	Annotated

abnormal aorta wall morphology	3,39E-08	N
abnormal bone mineralization	4,70E-08	N
increased cellular sensitivity to hydrogen peroxide	1,12E-07	N
abnormal aorta tunica media morphology	1,70E-07	N
increased brain weight	1,72E-07	N
abnormal compact bone morphology	2,25E-07	N
abnormal chondrocyte morphology	4,65E-07	N
decreased trabecular bone thickness	5,26E-07	N
abnormal skeleton physiology	5,96E-07	N
hyporesponsive to tactile stimuli	7,01E-07	N
abnormal bone structure	1,77E-06	N
decreased bone volume	3,45E-06	N
abnormal long bone epiphyseal plate morphology	3,85E-06	N
increased hepatocyte apoptosis	5,00E-06	N
increased lean body mass	5,32E-06	N
overexpanded pulmonary alveoli	6,26E-06	N
abnormal hippocampus layer morphology	6,70E-06	N
oxidative stress	1,03E-05	N
abnormal trabecular bone morphology	1,51E-05	N
abnormal enteric neuron morphology	1,70E-05	N

NPAS2

Term	P-value	Annotated
shortened circadian period	7,01E-16	N
increased incidence of corneal inflammation	6,87E-13	N
increased circulating aspartate transaminase level	9,77E-13	N
abnormal tail movements	2,61E-12	N
increased total fat pad weight	3,29E-12	N
abnormal circulating hormone level	5,60E-12	N
decreased uterus weight	2,06E-10	N
abnormal joint morphology	1,55E-09	N
early reproductive senescence	7,12E-09	N
increased bone resorption	8,64E-09	N
hypotension	1,17E-08	Y
increased circulating alanine transaminase level	5,77E-08	N
abnormal hair cycle	2,11E-07	N
decreased heart weight	2,33E-07	N
decreased mean systemic arterial blood pressure	3,28E-07	Y
abnormal metabolism	5,48E-07	N
abnormal response to injury	6,87E-07	Y
abnormal vertebral column morphology	1,38E-06	N
abnormal corneal stroma morphology	1,45E-06	N
osteoporosis	2,24E-06	N

KCNMA1		
Term	P-value	Annotated
myoclonus	2,27E-08	N
decreased vasoconstriction	6,72E-08	N
abnormal miniature excitatory postsynaptic currents	1,24E-07	N
abnormal heart left ventricle morphology	6,69E-07	N
abnormal patella morphology	6,76E-07	N
distended urinary bladder	1,79E-06	N
abnormal brain wave pattern	2,98E-06	N
abnormal cartilage development	3,24E-06	N
limb grasping	5,34E-06	N
intracerebral hemorrhage	8,26E-06	N
abnormal GABA-mediated receptor currents	9,18E-06	N
decreased mean systemic arterial blood pressure	1,03E-05	N
abnormal synaptic plasticity	1,08E-05	N
decreased length of long bones	1,21E-05	N
decreased aggression towards males	1,67E-05	N
abnormal pancreatic beta cell physiology	2,70E-05	N
abnormal tibia morphology	3,49E-05	N
abnormal long bone epiphysis morphology	3,54E-05	N
abnormal long bone hypertrophic chondrocyte zone	3,73E-05	N
abnormal skeleton physiology	3,93E-05	N

DEC1		
Term	P-value	Annotated
hydroencephaly	3,16E-03	N
abnormal startle reflex	5,63E-03	N
absent incisors	8,57E-03	N
abnormal supraoccipital bone morphology	1,35E-02	N
abnormal exocrine pancreas morphology	1,48E-02	N
decreased oocyte number	1,57E-02	N
abnormal pituitary gland morphology	1,66E-02	N
impaired passive avoidance behavior	1,74E-02	N
abnormal milk composition	2,14E-02	N
abnormal drinking behavior	2,18E-02	N
abnormal egg cylinder morphology	2,21E-02	N
absent distortion product otoacoustic emissions	2,50E-02	N
abnormal platelet physiology	2,76E-02	N
spinal hemorrhage	2,84E-02	N
intracerebral hemorrhage	2,92E-02	N
abnormal acrosome morphology	3,25E-02	N
muscle spasm	3,28E-02	N
abnormal eye distance/ position	3,43E-02	N
rib fusion	3,54E-02	N

stereotypic behavior	3,80E-02	N

SDCCAG8		
Term	P-value	Annotated
abnormal direction of heart looping	3,09E-04	N
dilated heart right ventricle	9,33E-04	N
extramedullary hematopoiesis	1,03E-03	N
decreased mature ovarian follicle number	1,26E-03	N
increased triglyceride level	1,40E-03	N
abnormal left-right axis patterning	1,71E-03	N
absent embryonic cilia	1,87E-03	N
myocardial necrosis	2,22E-03	N
increased pituitary adenoma incidence	2,35E-03	N
abnormal artery morphology	2,65E-03	N
prolonged PR interval	2,76E-03	N
reduced female fertility	3,07E-03	N
abnormal immune serum protein physiology	3,37E-03	N
increased leukocyte cell number	3,42E-03	N
abnormal bone marrow cavity morphology	4,31E-03	N
abnormal cochlear sensory epithelium morphology	4,51E-03	N
osteoporosis	4,64E-03	N
increased cellular sensitivity to gamma-irradiation	5,44E-03	N
abnormal osteoblast physiology	5,96E-03	N
abnormal enteric ganglia morphology	7,37E-03	N

AKT3		
Term	P-value	Annotated
abnormal hippocampus pyramidal cell layer	1,66E-13	N
small hippocampus	1,80E-08	N
abnormal neocortex morphology	5,64E-06	N
decreased neuron number	6,53E-06	N
placental labyrinth hypoplasia	1,09E-05	N
decreased circulating thyroxine level	1,46E-05	N
abnormal brain ventricle morphology	1,73E-05	N
abnormal heart septum morphology	2,56E-05	N
abnormal fluid regulation	8,97E-05	N
decreased circulating triiodothyronine level	1,46E-04	N
abnormal sensory capabilities/reflexes/nociception	1,73E-04	N
abnormal hippocampus morphology	1,87E-04	N
abnormal cerebellar foliation	1,95E-04	N
decreased triglyceride level	2,44E-04	N
abnormal postnatal subventricular zone morphology	2,53E-04	N
skin lesions	2,60E-04	N
impaired balance	2,63E-04	N

increased susceptibility to weight gain	2,77E-04	N
abnormal social/conspecific interaction	3,00E-04	N
abnormal foot pigmentation	3,25E-04	N

CRYZL1

Term	P-value	Annotated
increased incidence of induced tumors	5,06E-06	N
small seminiferous tubules	2,14E-05	N
decreased double-positive T cell number	8,41E-05	N
myopathy	9,57E-05	N
increased susceptibility to atherosclerosis	1,06E-04	N
abnormal cell-mediated immunity	1,77E-04	N
abnormal synaptic vesicle recycling	2,07E-04	N
abnormal adrenal gland secretion	2,27E-04	N
abnormal bone marrow cell physiology	2,88E-04	N
failure of initiation of embryo turning	3,45E-04	N
abnormal muscle fiber morphology	3,76E-04	N
decreased susceptibility to diet-induced obesity	3,89E-04	N
enlarged spleen	6,44E-04	N
abnormal pulmonary alveolus morphology	6,55E-04	N
abnormal emotion/affect behavior	7,16E-04	N
increased B cell number	7,26E-04	N
decreased birth weight	8,26E-04	N
abnormal Sertoli cell morphology	8,95E-04	N
decreased corpus callosum size	9,05E-04	N
abnormal T cell number	9,29E-04	N

ITSN1

Term	P-value	Annotated
increased susceptibility to noise-induced hearing loss	7,77E-08	N
decreased brain size	2,82E-07	N
increased liver triglyceride level	9,15E-07	N
increased percent body fat	2,85E-06	N
increased fat cell size	9,94E-06	N
abnormal behavior	3,11E-05	N
microgliosis	4,08E-05	N
increased spleen iron level	4,64E-05	N
abnormal crypts of Lieberkuhn morphology	6,53E-05	N
complete embryonic lethality	6,64E-05	N
abnormal hippocampal commissure morphology	7,24E-05	N
decreased circulating free fatty acid level	7,92E-05	N
decreased thymocyte apoptosis	1,00E-04	N
abnormal embryonic growth/weight/body size	1,03E-04	N
decreased hemoglobin content	1,14E-04	N

failure of primitive streak formation	1,19E-04	N
enlarged lateral ventricles	1,21E-04	N
ectopic Purkinje cell	1,29E-04	N
abnormal otic capsule morphology	1,47E-04	N
abnormal head morphology	1,67E-04	N

SON

Term	P-value	Annotated
decreased birth body size	2,36E-07	N
increased cellular sensitivity to ionizing radiation	1,62E-06	N
abnormal anterior visceral endoderm morphology	7,92E-06	N
abnormal DNA replication	1,12E-05	N
abnormal granulocyte differentiation	1,31E-05	N
increased incidence of induced tumors	1,32E-05	N
decreased fetal size	1,65E-05	N
incomplete embryo turning	2,20E-05	N
complete perinatal lethality	2,59E-05	N
pericardial effusion	2,66E-05	N
ventricular septal defect	3,52E-05	N
abnormal ectoderm development	3,62E-05	N
complete embryonic lethality	4,14E-05	N
partial postnatal lethality	5,08E-05	N
small branchial arch	5,15E-05	N
complete embryonic lethality during organogenesis	5,69E-05	N
increased mortality induced by gamma-irradiation	5,97E-05	N
abnormal brain internal capsule morphology	6,07E-05	N
abnormal visceral endoderm morphology	7,58E-05	N
decreased cell proliferation	7,77E-05	N

GART

Term	P-value	Annotated
complete embryonic lethality between implantation and placent	3,21E-05	N
abnormal DNA repair	3,46E-05	N
failure to form blastocele	7,42E-05	N
induced chromosome breakage	7,50E-05	N
absent inner cell mass	8,38E-05	N
complete embryonic lethality before somite formation	1,23E-04	N
increased cellular sensitivity to ionizing radiation	1,23E-04	N
decreased tumor latency	1,64E-04	N
decreased spleen red pulp amount	2,63E-04	N
inner cell mass degeneration	3,38E-04	N
abnormal food intake	7,30E-04	N
T cell derived lymphoma	8,00E-04	N
complete embryonic lethality before implantation	8,24E-04	N

abnormal cell cycle checkpoint function	8,32E-04	N
increased fibrosarcoma incidence	9,67E-04	N
increased susceptibility to noise-induced hearing loss	1,15E-03	N
decreased single-positive T cell number	1,19E-03	N
small hippocampus	1,40E-03	N
hyperactivity	1,46E-03	N
abnormal digit morphology	1,63E-03	N

DNAJC28

Term	P-value	Annotated
abnormal mitochondrial physiology	2,54E-04	N
abnormal femur morphology	5,63E-04	N
abnormal otic vesicle development	1,02E-03	N
abnormal ovarian folliculogenesis	1,21E-03	N
reduced female fertility	1,29E-03	N
partial perinatal lethality	1,37E-03	N
abnormal skeleton development	1,82E-03	N
early reproductive senescence	2,49E-03	N
abnormal ureteric bud morphology	2,49E-03	N
abnormal stationary movement	2,54E-03	N
abnormal corpus callosum morphology	2,59E-03	N
abnormal bone remodeling	3,33E-03	N
enlarged lateral ventricles	3,35E-03	N
abnormal thyroid cartilage morphology	3,97E-03	N
abnormal tibia morphology	4,01E-03	N
decreased primordial germ cell number	4,24E-03	N
abnormal kidney morphology	4,76E-03	N
abnormal reproductive system morphology	5,07E-03	N
short maxilla	5,22E-03	N
abnormal cochlear sensory epithelium morphology	6,08E-03	N

TMEM50B

Term	P-value	Annotated
increased susceptibility to ischemic brain injury	1,00E-04	N
abnormal DNA methylation	1,61E-04	N
arrested T cell differentiation	1,64E-04	N
partial perinatal lethality	1,84E-04	N
abnormal type II pneumocyte morphology	2,75E-04	N
increased cardiomyocyte apoptosis	2,88E-04	N
decreased double-negative T cell number	3,69E-04	N
abnormal somite development	4,47E-04	N
abnormal spongiotrophoblast layer morphology	5,59E-04	N
myocardial necrosis	7,18E-04	N
abnormal pericardium morphology	1,12E-03	N

abnormal vas deferens morphology	1,21E-03	N
abnormal cardiac muscle relaxation	1,32E-03	N
abnormal immune system organ morphology	1,34E-03	N
abnormal liver morphology	1,73E-03	N
abnormal T cell activation	1,84E-03	N
abnormal double-positive T cell morphology	2,02E-03	N
decreased gonadal fat pad weight	2,06E-03	N
increased bone mass	2,11E-03	N
increased cellular sensitivity to gamma-irradiation	2,13E-03	N

IFNGR2

Term	P-value	Annotated
abnormal macrophage physiology	4,19E-17	N
large intestinal inflammation	1,38E-15	N
decreased interleukin-12b secretion	6,30E-15	N
decreased interleukin-12 secretion	1,03E-12	N
myositis	5,23E-12	N
decreased circulating tumor necrosis factor level	9,28E-12	N
decreased tumor necrosis factor secretion	9,35E-12	N
abnormal tumor necrosis factor level	4,35E-11	N
increased IgM level	1,62E-10	N
abnormal mesenteric lymph node morphology	1,95E-10	N
increased marginal zone B cell number	2,06E-10	N
decreased interleukin-6 secretion	7,04E-10	N
decreased interferon-beta secretion	8,04E-10	N
impaired neutrophil phagocytosis	1,22E-09	N
abnormal interleukin level	1,89E-09	N
decreased dendritic cell number	2,15E-09	N
increased B cell proliferation	3,53E-09	N
decreased IgG2a level	3,61E-09	N
decreased susceptibility to induced colitis	4,56E-09	N
abnormal Peyer's patch morphology	5,21E-09	N

SBNO1

Term	P-value	Annotated
abnormal spermatocyte morphology	1,36E-05	N
abnormal spermatid morphology	2,91E-05	N
male germ cell apoptosis	3,53E-05	N
right aortic arch	3,82E-05	N
small testis	4,14E-05	N
arrest of spermatogenesis	8,46E-05	N
pericardial effusion	2,23E-04	N
decreased urine potassium level	8,89E-04	N
thymus atrophy	9,84E-04	N

spleen atrophy	1,01E-03	N
abnormal sperm head morphology	1,18E-03	N
skin papilloma	1,28E-03	N
abnormal hippocampal commissure morphology	1,39E-03	N
abnormal digestive system development	1,42E-03	N
abnormal sperm midpiece morphology	1,59E-03	N
complete embryonic lethality between implantation and placent	1,84E-03	N
decreased male germ cell number	1,91E-03	N
decreased urine sodium level	2,14E-03	N
decreased testis weight	2,34E-03	N
male infertility	2,93E-03	N

SETD8

Term	P-value	Annotated
abnormal brain internal capsule morphology	3,42E-04	N
decreased physiological sensitivity to xenobiotic	2,45E-03	N
skin papilloma	2,59E-03	N
abnormal nitric oxide homeostasis	2,97E-03	N
abnormal DNA replication	5,10E-03	N
abnormal visceral endoderm morphology	5,25E-03	N
polydipsia	5,66E-03	N
abnormal erythropoiesis	6,07E-03	N
abnormal ventral body wall morphology	6,33E-03	N
abnormal megakaryocyte differentiation	6,87E-03	N
polyploidy	6,94E-03	N
abnormal male reproductive system morphology	7,75E-03	N
abnormal apoptosis	7,93E-03	N
decreased follicle stimulating hormone level	8,40E-03	N
anovulation	8,82E-03	N
small ovary	9,64E-03	N
abnormal female reproductive system morphology	9,81E-03	N
abnormal bone marrow cell physiology	9,92E-03	N
decreased spleen germinal center size	1,09E-02	N
short premaxilla	1,17E-02	N

RILPL2

Term	P-value	Annotated
increased T cell proliferation	5,85E-11	N
increased interleukin-17 secretion	1,57E-10	N
enlarged lymph nodes	5,55E-09	N
increased IgE level	8,47E-09	N
decreased interleukin-2 secretion	2,14E-08	N
increased B cell proliferation	4,05E-08	N
abnormal thymocyte activation	5,10E-08	N

increased susceptibility to experimental autoimmune encephalor	6,40E-08	N
abnormal CD4-positive T cell physiology	8,56E-08	N
abnormal cytokine secretion	1,02E-07	N
increased IgA level	1,19E-07	N
abnormal regulatory T cell physiology	1,38E-07	N
decreased interleukin-4 secretion	2,45E-07	N
increased IgG2a level	2,61E-07	N
increased IgG1 level	2,66E-07	N
abnormal class switch recombination	3,53E-07	N
increased plasma cell number	3,56E-07	N
abnormal T cell physiology	3,66E-07	N
abnormal dendritic cell physiology	3,96E-07	N
decreased susceptibility to experimental autoimmune encephalo	8,26E-07	N

C12orf65

Term	P-value	Annotated
increased gastrointestinal tumor incidence	1,17E-03	N
impaired olfaction	5,98E-03	N
abnormal nervous system physiology	7,47E-03	N
abnormal colon morphology	7,61E-03	N
abnormal choroid pigmentation	8,08E-03	N
abnormal medulla oblongata morphology	8,19E-03	N
abnormal iris pigmentation	8,83E-03	N
abnormal chondrocyte morphology	1,04E-02	N
ovary atrophy	1,05E-02	N
irregular coat pigmentation	1,13E-02	N
transposition of great arteries	1,16E-02	N
abnormal neural tube closure	1,43E-02	N
abnormal seizure response to electrical stimulation	1,61E-02	N
abnormal hippocampus CA1 region morphology	1,71E-02	N
increased cardiomyocyte apoptosis	1,71E-02	N
absent distortion product otoacoustic emissions	1,76E-02	N
abnormal pancreas development	1,77E-02	N
increased drinking behavior	1,77E-02	N
decreased respiratory quotient	1,86E-02	N
abnormal intestinal mucosa morphology	1,92E-02	N

MPHOSPH9

Term	P-value	Annotated
abnormal mitotic spindle morphology	7,78E-06	N
abnormal chromosome morphology	1,53E-05	N
abnormal mitosis	2,10E-05	N
abnormal cell nucleus morphology	7,73E-05	N
increased tumor incidence	1,02E-04	N

abnormal spermatogonia proliferation	2,85E-04	N
small stomach	4,33E-04	N
abnormal mammary gland epithelium morphology	4,35E-04	N
cervical vertebral transformation	5,41E-04	N
increased transitional stage B cell number	7,79E-04	N
intestinal adenocarcinoma	7,92E-04	N
increased lymphoma incidence	9,61E-04	N
failure of zygotic cell division	1,09E-03	N
dystrophic muscle	1,15E-03	N
decreased B cell proliferation	1,17E-03	N
abnormal positive T cell selection	1,25E-03	N
delayed kidney development	1,31E-03	N
skin papilloma	1,66E-03	N
atrioventricular septal defect	1,68E-03	N
increased B cell apoptosis	1,72E-03	N

SNRNP35

Term	P-value	Annotated
decreased lymphocyte cell number	4,63E-04	N
intestinal inflammation	6,83E-04	N
abnormal brain morphology	7,10E-04	N
increased double-positive T cell number	1,23E-03	N
small placenta	1,34E-03	N
thymus hypoplasia	1,42E-03	N
abnormal action potential	1,47E-03	N
leukemia	2,07E-03	N
astrocytosis	2,12E-03	N
absent T cells	2,32E-03	N
neurodegeneration	2,54E-03	N
seminiferous tubule degeneration	2,81E-03	N
decreased double-positive T cell number	2,88E-03	N
increased circulating luteinizing hormone level	3,02E-03	N
abnormal cell physiology	3,33E-03	N
abnormal miniature inhibitory postsynaptic currents	3,44E-03	N
arrested T cell differentiation	3,61E-03	N
complete embryonic lethality	3,69E-03	N
decreased T cell number	3,80E-03	N
increased cellular sensitivity to ionizing radiation	3,91E-03	N

RILPL1

Term	P-value	Annotated
skeletal muscle fiber necrosis	2,97E-07	N
abnormal thymus involution	5,32E-06	N
absent mature B cells	5,38E-06	N

abnormal B cell morphology	1,08E-05	N
spleen hypoplasia	1,51E-05	N
decreased B cell number	4,02E-05	N
increased macrophage cell number	5,73E-05	N
arrested B cell differentiation	5,78E-05	N
increased skeletal muscle fiber size	6,78E-05	N
abnormal supraoccipital bone morphology	8,05E-05	N
centrally nucleated skeletal muscle fibers	9,80E-05	N
abnormal skeletal muscle morphology	9,97E-05	N
abnormal notochord morphology	1,01E-04	N
leukemia	1,19E-04	N
abnormal lymphopoiesis	1,25E-04	N
abnormal B cell differentiation	2,22E-04	N
abnormal muscle physiology	2,44E-04	N
small branchial arch	3,13E-04	N
increased cochlear inner hair cell number	3,40E-04	N
increased cochlear outer hair cell number	3,84E-04	N

PITPNM2

Term	P-value	Annotated
reduced long term depression	4,96E-06	N
decreased double-positive T cell number	1,03E-05	N
uterus hypoplasia	1,65E-05	N
abnormal T cell physiology	8,79E-05	N
abnormal behavior	1,16E-04	N
decreased T cell number	2,01E-04	N
increased bleeding time	2,27E-04	N
abnormal learning/ memory	2,34E-04	N
arrested T cell differentiation	2,56E-04	N
abnormal T cell differentiation	2,90E-04	N
abnormal trabecular bone morphology	3,62E-04	N
impaired cued conditioning behavior	4,34E-04	N
decreased chemically-elicited antinociception	5,06E-04	N
abnormal double-negative T cell morphology	5,12E-04	N
delayed female fertility	5,14E-04	N
abnormal excitatory postsynaptic potential	5,15E-04	N
impaired contextual conditioning behavior	6,63E-04	N
decreased thymocyte number	7,12E-04	N
abnormal calcium ion homeostasis	8,60E-04	N
abnormal estrous cycle	9,59E-04	N

STK24

Term	P-value	Annotated
abnormal immune system organ morphology	1,73E-05	N

small first branchial arch	3,72E-05	N
decreased cell proliferation	4,93E-05	N
abnormal immune system cell morphology	6,45E-05	N
premature aging	6,99E-05	N
increased cellular sensitivity to ultraviolet irradiation	8,26E-05	N
decreased spleen weight	1,08E-04	N
failure of chorioallantoic fusion	1,18E-04	N
increased single-positive T cell number	1,21E-04	N
increased energy expenditure	1,59E-04	N
abnormal placental labyrinth vasculature morphology	1,88E-04	N
wavy neural tube	2,09E-04	N
decreased thymus weight	2,99E-04	N
short premaxilla	3,07E-04	N
induced chromosome breakage	3,20E-04	N
abnormal cerebellar foliation	3,54E-04	N
liver hypoplasia	4,42E-04	N
small cerebellum	4,73E-04	N
B cell derived lymphoma	4,90E-04	N
embryonic growth retardation	5,17E-04	N

FARP1

Term	P-value	Annotated
anal atresia	4,60E-09	N
cleft secondary palate	3,03E-08	N
short mandible	3,56E-08	N
abnormal limb morphology	4,04E-08	N
abnormal ulna morphology	4,51E-08	N
decreased chondrocyte cell number	1,61E-07	N
short radius	1,66E-07	N
decreased tongue size	2,16E-07	N
short ulna	5,12E-07	N
abnormal frontal bone morphology	7,07E-07	N
dilated kidney collecting duct	9,06E-07	N
cleft palate	1,11E-06	N
impaired branching involved in ureteric bud morphogenesis	1,29E-06	N
short fibula	2,04E-06	N
delayed kidney development	2,63E-06	N
abnormal bile duct morphology	2,70E-06	N
abnormal tarsal bone morphology	3,22E-06	N
abnormal cell migration	3,77E-06	N
abnormal cranium morphology	3,92E-06	N
abnormal spine curvature	4,01E-06	N

SLC15A1

Term	P-value	Annotated
increased susceptibility to weight loss	3,41E-04	N
increased urine potassium level	1,41E-03	N
abnormal intestinal lipid absorption	1,48E-03	N
increased kidney weight	2,68E-03	N
partial embryonic lethality before turning of embryo	3,86E-03	N
disorganized photoreceptor outer segment	4,24E-03	N
abnormal sensory capabilities/reflexes/nociception	5,33E-03	N
abnormal hair cycle	5,59E-03	N
abnormal triglyceride level	5,84E-03	N
abnormal circulating lipid level	7,36E-03	N
abnormal lateral ventricle morphology	7,92E-03	N
abnormal PNS synaptic transmission	8,48E-03	N
impaired skin barrier function	9,23E-03	N
abnormal blood coagulation	9,73E-03	N
abnormal sperm physiology	1,01E-02	N
abnormal metatarsal bone morphology	1,05E-02	N
fusion of atlas and odontoid process	1,08E-02	N
small prostate gland	1,09E-02	N
abnormal cholesterol homeostasis	1,12E-02	N
abnormal thymus corticomedullary boundary morphology	1,13E-02	N

TANK

Term	P-value	Annotated
abnormal cytokine secretion	5,91E-13	N
abnormal Peyer's patch germinal center morphology	7,48E-12	N
abnormal Peyer's patch morphology	7,48E-11	N
skin inflammation	8,06E-11	N
increased IgM level	1,02E-10	Y
increased interleukin-2 secretion	1,25E-10	N
decreased IgG2a level	4,79E-10	N
increased T cell proliferation	5,11E-10	N
abnormal macrophage physiology	8,99E-10	Y
abnormal dendritic cell physiology	1,12E-09	Y
autoimmune response	1,13E-09	N
abnormal immune system morphology	1,66E-09	N
abnormal CD8-positive T cell physiology	9,70E-09	N
abnormal cytotoxic T cell physiology	1,15E-08	N
decreased susceptibility to endotoxin shock	1,38E-08	N
increased IgA level	1,40E-08	Y
absent spleen germinal center	1,70E-08	N
decreased IgE level	1,70E-08	N
abnormal mesenteric lymph node morphology	1,98E-08	N
increased IgG2a level	2,69E-08	Y

PSMD14		
Term	P-value	Annotated
complete embryonic lethality before implantation	7,61E-11	N
abnormal blastocyst morphology	7,32E-09	N
complete embryonic lethality before somite formation	1,61E-08	N
abnormal inner cell mass proliferation	3,99E-07	N
inner cell mass degeneration	1,42E-06	N
embryonic growth arrest	6,32E-06	N
absent chorion	4,32E-05	N
complete embryonic lethality before turning of embryo	4,82E-05	N
mammary adenocarcinoma	1,83E-04	N
thin retinal inner nuclear layer	2,46E-04	N
atrial septal defect	2,50E-04	N
abnormal embryonic-extraembryonic boundary morphology	3,44E-04	N
proportional dwarf	4,42E-04	N
failure of embryo implantation	4,65E-04	N
absent T cells	4,81E-04	N
paralysis	5,40E-04	N
decreased response of heart to induced stress	5,41E-04	N
increased infarction size	5,54E-04	N
short stride length	6,16E-04	N
absent amnion	6,21E-04	N

TBR1		
Term	P-value	Annotated
abnormal inhibitory postsynaptic currents	2,74E-22	N
reduced long term depression	3,24E-22	N
abnormal spatial learning	1,86E-20	N
abnormal brain wave pattern	1,07E-19	N
absent corpus callosum	4,73E-18	N
sporadic seizures	4,74E-16	N
increased startle reflex	4,78E-16	N
abnormal cerebral cortex morphology	7,08E-16	N
abnormal neocortex morphology	4,66E-15	N
abnormal long term depression	7,92E-15	N
hyperactivity	1,80E-14	N
abnormal CNS synaptic transmission	4,33E-14	N
increased anxiety-related response	4,38E-13	N
abnormal GABA-mediated receptor currents	5,06E-13	N
increased susceptibility to pharmacologically induced seizures	5,39E-13	N
abnormal synaptic vesicle number	5,89E-13	N
abnormal excitatory postsynaptic currents	2,19E-12	N
abnormal thalamus morphology	3,19E-12	N

abnormal telencephalon development	1,18E-11	N
abnormal excitatory postsynaptic potential	1,65E-11	N

POU3F2

Tissue	# samples	AUC	P-value
Neural Stem Cells	11	0,98	4 x 10-8
Spinal Cord	19	0,97	9 x 10-13
Substantia Nigra	22	0,97	2 x 10-14
Visual Cortex	34	0,97	5 x 10-21
Prefrontal Cortex	46	0,97	6 x 10-28
Occipital Lobe	42	0,97	1 x 10-25
Retinal Pigment Epithelium	12	0,97	2 x 10-8
Motor Neurons	12	0,97	2 x 10-8
Mesencephalon	41	0,96	8 x 10-25
Parietal Lobe	17	0,96	4 x 10-11
Frontal Lobe	62	0,96	4 x 10-36
Cerebral Cortex	276	0,96	5 x 10-151
Putamen	16	0,95	3 x 10-10
HEK293 Cells	100	0,95	3 x 10-55
Cell Line, Transformed	102	0,95	6 x 10-56
Cerebrum	344	0,95	2 x 10-180
Temporal Lobe	91	0,95	2 x 10-49
Entorhinal Cortex	83	0,95	4 x 10-45
Subthalamic Nucleus	12	0,95	9 x 10-8
Hippocampus	55	0,94	4 x 10-30

JMJD1C

Tissue	# samples	AUC	P-value
Neutrophils	216	0,92	3 x 10-101
Cerebellum	36	0,91	4 x 10-17
Sputum	151	0,9	1 x 10-65
Organelles	12	0,87	8 x 10-6
Induced Pluripotent Stem Cells	35	0,8	6 x 10-10
Precursor Cells, B-Lymphoid	14	0,79	2 x 10-4
Pluripotent Stem Cells	47	0,76	5 x 10-10
Hand	11	0,73	7 x 10-3
Aortic Valve	10	0,73	1 x 10-2
T-Lymphocytes, Regulatory	33	0,73	7 x 10-6
Knee	26	0,71	2 x 10-4
Prefrontal Cortex	46	0,66	2 x 10-4
Caco-2 Cells	44	0,65	5 x 10-4

REEP3

Tissue	# samples	AUC	P-value
Osteoblasts	26	0,96	3 x 10-16
Retinal Pigment Epithelium	12	0,96	4 x 10-8
Myocytes, Smooth Muscle	141	0,94	9 x 10-72

Muscle Cells	146	0,92	3 x 10-69
Conjunctiva	59	0,92	5 x 10-29
Caco-2 Cells	44	0,92	9 x 10-22
Keloid	10	0,92	5 x 10-6
Cicatrix	19	0,9	1 x 10-9
Macrophages, Alveolar	117	0,89	4 x 10-47
Chondrocytes	19	0,88	7 x 10-9
Ileum	59	0,88	6 x 10-24
Fibroblasts	392	0,88	5 x 10-146
Chorion	15	0,87	5 x 10-7
Keratinocytes	48	0,86	3 x 10-18
Mesenchymal Stem Cells	145	0,86	5 x 10-50
Foreskin	69	0,85	3 x 10-24
Neural Stem Cells	11	0,84	7 x 10-5
Adipocytes	81	0,83	7 x 10-25
Islets of Langerhans	60	0,83	2 x 10-18
Trophoblasts	11	0,83	2 x 10-4

LRRC14

Tissue	# samples	AUC	P-value
Jurkat Cells	21	0,84	6 x 10-8
Palatine Tonsil	72	0,83	9 x 10-22
Hela Cells	201	0,81	6 x 10-52
HEK293 Cells	100	0,79	2 x 10-24
Cell Line, Transformed	102	0,79	1 x 10-24
K562 Cells	37	0,78	3 x 10-9
Synovial Fluid	12	0,78	9 x 10-4
T-Lymphocytes, Regulatory	33	0,75	5 x 10-7
HL-60 Cells	12	0,73	6 x 10-3
Parotid Gland	19	0,73	6 x 10-4
Mammary Glands, Human	12	0,73	7 x 10-3
T-Lymphocytes	517	0,72	3 x 10-65
HCT116 Cells	96	0,72	2 x 10-13
Lymphocytes	1737	0,69	2 x 10-164
Granulocyte Precursor Cells	30	0,69	4 x 10-4
Killer Cells, Natural	84	0,68	5 x 10-9
B-Lymphocytes	851	0,68	10 x 10-70
Plasma	622	0,66	5 x 10-45
Plasma Cells	619	0,66	6 x 10-44
Salivary Glands	24	0,66	8 x 10-3

ARHGAP39

Tissue	# samples	AUC	P-value
Trachea	63	0,92	4 x 10-31

Nasal Mucosa	93	0,89	1 x 10-39
Hippocampus	55	0,88	5 x 10-22
Visual Cortex	34	0,87	7 x 10-14
Neural Stem Cells	11	0,87	3 x 10-5
Occipital Lobe	42	0,86	5 x 10-16
Parietal Lobe	17	0,86	3 x 10-7
Hypothalamus	15	0,85	4 x 10-6
Ganglia	11	0,83	2 x 10-4
Testis	37	0,82	10 x 10-12
Cerebral Cortex	276	0,82	2 x 10-75
Entorhinal Cortex	83	0,82	6 x 10-24
Cerebrum	344	0,82	1 x 10-91
Fallopian Tubes	273	0,82	2 x 10-72
Mammary Glands, Human	12	0,81	2 x 10-4
Temporal Lobe	91	0,81	1 x 10-24
Epithelium	183	0,8	9 x 10-45
HCT116 Cells	96	0,78	2 x 10-21
Brain	1274	0,78	1 x 10-252
Central Nervous System	1302	0,78	2 x 10-251

FOXH1

Tissue	# samples	AUC	P-value
Induced Pluripotent Stem Cells	35	0,99	1 x 10-23
Pluripotent Stem Cells	47	0,94	8 x 10-26
Embryonic Stem Cells	83	0,9	2 x 10-36
Putamen	16	0,9	3 x 10-8
Substantia Nigra	22	0,86	4 x 10-9
Subthalamic Nucleus	12	0,84	5 x 10-5
Thalamus	16	0,82	8 x 10-6
Muscle, Striated	162	0,81	1 x 10-41
Muscle, Skeletal	162	0,81	1 x 10-41
Blastocyst	14	0,8	9 x 10-5
Mesencephalon	41	0,8	4 x 10-11
Embryoid Bodies	11	0,79	1 x 10-3
Quadriceps Muscle	82	0,78	6 x 10-19
Parietal Lobe	17	0,77	9 x 10-5
Blood Platelets	30	0,76	5 x 10-7
Trophoblasts	11	0,75	4 x 10-3
Occipital Lobe	42	0,75	4 x 10-8
Visual Cortex	34	0,74	9 x 10-7
Muscles	723	0,74	1 x 10-111
Hypothalamus	15	0,74	2 x 10-3

KIFC2

Tissue	# samples	AUC	P-value
Putamen	16	0,99	9 x 10-12
Cerebellum	36	0,98	1 x 10-23
Frontal Lobe	62	0,98	3 x 10-39
Parietal Lobe	17	0,98	9 x 10-12
Prefrontal Cortex	46	0,98	4 x 10-29
Cerebral Cortex	276	0,97	6 x 10-162
Entorhinal Cortex	83	0,97	7 x 10-50
Temporal Lobe	91	0,97	3 x 10-54
Occipital Lobe	42	0,97	9 x 10-26
Visual Cortex	34	0,97	6 x 10-21
Hippocampus	55	0,96	6 x 10-32
Cerebrum	344	0,93	4 x 10-168
Hypothalamus	15	0,92	2 x 10-8
Thalamus	16	0,88	1 x 10-7
Brain	1274	0,82	< 10-300
Neural Stem Cells	11	0,81	3 x 10-4
Mouth Mucosa	94	0,81	1 x 10-25
Central Nervous System	1302	0,81	10 x 10-320
Nervous System	1358	0,81	7 x 10-323
Substantia Nigra	22	0,8	7 x 10-7

CYHR1

Tissue	# samples	AUC	P-value
Plasma Cells	619	0,91	9 x 10-274
Plasma	622	0,91	1 x 10-273
Neutrophils	216	0,83	5 x 10-63
Hypothalamus	15	0,82	1 x 10-5
B-Lymphocytes	851	0,78	1 x 10-176
Intestinal Mucosa	40	0,78	7 x 10-10
Putamen	16	0,78	1 x 10-4
Mammary Glands, Human	12	0,78	8 x 10-4
Salivary Glands	24	0,77	7 x 10-6
Parietal Lobe	17	0,74	7 x 10-4
Parotid Gland	19	0,73	4 x 10-4
Occipital Lobe	42	0,71	2 x 10-6
Visual Cortex	34	0,71	2 x 10-5
Cerebellum	36	0,7	3 x 10-5
Thalamus	16	0,7	7 x 10-3
Astrocytes	12	0,69	2 x 10-2
Adrenal Glands	129	0,68	4 x 10-12
Hippocampus	55	0,67	8 x 10-6
Osteoblasts	26	0,66	4 x 10-3
Adrenal Cortex	99	0,66	2 x 10-8

VPS28

Tissue	# samples	AUC	P-value
Synovial Fluid	12	0,8	3 x 10-4
Ileum	59	0,73	6 x 10-10
Intestine, Small	112	0,73	1 x 10-16
Neural Stem Cells	11	0,72	1 x 10-2
Mammary Glands, Human	12	0,72	9 x 10-3
Omentum	76	0,72	6 x 10-11
Peritoneum	89	0,71	6 x 10-12
Abdomen	103	0,71	2 x 10-13
Retina	27	0,71	2 x 10-4
Fallopian Tubes	273	0,69	2 x 10-28
Stomach	55	0,69	9 x 10-7
Thyroid Gland	85	0,68	1 x 10-8
Eye	157	0,67	6 x 10-14
Synovial Membrane	26	0,66	6 x 10-3
Joints	26	0,66	6 x 10-3
Ovary	699	0,65	1 x 10-44
Vulva	34	0,65	3 x 10-3
Prostate	352	0,64	2 x 10-20
Cecum	15	0,64	6 x 10-2
Endometrium	264	0,63	6 x 10-14

SCRT1

Tissue	# samples	AUC	P-value
Retinal Pigment Epithelium	1,20E+01	0,8	3 x 10-4
Chorion	1,50E+01	0,78	1 x 10-4
Sputum	1,51E+02	0,73	2 x 10-23
Chondrocytes	1,90E+01	0,72	1 x 10-3
K562 Cells	3,70E+01	0,69	7 x 10-5
Myocytes, Smooth Muscle	1,41E+02	0,68	3 x 10-13
HT29 Cells	1,70E+01	0,67	1 x 10-2
Mesenchymal Stem Cells	1,45E+02	0,67	2 x 10-12
Ileum	5,90E+01	0,66	1 x 10-5
Muscle Cells	1,46E+02	0,66	1 x 10-11
Intestinal Mucosa	4,00E+01	0,66	6 x 10-4
Clone Cells	1,15E+02	0,65	4 x 10-8
Plasma	6,22E+02	0,64	5 x 10-35
Caco-2 Cells	4,40E+01	0,64	10 x 10-4
Plasma Cells	6,19E+02	0,64	3 x 10-34
Jurkat Cells	2,10E+01	0,63	4 x 10-2
Fetal Blood	1,51E+02	0,63	2 x 10-8
Hep G2 Cells	1,02E+02	0,63	7 x 10-6

Retina	2,70E+01	0,63	2 x 10-2
Mouth Mucosa	9,40E+01	0,62	3 x 10-5

ATXN2L

Tissue	# samples	AUC	P-value
Organelles	12	0,86	1 x 10-5
Fetal Blood	151	0,76	5 x 10-28
Hep G2 Cells	102	0,75	9 x 10-18
Parotid Gland	19	0,74	4 x 10-4
Salivary Glands	24	0,73	1 x 10-4
Blood Platelets	30	0,73	2 x 10-5
Jurkat Cells	21	0,71	8 x 10-4
Precursor Cells, B-Lymphoid	14	0,71	6 x 10-3
Killer Cells, Natural	84	0,7	1 x 10-10
Cartilage	13	0,7	1 x 10-2
Retinal Pigment Epithelium	12	0,68	3 x 10-2
Putamen	16	0,68	1 x 10-2
Granulocyte Precursor Cells	30	0,67	1 x 10-3
T-Lymphocytes, Regulatory	33	0,67	9 x 10-4
Adrenal Cortex	99	0,65	2 x 10-7
Clone Cells	115	0,65	4 x 10-8
Trophoblasts	11	0,64	1 x 10-1
Bone Marrow Cells	809	0,63	4 x 10-39
Adrenal Glands	129	0,63	3 x 10-7
Neutrophils	216	0,63	5 x 10-11

TUFM

Tissue	# samples	AUC	P-value
HL-60 Cells	12	0,95	8 x 10-8
HCT116 Cells	96	0,92	1 x 10-46
K562 Cells	37	0,89	2 x 10-16
Neural Stem Cells	11	0,88	1 x 10-5
HEK293 Cells	100	0,87	4 x 10-38
Cell Line, Transformed	102	0,87	7 x 10-39
Hep G2 Cells	102	0,85	5 x 10-35
Hela Cells	201	0,82	3 x 10-54
Jurkat Cells	21	0,81	1 x 10-6
Cell Line, Tumor	674	0,79	4 x 10-151
Tongue	105	0,79	9 x 10-25
Palatine Tonsil	72	0,79	3 x 10-17
Hepatocytes	188	0,77	4 x 10-37
Glucagon-Secreting Cells	39	0,76	3 x 10-8
Clone Cells	115	0,74	1 x 10-19
Induced Pluripotent Stem Cells	35	0,74	1 x 10-6

Pluripotent Stem Cells	47	0,73	4 x 10-8
Granulocyte Precursor Cells	30	0,71	5 x 10-5
Astrocytes	12	0,71	1 x 10-2
Plasma Cells	619	0,71	4 x 10-73

SH2B1

Tissue	# samples	AUC	P-value
Hypothalamus	15	0,99	6 x 10-11
Thalamus	16	0,98	5 x 10-11
Putamen	16	0,96	3 x 10-10
Subthalamic Nucleus	12	0,95	5 x 10-8
Substantia Nigra	22	0,94	1 x 10-12
Ganglia	11	0,92	1 x 10-6
Mesencephalon	41	0,9	1 x 10-18
Salivary Glands	24	0,88	2 x 10-10
Organelles	12	0,86	1 x 10-5
Parotid Gland	19	0,85	2 x 10-7
Hippocampus	55	0,84	2 x 10-18
Parietal Lobe	17	0,8	2 x 10-5
Temporal Lobe	91	0,8	7 x 10-23
Cerebral Cortex	276	0,78	9 x 10-60
Entorhinal Cortex	83	0,78	4 x 10-19
Myometrium	105	0,77	5 x 10-22
Nasal Mucosa	93	0,75	3 x 10-17
Cerebellum	36	0,75	2 x 10-7
Neural Stem Cells	11	0,74	5 x 10-3
Muscles	723	0,74	8 x 10-111

NFATC2IP

Tissue	# samples	AUC	P-value
T-Lymphocytes, Regulatory	33	0,91	5 x 10-16
Precursor Cells, B-Lymphoid	14	0,9	2 x 10-7
Cerebellum	36	0,86	7 x 10-14
Blood Platelets	30	0,84	6 x 10-11
T-Lymphocytes	517	0,82	4 x 10-140
Synovial Fluid	12	0,82	2 x 10-4
Palatine Tonsil	72	0,81	1 x 10-19
Granulocyte Precursor Cells	30	0,8	8 x 10-9
Glucagon-Secreting Cells	39	0,78	2 x 10-9
HL-60 Cells	12	0,75	2 x 10-3
Killer Cells, Natural	84	0,73	9 x 10-14
Lymphoid Tissue	818	0,72	2 x 10-101
Hematopoietic Stem Cells	106	0,71	6 x 10-14
Lymph Nodes	671	0,7	1 x 10-69

Lymph	683	0,69	8 x 10-68
Spleen	23	0,68	2 x 10-3
HEK293 Cells	100	0,68	3 x 10-10
Cell Line, Transformed	102	0,67	1 x 10-9
Induced Pluripotent Stem Cells	35	0,66	8 x 10-4
Mammary Glands, Human	12	0,66	5 x 10-2

SPNS1

Tissue	# samples	AUC	P-value
Macrophages, Alveolar	117	0,95	4 x 10-63
Macrophages	342	0,94	2 x 10-175
Hep G2 Cells	102	0,88	6 x 10-40
Neural Stem Cells	11	0,87	2 x 10-5
Chorion	15	0,84	7 x 10-6
U937 Cells	57	0,83	7 x 10-18
Synovial Fluid	12	0,82	1 x 10-4
Monocytes	506	0,81	2 x 10-128
Umbilical Veins	113	0,8	6 x 10-28
Retinal Pigment Epithelium	12	0,8	4 x 10-4
Endothelial Cells	196	0,79	2 x 10-45
Clone Cells	115	0,79	4 x 10-27
Veins	133	0,79	6 x 10-31
Hepatocytes	188	0,78	9 x 10-40
Hela Cells	201	0,76	5 x 10-37
Caco-2 Cells	44	0,76	3 x 10-9
Myocytes, Smooth Muscle	141	0,76	9 x 10-26
Mesenchymal Stem Cells	145	0,75	2 x 10-25
HL-60 Cells	12	0,74	4 x 10-3
Blood Vessels	171	0,74	2 x 10-27

LAT

Tissue	# samples	AUC	P-value
Blood Platelets	30	0,98	2 x 10-19
Jurkat Cells	21	0,96	3 x 10-13
T-Lymphocytes, Regulatory	33	0,96	5 x 10-20
T-Lymphocytes	517	0,96	3 x 10-282
Synovial Fluid	12	0,95	5 x 10-8
Palatine Tonsil	72	0,86	7 x 10-26
U937 Cells	57	0,86	2 x 10-20
Killer Cells, Natural	84	0,84	9 x 10-27
Macrophages	342	0,82	1 x 10-89
Spleen	23	0,8	7 x 10-7
Lymphoid Tissue	818	0,79	2 x 10-183
Lymph	683	0,79	4 x 10-146

Lymph Nodes	671	0,78	2 x 10-138
Sputum	151	0,76	5 x 10-29
Macrophages, Alveolar	117	0,75	2 x 10-20
Lymphocytes	1737	0,73	8 x 10-239
Monocytes	506	0,73	6 x 10-73
Synovial Membrane	26	0,73	6 x 10-5
Joints	26	0,73	6 x 10-5
Myeloid Cells	997	0,73	8 x 10-131

SULT1A1
SULT1A2

Tissue	# samples	AUC	P-value
Intestinal Mucosa	40	0,97	9 x 10-25
Hep G2 Cells	102	0,97	6 x 10-60
Ileum	59	0,94	3 x 10-32
Hepatocytes	188	0,91	2 x 10-84
Abdominal Fat	69	0,87	1 x 10-26
Subcutaneous Fat, Abdominal	69	0,87	1 x 10-26
Liver	569	0,85	3 x 10-185
Neutrophils	216	0,84	5 x 10-68
Subcutaneous Fat	120	0,84	5 x 10-38
Hypothalamus	15	0,83	9 x 10-6
Adipose Tissue	165	0,83	8 x 10-49
Putamen	16	0,82	8 x 10-6
Substantia Nigra	22	0,76	3 x 10-5
Colon, Sigmoid	27	0,76	4 x 10-6
Trachea	63	0,75	3 x 10-12
Ganglia	11	0,75	4 x 10-3
U937 Cells	57	0,75	1 x 10-10
Thalamus	16	0,74	8 x 10-4
Mammary Glands, Human	12	0,73	7 x 10-3
Caco-2 Cells	44	0,73	2 x 10-7

CCDC101

Tissue	# samples	AUC	P-value
Quadriceps Muscle	82	0,87	4 x 10-31
U937 Cells	57	0,86	3 x 10-21
Muscle, Skeletal	162	0,82	2 x 10-45
Muscle, Striated	162	0,82	2 x 10-45
Palatine Tonsil	72	0,8	5 x 10-19
Synovial Fluid	12	0,79	4 x 10-4
Hematopoietic Stem Cells	106	0,78	4 x 10-23
T-Lymphocytes, Regulatory	33	0,75	4 x 10-7
Myometrium	105	0,75	3 x 10-19

Plasma Cells	619	0,73	3 x 10-88
Plasma	622	0,73	1 x 10-88
Muscles	723	0,73	2 x 10-101
B-Lymphocytes	851	0,71	1 x 10-95
T-Lymphocytes	517	0,7	3 x 10-55
Granulocyte Precursor Cells	30	0,7	2 x 10-4
Intestinal Mucosa	40	0,69	2 x 10-5
Synovial Membrane	26	0,69	10 x 10-4
Joints	26	0,69	10 x 10-4
Mammary Glands, Human	12	0,69	3 x 10-2
Jurkat Cells	21	0,69	3 x 10-3

NRXN1

Tissue	# samples	AUC	P-value
Prefrontal Cortex	46	1	2 x 10-31
Frontal Lobe	62	0,99	2 x 10-41
Cerebellum	36	0,99	2 x 10-24
Cerebral Cortex	276	0,99	5 x 10-174
Temporal Lobe	91	0,99	5 x 10-58
Entorhinal Cortex	83	0,99	5 x 10-53
Occipital Lobe	42	0,99	1 x 10-27
Hippocampus	55	0,99	1 x 10-35
Visual Cortex	34	0,98	1 x 10-22
Parietal Lobe	17	0,98	5 x 10-12
Ganglia	11	0,98	4 x 10-8
Thalamus	16	0,97	6 x 10-11
Cerebrum	344	0,97	4 x 10-195
Mesencephalon	41	0,97	6 x 10-25
Putamen	16	0,96	1 x 10-10
Substantia Nigra	22	0,96	6 x 10-14
Hypothalamus	15	0,96	6 x 10-10
Motor Neurons	12	0,95	5 x 10-8
Subthalamic Nucleus	12	0,95	8 x 10-8
Atrial Appendage	10	0,94	1 x 10-6

NUPR1

Tissue	# samples	AUC	P-value
Keloid	10	0,95	8 x 10-7
Cicatrix	19	0,95	1 x 10-11
Cartilage	13	0,93	1 x 10-7
Abdominal Fat	69	0,91	1 x 10-32
Subcutaneous Fat, Abdominal	69	0,91	1 x 10-32
Adipocytes	81	0,9	2 x 10-36
Subcutaneous Fat	120	0,9	1 x 10-50

Salivary Glands	24	0,88	7 x 10-11
Intestinal Mucosa	40	0,88	4 x 10-17
Prostate	352	0,88	4 x 10-136
Adipose Tissue	165	0,88	2 x 10-64
Mammary Glands, Human	12	0,88	6 x 10-6
Parotid Gland	19	0,87	3 x 10-8
Telomere	30	0,86	6 x 10-12
Myometrium	105	0,86	9 x 10-38
Fibroblasts	392	0,86	1 x 10-132
Mesenchymal Stem Cells	145	0,86	2 x 10-50
Knee	26	0,86	3 x 10-10
Chondrocytes	19	0,85	9 x 10-8
Sputum	151	0,84	4 x 10-48

NPAS2

Tissue	# samples	AUC	P-value
Prefrontal Cortex	46	0,93	3 x 10-24
Cartilage	13	0,92	2 x 10-7
Umbilical Veins	113	0,92	1 x 10-52
Hepatocytes	188	0,91	2 x 10-85
Frontal Lobe	62	0,91	1 x 10-28
Veins	133	0,91	1 x 10-58
Putamen	16	0,9	3 x 10-8
Hep G2 Cells	102	0,9	3 x 10-44
Muscle Cells	146	0,9	9 x 10-62
Myocytes, Smooth Muscle	141	0,9	1 x 10-59
Heart Ventricles	124	0,89	3 x 10-51
Umbilical Cord	180	0,89	1 x 10-71
Retinal Pigment Epithelium	12	0,88	4 x 10-6
Mouth Mucosa	94	0,88	2 x 10-36
Blood Vessels	171	0,86	4 x 10-59
Heart	217	0,86	1 x 10-73
Endothelial Cells	196	0,86	2 x 10-66
Entorhinal Cortex	83	0,85	5 x 10-28
Hippocampus	55	0,85	6 x 10-19
Cerebral Cortex	276	0,84	3 x 10-86

KCNMA1

Tissue	# samples	AUC	P-value
Myometrium	105	0,98	2 x 10-64
Osteoblasts	26	0,97	8 x 10-17
Retinal Pigment Epithelium	12	0,96	3 x 10-8
Cartilage	13	0,96	1 x 10-8
Visual Cortex	34	0,95	7 x 10-20

Occipital Lobe	42	0,94	4 x 10-23
Prefrontal Cortex	46	0,93	2 x 10-24
Entorhinal Cortex	83	0,93	7 x 10-42
Aortic Valve	10	0,93	2 x 10-6
Mesenchymal Stem Cells	145	0,93	2 x 10-70
Temporal Lobe	91	0,92	4 x 10-44
Muscle, Smooth	248	0,92	1 x 10-115
Cerebral Cortex	276	0,92	2 x 10-125
Keloid	10	0,91	6 x 10-6
Frontal Lobe	62	0,91	10 x 10-29
Hippocampus	55	0,9	6 x 10-25
Sputum	151	0,9	3 x 10-65
Chondrocytes	19	0,9	2 x 10-9
Cicatrix	19	0,88	7 x 10-9
Prostate	352	0,88	1 x 10-134

DEC1

Tissue	# samples	AUC	P-value
Nasopharynx	30	0,87	4 x 10-12
Heart Ventricles	124	0,78	5 x 10-28
Substantia Nigra	22	0,78	6 x 10-6
HCT116 Cells	96	0,77	1 x 10-20
Thalamus	16	0,75	5 x 10-4
Organelles	12	0,75	3 x 10-3
Mesencephalon	41	0,74	7 x 10-8
Embryoid Bodies	11	0,74	6 x 10-3
Myocytes, Smooth Muscle	141	0,73	1 x 10-21
Hypothalamus	15	0,73	2 x 10-3
Hep G2 Cells	102	0,73	1 x 10-15
Muscle Cells	146	0,71	4 x 10-19
Quadriceps Muscle	82	0,71	4 x 10-11
Neutrophils	216	0,71	3 x 10-26
Neck	138	0,7	2 x 10-16
Blastocyst	14	0,7	9 x 10-3
Heart	217	0,69	2 x 10-21
Umbilical Cord	180	0,68	1 x 10-17
Subthalamic Nucleus	12	0,68	3 x 10-2
Heart Atria	13	0,68	2 x 10-2

SDCCAG8

Tissue	# samples	AUC	P-value
Sputum	151	0,96	4 x 10-85
Aortic Valve	10	0,89	2 x 10-5
Macrophages, Alveolar	117	0,87	2 x 10-43

Foot	34	0,81	4 x 10-10
Hand	11	0,81	4 x 10-4
Macrophages	342	0,8	5 x 10-82
Chorion	15	0,78	2 x 10-4
K562 Cells	37	0,78	6 x 10-9
Knee	26	0,75	9 x 10-6
Dendritic Cells	277	0,74	5 x 10-42
Tongue	105	0,73	3 x 10-16
HEK293 Cells	100	0,72	2 x 10-14
Synovial Fluid	12	0,72	9 x 10-3
Cell Line, Transformed	102	0,72	6 x 10-14
Retinal Pigment Epithelium	12	0,69	2 x 10-2
Testis	37	0,68	1 x 10-4
Clone Cells	115	0,68	1 x 10-11
U937 Cells	57	0,67	8 x 10-6
HCT116 Cells	96	0,67	9 x 10-9
Endothelial Cells	196	0,66	5 x 10-15

AKT3

Tissue	# samples	AUC	P-value
Prefrontal Cortex	46	0,98	6 x 10-30
Retinal Pigment Epithelium	12	0,97	2 x 10-8
Frontal Lobe	62	0,95	3 x 10-35
Retina	27	0,95	1 x 10-15
Visual Cortex	34	0,94	3 x 10-19
Occipital Lobe	42	0,94	5 x 10-23
Cerebral Cortex	276	0,94	3 x 10-140
Entorhinal Cortex	83	0,94	2 x 10-43
Temporal Lobe	91	0,94	5 x 10-47
Cerebellum	36	0,93	3 x 10-19
Hippocampus	55	0,93	7 x 10-28
Cerebrum	344	0,92	3 x 10-160
Osteoblasts	26	0,92	2 x 10-13
Parietal Lobe	17	0,91	5 x 10-9
Veins	133	0,91	5 x 10-60
Umbilical Veins	113	0,91	3 x 10-51
Aortic Valve	10	0,9	1 x 10-5
Blood Vessels	171	0,9	4 x 10-73
HEK293 Cells	100	0,9	3 x 10-43
Cicatrix	19	0,9	2 x 10-9

CRYZL1

Tissue	# samples	AUC	P-value
Prefrontal Cortex	46	0,95	6 x 10-26

Subcutaneous Fat	120	0,91	3 x 10-54
Abdominal Fat	69	0,9	3 x 10-30
Subcutaneous Fat, Abdominal	69	0,9	3 x 10-30
Chorion	15	0,87	8 x 10-7
Frontal Lobe	62	0,86	1 x 10-22
Cerebellum	36	0,86	9 x 10-14
K562 Cells	37	0,85	2 x 10-13
Adipose Tissue	165	0,84	1 x 10-52
Hand	11	0,81	4 x 10-4
Jurkat Cells	21	0,8	2 x 10-6
Knee	26	0,79	2 x 10-7
Trachea	63	0,77	1 x 10-13
Retina	27	0,76	3 x 10-6
Foot	34	0,74	8 x 10-7
Mammary Glands, Human	12	0,73	5 x 10-3
Substantia Nigra	22	0,73	2 x 10-4
Myometrium	105	0,72	2 x 10-15
Chondrocytes	19	0,72	10 x 10-4
HEK293 Cells	100	0,71	2 x 10-13

ITSN1

Tissue	# samples	AUC	P-value
Abdominal Fat	69	0,99	2 x 10-44
Subcutaneous Fat, Abdominal	69	0,99	2 x 10-44
Subcutaneous Fat	120	0,98	4 x 10-75
Visual Cortex	34	0,98	4 x 10-22
Adipose Tissue	165	0,98	4 x 10-100
Motor Neurons	12	0,98	1 x 10-8
Occipital Lobe	42	0,97	4 x 10-26
Prefrontal Cortex	46	0,97	8 x 10-28
Aortic Valve	10	0,96	4 x 10-7
Frontal Lobe	62	0,96	1 x 10-35
Entorhinal Cortex	83	0,96	4 x 10-47
Cerebral Cortex	276	0,96	1 x 10-150
Temporal Lobe	91	0,95	7 x 10-51
Hippocampus	55	0,95	7 x 10-31
Spinal Cord	19	0,94	2 x 10-11
Cerebrum	344	0,94	5 x 10-175
Cicatrix	19	0,94	3 x 10-11
Parietal Lobe	17	0,94	4 x 10-10
Keloid	10	0,93	3 x 10-6
Cerebellum	36	0,92	1 x 10-18

SON

Tissue	# samples	AUC	P-value
Precursor Cells, B-Lymphoid	14	0,9	2 x 10-7
T-Lymphocytes, Regulatory	33	0,88	3 x 10-14
Synovial Membrane	26	0,78	8 x 10-7
Joints	26	0,78	8 x 10-7
Aortic Valve	10	0,77	3 x 10-3
Synovial Fluid	12	0,77	1 x 10-3
Killer Cells, Natural	84	0,76	2 x 10-16
Neutrophils	216	0,76	2 x 10-39
T-Lymphocytes	517	0,75	6 x 10-82
Nasal Mucosa	93	0,73	4 x 10-14
Sputum	151	0,73	9 x 10-22

GART

Tissue	# samples	AUC	P-value
K562 Cells	37	0,99	3 x 10-25
Jurkat Cells	21	0,93	1 x 10-11
Cell Line, Transformed	102	0,9	2 x 10-45
HEK293 Cells	100	0,9	4 x 10-44
HCT116 Cells	96	0,87	2 x 10-36
Induced Pluripotent Stem Cells	35	0,86	9 x 10-14
Glucagon-Secreting Cells	39	0,86	6 x 10-15
HL-60 Cells	12	0,85	3 x 10-5
Pluripotent Stem Cells	47	0,83	6 x 10-15
Hela Cells	201	0,81	1 x 10-52
U937 Cells	57	0,81	4 x 10-16
Clone Cells	115	0,79	2 x 10-27
Cell Line, Tumor	674	0,77	2 x 10-130
Mammary Glands, Human	12	0,77	1 x 10-3
Embryonic Stem Cells	83	0,74	1 x 10-14
Islets of Langerhans	60	0,73	3 x 10-10
Femur	15	0,73	2 x 10-3
Fallopian Tubes	273	0,73	9 x 10-39
Hematopoietic Stem Cells	106	0,69	2 x 10-11
Neural Stem Cells	11	0,69	3 x 10-2

DNAJC28

Tissue	# samples	AUC	P-value
Atrial Appendage	10	0,95	7 x 10-7
Induced Pluripotent Stem Cells	35	0,92	1 x 10-17
Conjunctiva	59	0,89	3 x 10-25
Pluripotent Stem Cells	47	0,86	3 x 10-17
Heart Atria	13	0,84	2 x 10-5
Sputum	151	0,82	6 x 10-43

Mammary Glands, Human	12	0,81	2 x 10-4
Testis	37	0,8	2 x 10-10
Retinal Pigment Epithelium	12	0,79	6 x 10-4
Heart Ventricles	124	0,78	5 x 10-27
Adipocytes	81	0,77	6 x 10-17
Heart	217	0,77	2 x 10-42
Cumulus Cells	38	0,77	1 x 10-8
Jurkat Cells	21	0,77	3 x 10-5
Embryonic Stem Cells	83	0,76	2 x 10-16
Muscle, Skeletal	162	0,76	2 x 10-29
Muscle, Striated	162	0,76	2 x 10-29
HEK293 Cells	100	0,75	3 x 10-18
Cell Line, Transformed	102	0,75	1 x 10-17
Mouth Mucosa	94	0,74	1 x 10-15

TMEM50B

Tissue	# samples	AUC	P-value
Trachea	63	0,95	4 x 10-35
Thyroid Gland	85	0,89	9 x 10-36
Nasal Mucosa	93	0,89	4 x 10-38
Motor Neurons	12	0,89	4 x 10-6
Plasma	622	0,88	1 x 10-228
Plasma Cells	619	0,88	4 x 10-227
Thalamus	16	0,87	3 x 10-7
Cerebellum	36	0,87	2 x 10-14
Neural Stem Cells	11	0,84	8 x 10-5
Synovial Fluid	12	0,81	2 x 10-4
Ganglia	11	0,81	4 x 10-4
Heart Ventricles	124	0,8	4 x 10-30
Prostate	352	0,79	2 x 10-80
Spinal Cord	19	0,78	2 x 10-5
Mammary Glands, Human	12	0,78	8 x 10-4
Ileum	59	0,78	1 x 10-13
Subcutaneous Fat	120	0,77	2 x 10-24
Heart	217	0,77	2 x 10-41
Adipose Tissue	165	0,76	2 x 10-31
Neurons	37	0,76	7 x 10-8

IFNGR2

Tissue	# samples	AUC	P-value
Neutrophils	216	0,97	6 x 10-124
Sputum	151	0,94	7 x 10-79
Monocytes	506	0,91	9 x 10-222
Myeloid Cells	997	0,89	< 10-300

Bone Marrow Cells	809	0,89	9 x 10-315
Trophoblasts	11	0,86	4 x 10-5
Cartilage	13	0,84	3 x 10-5
Dendritic Cells	277	0,84	4 x 10-83
Macrophages	342	0,81	9 x 10-85
Organelles	12	0,81	2 x 10-4
Ileum	59	0,77	5 x 10-13
Femur	15	0,74	1 x 10-3
Telomere	30	0,71	7 x 10-5
Knee	26	0,71	3 x 10-4
Macrophages, Alveolar	117	0,69	4 x 10-13
Abdominal Fat	69	0,69	3 x 10-8
Subcutaneous Fat, Abdominal	69	0,69	3 x 10-8
Spleen	23	0,69	2 x 10-3
Cicatrix	19	0,69	5 x 10-3
Intestinal Mucosa	40	0,68	6 x 10-5

SBNO1

Tissue	# samples	AUC	P-value
HL-60 Cells	12	0,96	4 x 10-8
K562 Cells	37	0,96	8 x 10-22
Precursor Cells, B-Lymphoid	14	0,92	4 x 10-8
Cerebellum	36	0,87	9 x 10-15
Granulocyte Precursor Cells	30	0,86	5 x 10-12
Caco-2 Cells	44	0,82	1 x 10-13
Prefrontal Cortex	46	0,82	4 x 10-14
Testis	37	0,81	4 x 10-11
Visual Cortex	34	0,8	8 x 10-10
Pluripotent Stem Cells	47	0,79	6 x 10-12
Induced Pluripotent Stem Cells	35	0,79	3 x 10-9
Cumulus Cells	38	0,79	7 x 10-10
Jurkat Cells	21	0,79	5 x 10-6
Osteoblasts	26	0,78	7 x 10-7
Hematopoietic Stem Cells	106	0,78	6 x 10-23
T-Lymphocytes, Regulatory	33	0,78	4 x 10-8
Motor Neurons	12	0,76	2 x 10-3
Frontal Lobe	62	0,76	9 x 10-13
Occipital Lobe	42	0,76	7 x 10-9
Embryonic Stem Cells	83	0,76	7 x 10-16

SETD8

Tissue	# samples	AUC	P-value
Sputum	151	0,93	2 x 10-75
K562 Cells	37	0,91	9 x 10-18

Myocytes, Smooth Muscle	141	0,84	5 x 10-45
Jurkat Cells	21	0,82	3 x 10-7
Muscle Cells	146	0,82	5 x 10-40
Prostate	352	0,81	4 x 10-92
Quadriceps Muscle	82	0,78	6 x 10-19
HCT116 Cells	96	0,78	1 x 10-21
Cell Line, Transformed	102	0,77	9 x 10-22
HEK293 Cells	100	0,77	3 x 10-21
Trophoblasts	11	0,77	2 x 10-3
Hela Cells	201	0,77	1 x 10-38
Synovial Fluid	12	0,76	2 x 10-3
Granulocyte Precursor Cells	30	0,74	5 x 10-6
Keratinocytes	48	0,71	3 x 10-7
Blastocyst	14	0,71	6 x 10-3
HT29 Cells	17	0,7	4 x 10-3
Muscle, Smooth	248	0,7	10 x 10-28
Astrocytes	12	0,69	2 x 10-2
Organelles	12	0,69	3 x 10-2

RILPL2

Tissue	# samples	AUC	P-value
Neutrophils	216	0,95	1 x 10-113
Granulocyte Precursor Cells	30	0,89	9 x 10-14
Sputum	151	0,89	6 x 10-61
HL-60 Cells	12	0,89	4 x 10-6
Bone Marrow Cells	809	0,86	1 x 10-264
Myeloid Cells	997	0,85	1 x 10-309
Monocytes	506	0,81	1 x 10-129
Macrophages	342	0,8	2 x 10-83
Hematopoietic Stem Cells	106	0,78	8 x 10-24
Macrophages, Alveolar	117	0,78	8 x 10-26
U937 Cells	57	0,78	3 x 10-13
Parotid Gland	19	0,77	4 x 10-5
Salivary Glands	24	0,75	2 x 10-5
Aortic Valve	10	0,72	1 x 10-2
Synovial Fluid	12	0,72	7 x 10-3
Conjunctiva	59	0,71	1 x 10-8
T-Lymphocytes	517	0,71	2 x 10-59
Palatine Tonsil	72	0,7	2 x 10-9
Blood Platelets	30	0,7	2 x 10-4
Osteoblasts	26	0,7	6 x 10-4

C12orf65

Tissue	# samples	AUC	P-value

Jurkat Cells	21	0,89	5 x 10-10
K562 Cells	37	0,88	2 x 10-15
T-Lymphocytes, Regulatory	33	0,87	9 x 10-14
T-Lymphocytes	517	0,87	10 x 10-180
Oocytes	15	0,84	4 x 10-6
Precursor Cells, B-Lymphoid	14	0,83	2 x 10-5
Hela Cells	201	0,79	1 x 10-45
Cell Line, Transformed	102	0,76	1 x 10-19
HCT116 Cells	96	0,76	5 x 10-18
HEK293 Cells	100	0,76	1 x 10-18
Palatine Tonsil	72	0,74	3 x 10-12
Lymphocytes	1737	0,73	4 x 10-239
HL-60 Cells	12	0,72	8 x 10-3
Clone Cells	115	0,72	6 x 10-16
Killer Cells, Natural	84	0,72	9 x 10-12
Germ Cells	33	0,71	4 x 10-5
Hypothalamus	15	0,68	1 x 10-2
HT29 Cells	17	0,67	2 x 10-2
Synovial Fluid	12	0,67	5 x 10-2
Intestinal Mucosa	40	0,66	5 x 10-4

MPHOSPH9

Tissue	# samples	AUC	P-value
Jurkat Cells	21	0,92	2 x 10-11
K562 Cells	37	0,89	3 x 10-16
T-Lymphocytes, Regulatory	33	0,86	6 x 10-13
Granulocyte Precursor Cells	30	0,85	3 x 10-11
HEK293 Cells	100	0,85	1 x 10-33
Cell Line, Transformed	102	0,85	4 x 10-34
HL-60 Cells	12	0,84	6 x 10-5
Visual Cortex	34	0,82	5 x 10-11
Precursor Cells, B-Lymphoid	14	0,79	2 x 10-4
Cerebellum	36	0,78	3 x 10-9
T-Lymphocytes	517	0,76	2 x 10-89
Induced Pluripotent Stem Cells	35	0,74	7 x 10-7
Neural Stem Cells	11	0,74	6 x 10-3
HCT116 Cells	96	0,74	4 x 10-16
Occipital Lobe	42	0,74	1 x 10-7
Synovial Fluid	12	0,72	8 x 10-3
Embryonic Stem Cells	83	0,71	2 x 10-11
Pluripotent Stem Cells	47	0,7	1 x 10-6
Hela Cells	201	0,68	4 x 10-18
Retina	27	0,65	9 x 10-3

SNRNP35

Tissue	# samples	AUC	P-value
Blood Platelets	30	0,99	2 x 10-20
Quadriceps Muscle	82	0,97	2 x 10-48
Muscle, Skeletal	162	0,92	5 x 10-76
Muscle, Striated	162	0,92	5 x 10-76
Atrial Appendage	10	0,91	6 x 10-6
Heart Atria	13	0,9	6 x 10-7
Muscles	723	0,85	1 x 10-224
Palatine Tonsil	72	0,84	9 x 10-24
Visual Cortex	34	0,83	2 x 10-11
Neutrophils	216	0,82	2 x 10-58
Occipital Lobe	42	0,81	2 x 10-12
T-Lymphocytes, Regulatory	33	0,81	1 x 10-9
Synovial Fluid	12	0,78	9 x 10-4
Subthalamic Nucleus	12	0,76	2 x 10-3
Nasopharynx	30	0,76	7 x 10-7
Conjunctiva	59	0,76	1 x 10-11
Hypothalamus	15	0,75	7 x 10-4
Arteries	25	0,75	1 x 10-5
Salivary Glands	24	0,73	7 x 10-5
Parotid Gland	19	0,73	4 x 10-4

RILPL1

Tissue	# samples	AUC	P-value
Atrial Appendage	10	1	5 x 10-8
Heart Atria	13	1	5 x 10-10
Heart Ventricles	124	0,99	2 x 10-80
Quadriceps Muscle	82	0,99	4 x 10-53
Muscle, Skeletal	162	0,98	6 x 10-101
Muscle, Striated	162	0,98	6 x 10-101
Heart	217	0,98	7 x 10-134
Subthalamic Nucleus	12	0,97	2 x 10-8
Substantia Nigra	22	0,96	7 x 10-14
Muscles	723	0,96	< 10-300
Mesencephalon	41	0,96	5 x 10-24
Thalamus	16	0,95	4 x 10-10
Putamen	16	0,94	8 x 10-10
Parietal Lobe	17	0,94	4 x 10-10
Embryoid Bodies	11	0,93	6 x 10-7
Temporal Lobe	91	0,93	1 x 10-45
Spinal Cord	19	0,93	9 x 10-11
Entorhinal Cortex	83	0,93	4 x 10-41
Neural Stem Cells	11	0,92	1 x 10-6

Cerebral Cortex	276	0,92	4 x 10-129

PITPNM2

Tissue	# samples	AUC	P-value
Hep G2 Cells	102	0,89	3 x 10-43
Frontal Lobe	62	0,88	1 x 10-24
Hippocampus	55	0,87	9 x 10-22
Prefrontal Cortex	46	0,87	7 x 10-18
Hepatocytes	188	0,86	7 x 10-65
Jurkat Cells	21	0,83	1 x 10-7
Putamen	16	0,81	1 x 10-5
Temporal Lobe	91	0,8	1 x 10-23
Cerebral Cortex	276	0,8	8 x 10-67
Entorhinal Cortex	83	0,8	8 x 10-21
Heart Ventricles	124	0,79	1 x 10-28
Retinal Pigment Epithelium	12	0,78	7 x 10-4
Hypothalamus	15	0,78	2 x 10-4
Trophoblasts	11	0,78	2 x 10-3
Cerebrum	344	0,75	3 x 10-56
Synovial Membrane	26	0,74	2 x 10-5
Joints	26	0,74	2 x 10-5
Endothelial Cells	196	0,74	7 x 10-31
Myocytes, Smooth Muscle	141	0,74	4 x 10-22
Synovial Fluid	12	0,73	5 x 10-3

STK24

Tissue	# samples	AUC	P-value
Conjunctiva	59	0,94	3 x 10-32
Blood Platelets	30	0,94	1 x 10-16
Precursor Cells, B-Lymphoid	14	0,92	6 x 10-8
Nasal Mucosa	93	0,9	9 x 10-40
Caco-2 Cells	44	0,88	7 x 10-18
Mouth Mucosa	94	0,87	3 x 10-36
T-Lymphocytes, Regulatory	33	0,86	5 x 10-13
Neck	138	0,84	2 x 10-43
Mucous Membrane	480	0,82	2 x 10-130
Ileum	59	0,81	1 x 10-16
Keratinocytes	48	0,81	2 x 10-13
Head	297	0,8	10 x 10-72
Urinary Bladder	70	0,79	3 x 10-17
Membranes	521	0,79	7 x 10-111
U937 Cells	57	0,78	2 x 10-13
Neutrophils	216	0,78	8 x 10-45
Vulva	34	0,77	4 x 10-8

Sputum	151	0,77	9 x 10-31
Pelvis	10	0,77	4 x 10-3
Intestinal Mucosa	40	0,76	1 x 10-8

FARP1

Tissue	# samples	AUC	P-value
Neural Stem Cells	11	0,96	1 x 10-7
Hep G2 Cells	102	0,94	2 x 10-52
Cicatrix	19	0,94	5 x 10-11
Embryoid Bodies	11	0,93	10 x 10-7
Keloid	10	0,91	6 x 10-6
Osteoblasts	26	0,89	7 x 10-12
Retinal Pigment Epithelium	12	0,89	3 x 10-6
Parotid Gland	19	0,88	7 x 10-9
Salivary Glands	24	0,88	1 x 10-10
Fibroblasts	392	0,86	3 x 10-133
Hepatocytes	188	0,86	7 x 10-64
Endometrium	264	0,85	3 x 10-84
Astrocytes	12	0,84	4 x 10-5
Thyroid Gland	85	0,84	2 x 10-27
Liver	569	0,84	2 x 10-170
Embryonic Stem Cells	83	0,82	2 x 10-24
Organelles	12	0,82	1 x 10-4
Kidney	614	0,82	10 x 10-163
Myocytes, Smooth Muscle	141	0,82	7 x 10-39
Chondrocytes	19	0,82	2 x 10-6

SLC15A1

Tissue	# samples	AUC	P-value
Thalamus	16	0,85	2 x 10-6
Putamen	16	0,82	1 x 10-5
Ganglia	11	0,8	5 x 10-4
Pelvis	10	0,78	2 x 10-3
Cervix Uteri	38	0,75	9 x 10-8
Palatine Tonsil	72	0,75	6 x 10-13
Subthalamic Nucleus	12	0,74	4 x 10-3
Cecum	15	0,73	2 x 10-3
Esophagus	13	0,73	4 x 10-3
Killer Cells, Natural	84	0,71	1 x 10-11
Thyroid Gland	85	0,71	1 x 10-11
Ileum	59	0,71	3 x 10-8
Neutrophils	216	0,7	7 x 10-24
Omentum	76	0,7	3 x 10-9
Abdomen	103	0,69	8 x 10-12

Mesencephalon	41	0,69	2 x 10-5
Substantia Nigra	22	0,69	2 x 10-3
Precursor Cells, B-Lymphoid	14	0,69	2 x 10-2
Peritoneum	89	0,68	3 x 10-9
Hypothalamus	15	0,68	2 x 10-2

TANK

Tissue	# samples	AUC	P-value
Sputum	151	0,95	7 x 10-83
Neutrophils	216	0,94	1 x 10-111
HT29 Cells	17	0,89	2 x 10-8
Myeloid Cells	997	0,85	2 x 10-312
Bone Marrow Cells	809	0,85	3 x 10-254
Synovial Fluid	12	0,85	3 x 10-5
Monocytes	506	0,84	2 x 10-152
Macrophages	342	0,81	4 x 10-85
Chorion	15	0,78	2 x 10-4
Umbilical Veins	113	0,78	3 x 10-24
Killer Cells, Natural	84	0,77	4 x 10-18
Cicatrix	19	0,77	4 x 10-5
Dendritic Cells	277	0,77	3 x 10-54
Precursor Cells, B-Lymphoid	14	0,75	1 x 10-3
Macrophages, Alveolar	117	0,75	8 x 10-21
Oocytes	15	0,74	1 x 10-3
Keloid	10	0,74	9 x 10-3
HCT116 Cells	96	0,73	2 x 10-15
Veins	133	0,73	1 x 10-20
Fetal Blood	151	0,72	6 x 10-21

PSMD14

Tissue	# samples	AUC	P-value
K562 Cells	37	0,97	9 x 10-23
HCT116 Cells	96	0,97	4 x 10-56
U937 Cells	57	0,95	2 x 10-31
Jurkat Cells	21	0,92	3 x 10-11
HL-60 Cells	12	0,89	4 x 10-6
Tongue	105	0,87	5 x 10-39
Glucagon-Secreting Cells	39	0,84	2 x 10-13
Clone Cells	115	0,83	4 x 10-35
Cell Line, Tumor	674	0,83	9 x 10-191
Nasopharynx	30	0,81	2 x 10-9
Pluripotent Stem Cells	47	0,81	2 x 10-13
HT29 Cells	17	0,81	1 x 10-5
Islets of Langerhans	60	0,8	3 x 10-16

Induced Pluripotent Stem Cells	35	0,8	4 x 10-10
Cell Line, Transformed	102	0,8	2 x 10-26
HEK293 Cells	100	0,8	1 x 10-25
Neural Stem Cells	11	0,79	8 x 10-4
Hela Cells	201	0,77	3 x 10-41
Hep G2 Cells	102	0,77	5 x 10-21
Stromal Cells	54	0,77	8 x 10-12

TBR1

Tissue	# samples	AUC	P-value
Prefrontal Cortex	46	0,99	1 x 10-30
Frontal Lobe	62	0,99	2 x 10-40
Hippocampus	55	0,92	4 x 10-27
Parietal Lobe	17	0,89	3 x 10-8
Cerebral Cortex	276	0,88	2 x 10-104
Temporal Lobe	91	0,86	1 x 10-32
Entorhinal Cortex	83	0,85	4 x 10-28
Nasopharynx	30	0,84	8 x 10-11
Keloid	10	0,84	2 x 10-4
Trophoblasts	11	0,83	1 x 10-4
Heart Ventricles	124	0,83	2 x 10-36
Blastocyst	14	0,83	2 x 10-5
Subthalamic Nucleus	12	0,81	2 x 10-4
Cerebrum	344	0,79	3 x 10-78
Myocytes, Smooth Muscle	141	0,78	2 x 10-31
Cicatrix	19	0,78	2 x 10-5
Thalamus	16	0,78	1 x 10-4
Muscle Cells	146	0,76	4 x 10-27
Brain	1274	0,75	2 x 10-206
Central Nervous System	1302	0,75	7 x 10-200

Related to neuronal function	Gene Set ID	Gene Set Name
0	GO:0051084	'De Novo' Posttranslational Protein Folding
0	GO:0006458	'De Novo' Protein Folding
0	GO:0005545	1-Phosphatidylinositol Binding
0	GO:0016303	1-Phosphatidylinositol-3-Kinase Activity
0	GO:0051537	2 Iron, 2 Sulfur Cluster Binding
0	GO:0006103	2-Oxoglutarate Metabolic Process
0	GO:0009394	2'-Deoxyribonucleotide Metabolic Process
0	GO:0003854	3-Beta-Hydroxy-Delta5-Steroid Dehydrogenase Activity
0	GO:0008408	3'-5' Exonuclease Activity
0	GO:0000175	3'-5'-Exoribonuclease Activity
0	GO:0050427	3'-Phosphoadenosine 5'-Phosphosulfate Metabolic Process
0	GO:0004115	3',5'-Cyclic-Amp Phosphodiesterase Activity
0	GO:0047555	3',5'-Cyclic-Gmp Phosphodiesterase Activity
0	GO:0004114	3',5'-Cyclic-Nucleotide Phosphodiesterase Activity
0	GO:0051539	4 Iron, 4 Sulfur Cluster Binding
0	GO:0031672	A Band
0	GO:0006085	Acetyl-Coa Biosynthetic Process
0	GO:0006086	Acetyl-Coa Biosynthetic Process From Pyruvate
0	GO:0046356	Acetyl-Coa Catabolic Process
0	GO:0006084	Acetyl-Coa Metabolic Process
1	GO:0042166	Acetylcholine Binding
1	GO:0015464	Acetylcholine Receptor Activity
1	GO:0004889	Acetylcholine-Activated Cation-Selective Channel Activity
1	GO:0005892	Acetylcholine-Gated Channel Complex
0	GO:0008376	Acetylgalactosaminyltransferase Activity
0	GO:0008375	Acetylglucosaminyltransferase Activity
0	GO:0016407	Acetyltransferase Activity
0	GO:0003993	Acid Phosphatase Activity
0	GO:0046717	Acid Secretion
0	GO:0016881	Acid-Amino Acid Ligase Activity
0	GO:0016878	Acid-Thiol Ligase Activity
0	GO:0015172	Acidic Amino Acid Transmembrane Transporter Activity
0	GO:0015800	Acidic Amino Acid Transport
0	GO:0002080	Acrosomal Membrane
0	GO:0001669	Acrosomal Vesicle
0	GO:0007340	Acrosome Reaction
0	GO:0003779	Actin Binding
0	GO:0015629	Actin Cytoskeleton
0	GO:0030036	Actin Cytoskeleton Organization
0	GO:0031532	Actin Cytoskeleton Reorganization
0	GO:0005884	Actin Filament
0	GO:0051015	Actin Filament Binding
0	GO:0032432	Actin Filament Bundle
0	GO:0051017	Actin Filament Bundle Assembly
0	GO:0051693	Actin Filament Capping
0	GO:0030042	Actin Filament Depolymerization
0	GO:0007015	Actin Filament Organization
0	GO:0030041	Actin Filament Polymerization
0	GO:0030048	Actin Filament-Based Movement
0	GO:0030029	Actin Filament-Based Process
0	GO:0003785	Actin Monomer Binding
0	GO:0008154	Actin Polymerization Or Depolymerization
0	GO:0070252	Actin-Mediated Cell Contraction
0	GO:0033275	Actin-Myosin Filament Sliding

0	GO:0042805	Actinin Binding
0	GO:0050798	Activated T Cell Proliferation
0	GO:0033613	Activating Transcription Factor Binding
0	GO:0007190	Activation Of Adenylate Cyclase Activity
0	GO:0006919	Activation Of Cysteine-Type Endopeptidase Activity Involved In Apoptotic Process
0	GO:0008635	Activation Of Cysteine-Type Endopeptidase Activity Involved In Apoptotic Process By Cytochrome C
0	GO:0002253	Activation Of Immune Response
0	GO:0002218	Activation Of Innate Immune Response
0	GO:0042976	Activation Of Janus Kinase Activity
0	GO:0007257	Activation Of Jun Kinase Activity
0	GO:0000187	Activation Of Mapk Activity
0	GO:0000186	Activation Of Mapkk Activity
0	GO:0007250	Activation Of Nf-Kappab-Inducing Kinase Activity
0	GO:0007202	Activation Of Phospholipase C Activity
0	GO:0008633	Activation Of Pro-Apoptotic Gene Products
0	GO:0034199	Activation Of Protein Kinase A Activity
0	GO:0032147	Activation Of Protein Kinase Activity
0	GO:0032148	Activation Of Protein Kinase B Activity
0	GO:0032856	Activation Of Ras Gtpase Activity
0	GO:0032862	Activation Of Rho Gtpase Activity
0	GO:0022804	Active Transmembrane Transporter Activity
0	GO:0048185	Activin Binding
0	GO:0032924	Activin Receptor Signaling Pathway
0	GO:0017002	Activin-Activated Receptor Activity
0	GO:0042641	Actomyosin
0	GO:0031032	Actomyosin Structure Organization
0	GO:0002526	Acute Inflammatory Response
0	GO:0002438	Acute Inflammatory Response To Antigenic Stimulus
0	GO:0006953	Acute-Phase Response
0	GO:0071616	Acyl-Coa Biosynthetic Process
0	GO:0003995	Acyl-Coa Dehydrogenase Activity
0	GO:0006637	Acyl-Coa Metabolic Process
0	GO:0046463	Acylglycerol Biosynthetic Process
0	GO:0046464	Acylglycerol Catabolic Process
0	GO:0006639	Acylglycerol Metabolic Process
0	GO:0016411	Acylglycerol O-Acyltransferase Activity
0	GO:0005671	Ada2/Gcn5/Ada3 Transcription Activator Complex
0	GO:0023058	Adaptation Of Signaling Pathway
0	GO:0002250	Adaptive Immune Response
0	GO:0002460	Adaptive Immune Response Based On Somatic Recombination Of Immune Receptors Built From Immunoglobulin Superfamily Domains
0	GO:0021984	Adenohypophysis Development
0	GO:0004016	Adenylate Cyclase Activity
0	GO:0007189	Adenylate Cyclase-Activating G-Protein Coupled Receptor Signaling Pathway
0	GO:0007193	Adenylate Cyclase-Inhibiting G-Protein Coupled Receptor Signaling Pathway
0	GO:0007188	Adenylate Cyclase-Modulating G-Protein Coupled Receptor Signaling Pathway
0	GO:0070566	Adenylyltransferase Activity
0	GO:0005912	Adherens Junction
0	GO:0034332	Adherens Junction Organization
0	GO:0060612	Adipose Tissue Development
0	GO:0043531	Adp Binding
0	GO:0030325	Adrenal Gland Development
1	GO:0030534	Adult Behavior
1	GO:0008343	Adult Feeding Behavior
0	GO:0007512	Adult Heart Development
0	GO:0008344	Adult Locomotory Behavior
0	GO:0007628	Adult Walking Behavior

0	GO:0009060	Aerobic Respiration
0	GO:0016235	Aggresome
0	GO:0007568	Aging
0	GO:0043178	Alcohol Binding
0	GO:0046165	Alcohol Biosynthetic Process
0	GO:0046164	Alcohol Catabolic Process
0	GO:0019400	Alditol Metabolic Process
0	GO:0004033	Aldo-Keto Reductase (Nadp) Activity
0	GO:0043450	Alkene Biosynthetic Process
0	GO:0032281	Alpha-Amino-3-Hydroxy-5-Methyl-4-Isoxazolepropionic Acid Selective Glutamate Receptor Complex
0	GO:0046631	Alpha-Beta T Cell Activation
0	GO:0002287	Alpha-Beta T Cell Activation Involved In Immune Response
0	GO:0046632	Alpha-Beta T Cell Differentiation
0	GO:0002293	Alpha-Beta T Cell Differentiation Involved In Immune Response
0	GO:0046633	Alpha-Beta T Cell Proliferation
0	GO:0043014	Alpha-Tubulin Binding
0	GO:0000380	Alternative Nuclear Mrna Splicing, Via Spliceosome
0	GO:0001667	Ameboidal Cell Migration
0	GO:0043176	Amine Binding
0	GO:0009309	Amine Biosynthetic Process
0	GO:0009310	Amine Catabolic Process
0	GO:0005275	Amine Transmembrane Transporter Activity
0	GO:0015837	Amine Transport
0	GO:0043038	Amino Acid Activation
0	GO:0016597	Amino Acid Binding
0	GO:0043090	Amino Acid Import
0	GO:0003333	Amino Acid Transmembrane Transport
0	GO:0015171	Amino Acid Transmembrane Transporter Activity
0	GO:0006865	Amino Acid Transport
0	GO:0006040	Amino Sugar Metabolic Process
0	GO:0004812	Aminoacyl-Trna Ligase Activity
0	GO:0006023	Aminoglycan Biosynthetic Process
0	GO:0006026	Aminoglycan Catabolic Process
0	GO:0006022	Aminoglycan Metabolic Process
0	GO:0004177	Aminopeptidase Activity
0	GO:0016208	Amp Binding
0	GO:0042987	Amyloid Precursor Protein Catabolic Process
0	GO:0042982	Amyloid Precursor Protein Metabolic Process
0	GO:0042640	Anagen
0	GO:0051322	Anaphase
0	GO:0005680	Anaphase-Promoting Complex
0	GO:0031145	Anaphase-Promoting Complex-Dependent Proteasomal Ubiquitin-Dependent Protein Catabolic Process
0	GO:0048532	Anatomical Structure Arrangement
0	GO:0060249	Anatomical Structure Homeostasis
0	GO:0071695	Anatomical Structure Maturation
0	GO:0031362	Anchored To External Side Of Plasma Membrane
0	GO:0031225	Anchored To Membrane
0	GO:0046658	Anchored To Plasma Membrane
0	GO:0030934	Anchoring Collagen
0	GO:0070161	Anchoring Junction
0	GO:0006702	Androgen Biosynthetic Process
0	GO:0008209	Androgen Metabolic Process
0	GO:0050681	Androgen Receptor Binding
0	GO:0030521	Androgen Receptor Signaling Pathway
0	GO:0001525	Angiogenesis
0	GO:0060055	Angiogenesis Involved In Wound Healing

0	GO:0043168	Anion Binding
0	GO:0005253	Anion Channel Activity
0	GO:0055081	Anion Homeostasis
0	GO:0008509	Anion Transmembrane Transporter Activity
0	GO:0006820	Anion Transport
0	GO:0015301	Anion:Anion Antiporter Activity
0	GO:0015296	Anion:Cation Symporter Activity
0	GO:0009948	Anterior/Posterior Axis Specification
0	GO:0008595	Anterior/Posterior Axis Specification, Embryo
0	GO:0009952	Anterior/Posterior Pattern Specification
0	GO:0006916	Anti-Apoptosis
0	GO:0003823	Antigen Binding
0	GO:0019882	Antigen Processing And Presentation
0	GO:0019884	Antigen Processing And Presentation Of Exogenous Antigen
0	GO:0002478	Antigen Processing And Presentation Of Exogenous Peptide Antigen
0	GO:0048002	Antigen Processing And Presentation Of Peptide Antigen
0	GO:0002474	Antigen Processing And Presentation Of Peptide Antigen Via Mhc Class I
0	GO:0002495	Antigen Processing And Presentation Of Peptide Antigen Via Mhc Class Ii
0	GO:0002504	Antigen Processing And Presentation Of Peptide Or Polysaccharide Antigen Via Mhc Class Ii
0	GO:0050851	Antigen Receptor-Mediated Signaling Pathway
0	GO:0016209	Antioxidant Activity
0	GO:0015297	Antiporter Activity
0	GO:0035904	Aorta Development
0	GO:0035909	Aorta Morphogenesis
0	GO:0030119	Ap-Type Membrane Coat Adaptor Complex
0	GO:0043297	Apical Junction Assembly
0	GO:0043296	Apical Junction Complex
0	GO:0045177	Apical Part Of Cell
0	GO:0016324	Apical Plasma Membrane
0	GO:0045176	Apical Protein Localization
0	GO:0016327	Apicolateral Plasma Membrane
0	GO:0034185	Apolipoprotein Binding
0	GO:0043277	Apoptotic Cell Clearance
0	GO:0006309	Apoptotic Dna Fragmentation
0	GO:0008637	Apoptotic Mitochondrial Changes
0	GO:0030262	Apoptotic Nuclear Change
0	GO:0060561	Apoptotic Process Involved In Morphogenesis
0	GO:0016505	Apoptotic Protease Activator Activity
0	GO:0048736	Appendage Development
0	GO:0035107	Appendage Morphogenesis
0	GO:0050482	Arachidonic Acid Secretion
0	GO:0008060	Arf Gtpase Activator Activity
0	GO:0005086	Arf Guanyl-Nucleotide Exchange Factor Activity
0	GO:0032011	Arf Protein Signal Transduction
0	GO:0006525	Arginine Metabolic Process
0	GO:0070330	Aromatase Activity
0	GO:0009074	Aromatic Amino Acid Family Catabolic Process
0	GO:0009072	Aromatic Amino Acid Family Metabolic Process
0	GO:0019438	Aromatic Compound Biosynthetic Process
0	GO:0019439	Aromatic Compound Catabolic Process
0	GO:0060840	Artery Development
0	GO:0048844	Artery Morphogenesis
0	GO:0004065	Arylsulfatase Activity
0	GO:0009067	Aspartate Family Amino Acid Biosynthetic Process
0	GO:0009068	Aspartate Family Amino Acid Catabolic Process
0	GO:0009066	Aspartate Family Amino Acid Metabolic Process

0	GO:0004190	Aspartic-Type Endopeptidase Activity
0	GO:0070001	Aspartic-Type Peptidase Activity
0	GO:0008306	Associative Learning
1	GO:0014002	Astrocyte Development
1	GO:0048708	Astrocyte Differentiation
0	GO:0008105	Asymmetric Protein Localization
0	GO:0032279	Asymmetric Synapse
0	GO:0006754	Atp Biosynthetic Process
0	GO:0006200	Atp Catabolic Process
0	GO:0015991	Atp Hydrolysis Coupled Proton Transport
0	GO:0046034	Atp Metabolic Process
0	GO:0042773	Atp Synthesis Coupled Electron Transport
0	GO:0015986	Atp Synthesis Coupled Proton Transport
0	GO:0043044	Atp-Dependent Chromatin Remodeling
0	GO:0004003	Atp-Dependent Dna Helicase Activity
0	GO:0008026	Atp-Dependent Helicase Activity
0	GO:0004004	Atp-Dependent Rna Helicase Activity
0	GO:0016887	Atpase Activity
0	GO:0042623	Atpase Activity, Coupled
0	GO:0043492	Atpase Activity, Coupled To Movement Of Substances
0	GO:0042625	Atpase Activity, Coupled To Transmembrane Movement Of Ions
0	GO:0015662	Atpase Activity, Coupled To Transmembrane Movement Of Ions, Phosphorylative Mechanism
0	GO:0042626	Atpase Activity, Coupled To Transmembrane Movement Of Substances
0	GO:0051117	Atpase Binding
0	GO:0060590	Atpase Regulator Activity
0	GO:0051313	Attachment Of Spindle Microtubules To Chromosome
0	GO:0008608	Attachment Of Spindle Microtubules To Kinetochore
0	GO:0017091	Au-Rich Element Binding
0	GO:0060117	Auditory Receptor Cell Development
0	GO:0042491	Auditory Receptor Cell Differentiation
0	GO:0048483	Autonomic Nervous System Development
0	GO:0005776	Autophagic Vacuole
0	GO:0000045	Autophagic Vacuole Assembly
0	GO:0000421	Autophagic Vacuole Membrane
0	GO:0006914	Autophagy
0	GO:0003401	Axis Elongation
0	GO:0009798	Axis Specification
0	GO:0030673	Axolemma
1	GO:0030424	Axon
1	GO:0008088	Axon Cargo Transport
1	GO:0008366	Axon Ensheathment
1	GO:0032291	Axon Ensheathment In Central Nervous System
1	GO:0048675	Axon Extension
1	GO:0048846	Axon Extension Involved In Axon Guidance
1	GO:0007411	Axon Guidance
1	GO:0033267	Axon Part
1	GO:0031103	Axon Regeneration
1	GO:0043679	Axon Terminus
1	GO:0007413	Axonal Fasciculation
0	GO:0005858	Axonemal Dynein Complex
0	GO:0005930	Axoneme
0	GO:0044447	Axoneme Part
1	GO:0007409	Axonogenesis
0	GO:0042113	B Cell Activation
0	GO:0002312	B Cell Activation Involved In Immune Response
0	GO:0001783	B Cell Apoptotic Process

0	GO:0030183	B Cell Differentiation
0	GO:0001782	B Cell Homeostasis
0	GO:0019724	B Cell Mediated Immunity
0	GO:0042100	B Cell Proliferation
0	GO:0050853	B Cell Receptor Signaling Pathway
0	GO:0051635	Bacterial Cell Surface Binding
0	GO:0005605	Basal Lamina
0	GO:0045178	Basal Part Of Cell
0	GO:0009925	Basal Plasma Membrane
0	GO:0006284	Base-Excision Repair
0	GO:0005604	Basement Membrane
0	GO:0015802	Basic Amino Acid Transport
0	GO:0016323	Basolateral Plasma Membrane
1	GO:0007610	Behavior
1	GO:0002209	Behavioral Defense Response
1	GO:0001662	Behavioral Fear Response
0	GO:0051705	Behavioral Interaction Between Organisms
1	GO:0048266	Behavioral Response To Pain
0	GO:0042537	Benzene-Containing Compound Metabolic Process
0	GO:0001540	Beta-Amyloid Binding
0	GO:0008013	Beta-Catenin Binding
0	GO:0048487	Beta-Tubulin Binding
0	GO:0015838	Betaine Transport
0	GO:0043425	Bhlh Transcription Factor Binding
0	GO:0015701	Bicarbonate Transport
0	GO:0015721	Bile Acid And Bile Salt Transport
0	GO:0006699	Bile Acid Biosynthetic Process
0	GO:0008206	Bile Acid Metabolic Process
0	GO:0007339	Binding Of Sperm To Zona Pellucida
0	GO:0060090	Binding, Bridging
0	GO:0031214	Biomineral Tissue Development
0	GO:0001824	Blastocyst Development
0	GO:0001825	Blastocyst Formation
0	GO:0001832	Blastocyst Growth
0	GO:0007350	Blastoderm Segmentation
0	GO:0008015	Blood Circulation
0	GO:0007596	Blood Coagulation
0	GO:0072378	Blood Coagulation, Fibrin Clot Formation
0	GO:0007597	Blood Coagulation, Intrinsic Pathway
0	GO:0001568	Blood Vessel Development
0	GO:0043534	Blood Vessel Endothelial Cell Migration
0	GO:0048514	Blood Vessel Morphogenesis
0	GO:0001974	Blood Vessel Remodeling
0	GO:0030509	Bmp Signaling Pathway
0	GO:0007589	Body Fluid Secretion
0	GO:0010171	Body Morphogenesis
0	GO:0060348	Bone Development
0	GO:0030282	Bone Mineralization
0	GO:0060349	Bone Morphogenesis
0	GO:0046849	Bone Remodeling
0	GO:0045453	Bone Resorption
1	GO:0007420	Brain Development
1	GO:0048854	Brain Morphogenesis
0	GO:0060602	Branch Elongation Of An Epithelium
0	GO:0009083	Branched Chain Family Amino Acid Catabolic Process
0	GO:0009081	Branched Chain Family Amino Acid Metabolic Process

0	GO:0060444	Branching Involved In Mammary Gland Duct Morphogenesis
0	GO:0060442	Branching Involved In Prostate Gland Morphogenesis
0	GO:0060445	Branching Involved In Salivary Gland Morphogenesis
0	GO:0001658	Branching Involved In Ureteric Bud Morphogenesis
0	GO:0048754	Branching Morphogenesis Of A Tube
0	GO:0050873	Brown Fat Cell Differentiation
0	GO:0005903	Brush Border
0	GO:0031526	Brush Border Membrane
0	GO:0016408	C-Acyltransferase Activity
0	GO:0016493	C-C Chemokine Receptor Activity
0	GO:0018410	C-Terminal Protein Amino Acid Modification
0	GO:0006501	C-Terminal Protein Lipidation
0	GO:0006700	C21-Steroid Hormone Biosynthetic Process
0	GO:0008207	C21-Steroid Hormone Metabolic Process
0	GO:0070742	C2H2 Zinc Finger Domain Binding
0	GO:0045296	Cadherin Binding
1	GO:0015030	Cajal Body
1	GO:0005227	Calcium Activated Cation Channel Activity
1	GO:0005262	Calcium Channel Activity
1	GO:0034704	Calcium Channel Complex
1	GO:0005246	Calcium Channel Regulator Activity
0	GO:0055074	Calcium Ion Homeostasis
0	GO:0070509	Calcium Ion Import
1	GO:0070588	Calcium Ion Transmembrane Transport
1	GO:0015085	Calcium Ion Transmembrane Transporter Activity
0	GO:0006816	Calcium Ion Transport
0	GO:0060402	Calcium Ion Transport Into Cytosol
1	GO:0017156	Calcium Ion-Dependent Exocytosis
1	GO:0015269	Calcium-Activated Potassium Channel Activity
1	GO:0016339	Calcium-Dependent Cell-Cell Adhesion
0	GO:0004198	Calcium-Dependent Cysteine-Type Endopeptidase Activity
0	GO:0005544	Calcium-Dependent Phospholipid Binding
0	GO:0048306	Calcium-Dependent Protein Binding
0	GO:0016338	Calcium-Independent Cell-Cell Adhesion
1	GO:0019722	Calcium-Mediated Signaling
1	GO:0015278	Calcium-Release Channel Activity
0	GO:0005516	Calmodulin Binding
0	GO:0004683	Calmodulin-Dependent Protein Kinase Activity
0	GO:0043010	Camera-Type Eye Development
0	GO:0048593	Camera-Type Eye Morphogenesis
0	GO:0060219	Camera-Type Eye Photoreceptor Cell Differentiation
0	GO:0030552	Camp Binding
0	GO:0006171	Camp Biosynthetic Process
0	GO:0006198	Camp Catabolic Process
0	GO:0046058	Camp Metabolic Process
0	GO:0004691	Camp-Dependent Protein Kinase Activity
0	GO:0005952	Camp-Dependent Protein Kinase Complex
0	GO:0008603	Camp-Dependent Protein Kinase Regulator Activity
0	GO:0019933	Camp-Mediated Signaling
0	GO:0060070	Canonical Wnt Receptor Signaling Pathway
0	GO:0030246	Carbohydrate Binding
0	GO:0016051	Carbohydrate Biosynthetic Process
0	GO:0016052	Carbohydrate Catabolic Process
0	GO:0033500	Carbohydrate Homeostasis
0	GO:0019200	Carbohydrate Kinase Activity
0	GO:0019203	Carbohydrate Phosphatase Activity

0	GO:0015144	Carbohydrate Transmembrane Transporter Activity
0	GO:0008643	Carbohydrate Transport
0	GO:0016830	Carbon-Carbon Lyase Activity
0	GO:0016884	Carbon-Nitrogen Ligase Activity, With Glutamine As Amido-N-Donor
0	GO:0016840	Carbon-Nitrogen Lyase Activity
0	GO:0016835	Carbon-Oxygen Lyase Activity
0	GO:0016846	Carbon-Sulfur Lyase Activity
0	GO:0004089	Carbonate Dehydratase Activity
0	GO:0016831	Carboxy-Lyase Activity
0	GO:0004091	Carboxylesterase Activity
0	GO:0031406	Carboxylic Acid Binding
0	GO:0046394	Carboxylic Acid Biosynthetic Process
0	GO:0046395	Carboxylic Acid Catabolic Process
0	GO:0046943	Carboxylic Acid Transmembrane Transporter Activity
0	GO:0046942	Carboxylic Acid Transport
0	GO:0052689	Carboxylic Ester Hydrolase Activity
0	GO:0004180	Carboxypeptidase Activity
0	GO:0003230	Cardiac Atrium Development
0	GO:0003209	Cardiac Atrium Morphogenesis
0	GO:0055006	Cardiac Cell Development
0	GO:0035051	Cardiac Cell Differentiation
0	GO:0003205	Cardiac Chamber Development
0	GO:0003207	Cardiac Chamber Formation
0	GO:0003206	Cardiac Chamber Morphogenesis
0	GO:0060317	Cardiac Epithelial To Mesenchymal Transition
0	GO:0010659	Cardiac Muscle Cell Apoptotic Process
0	GO:0055013	Cardiac Muscle Cell Development
0	GO:0055007	Cardiac Muscle Cell Differentiation
0	GO:0060038	Cardiac Muscle Cell Proliferation
0	GO:0060048	Cardiac Muscle Contraction
0	GO:0003300	Cardiac Muscle Hypertrophy
0	GO:0048738	Cardiac Muscle Tissue Development
0	GO:0055017	Cardiac Muscle Tissue Growth
0	GO:0055008	Cardiac Muscle Tissue Morphogenesis
0	GO:0055003	Cardiac Myofibril Assembly
0	GO:0003215	Cardiac Right Ventricle Morphogenesis
0	GO:0003279	Cardiac Septum Development
0	GO:0060411	Cardiac Septum Morphogenesis
0	GO:0003231	Cardiac Ventricle Development
0	GO:0003211	Cardiac Ventricle Formation
0	GO:0003208	Cardiac Ventricle Morphogenesis
0	GO:0010002	Cardioblast Differentiation
0	GO:0038024	Cargo Receptor Activity
0	GO:0015879	Carnitine Transport
0	GO:0001502	Cartilage Condensation
0	GO:0051216	Cartilage Development
0	GO:0060351	Cartilage Development Involved In Endochondral Bone Morphogenesis
0	GO:0060536	Cartilage Morphogenesis
0	GO:0071013	Catalytic Step 2 Spliceosome
0	GO:0009713	Catechol-Containing Compound Biosynthetic Process
0	GO:0009712	Catechol-Containing Compound Metabolic Process
0	GO:0042423	Catecholamine Biosynthetic Process
0	GO:0006584	Catecholamine Metabolic Process
0	GO:0050432	Catecholamine Secretion
0	GO:0051937	Catecholamine Transport
0	GO:0035411	Catenin Import Into Nucleus

0	GO:0005261	Cation Channel Activity
0	GO:0034703	Cation Channel Complex
0	GO:0055080	Cation Homeostasis
0	GO:0019829	Cation-Transporting Atpase Activity
0	GO:0005416	Cation:Amino Acid Symporter Activity
0	GO:0015491	Cation:Cation Antiporter Activity
0	GO:0005901	Caveola
0	GO:0048020	Ccr Chemokine Receptor Binding
0	GO:0035710	Cd4-Positive, Alpha-Beta T Cell Activation
0	GO:0043367	Cd4-Positive, Alpha-Beta T Cell Differentiation
0	GO:0002294	Cd4-Positive, Alpha-Beta T Cell Differentiation Involved In Immune Response
0	GO:0002263	Cell Activation Involved In Immune Response
0	GO:0033627	Cell Adhesion Mediated By Integrin
0	GO:0050839	Cell Adhesion Molecule Binding
0	GO:0007569	Cell Aging
0	GO:0044297	Cell Body
0	GO:0060326	Cell Chemotaxis
0	GO:0005938	Cell Cortex
0	GO:0044448	Cell Cortex Part
0	GO:0007050	Cell Cycle Arrest
0	GO:0000075	Cell Cycle Checkpoint
0	GO:0033205	Cell Cycle Cytokinesis
1	GO:0021533	Cell Differentiation In Hindbrain
1	GO:0021515	Cell Differentiation In Spinal Cord
0	GO:0060706	Cell Differentiation Involved In Embryonic Placenta Development
0	GO:0061005	Cell Differentiation Involved In Kidney Development
0	GO:0072202	Cell Differentiation Involved In Metanephros Development
0	GO:0051301	Cell Division
0	GO:0032153	Cell Division Site
0	GO:0032155	Cell Division Site Part
0	GO:0030313	Cell Envelope
0	GO:0045165	Cell Fate Commitment
0	GO:0060795	Cell Fate Commitment Involved In Formation Of Primary Germ Layer
0	GO:0001709	Cell Fate Determination
0	GO:0001708	Cell Fate Specification
0	GO:0016049	Cell Growth
0	GO:0034329	Cell Junction Assembly
0	GO:0034330	Cell Junction Organization
0	GO:0001906	Cell Killing
0	GO:0031252	Cell Leading Edge
0	GO:0048469	Cell Maturation
0	GO:0042074	Cell Migration Involved In Gastrulation
0	GO:0002042	Cell Migration Involved In Sprouting Angiogenesis
0	GO:0030031	Cell Projection Assembly
0	GO:0032838	Cell Projection Cytoplasm
0	GO:0031253	Cell Projection Membrane
1	GO:0021846	Cell Proliferation In Forebrain
0	GO:0072111	Cell Proliferation Involved In Kidney Development
0	GO:0072203	Cell Proliferation Involved In Metanephros Development
0	GO:0008037	Cell Recognition
0	GO:0045454	Cell Redox Homeostasis
0	GO:0009986	Cell Surface
0	GO:0043498	Cell Surface Binding
0	GO:0061311	Cell Surface Receptor Signaling Pathway Involved In Heart Development
0	GO:0006884	Cell Volume Homeostasis
0	GO:0016998	Cell Wall Macromolecule Catabolic Process

0	GO:0044036	Cell Wall Macromolecule Metabolic Process
0	GO:0071554	Cell Wall Organization Or Biogenesis
0	GO:0005913	Cell-Cell Adherens Junction
0	GO:0016337	Cell-Cell Adhesion
0	GO:0033631	Cell-Cell Adhesion Mediated By Integrin
0	GO:0044291	Cell-Cell Contact Zone
0	GO:0005911	Cell-Cell Junction
0	GO:0007043	Cell-Cell Junction Assembly
0	GO:0045216	Cell-Cell Junction Organization
0	GO:0009988	Cell-Cell Recognition
0	GO:0045168	Cell-Cell Signaling Involved In Cell Fate Commitment
0	GO:0007160	Cell-Matrix Adhesion
0	GO:0005924	Cell-Substrate Adherens Junction
0	GO:0031589	Cell-Substrate Adhesion
0	GO:0030055	Cell-Substrate Junction
0	GO:0007044	Cell-Substrate Junction Assembly
0	GO:0006081	Cellular Aldehyde Metabolic Process
0	GO:0043449	Cellular Alkene Metabolic Process
0	GO:0043603	Cellular Amide Metabolic Process
0	GO:0044106	Cellular Amine Metabolic Process
0	GO:0008652	Cellular Amino Acid Biosynthetic Process
0	GO:0009063	Cellular Amino Acid Catabolic Process
0	GO:0006520	Cellular Amino Acid Metabolic Process
0	GO:0030002	Cellular Anion Homeostasis
0	GO:0006725	Cellular Aromatic Compound Metabolic Process
0	GO:0042401	Cellular Biogenic Amine Biosynthetic Process
0	GO:0042402	Cellular Biogenic Amine Catabolic Process
0	GO:0006576	Cellular Biogenic Amine Metabolic Process
0	GO:0006874	Cellular Calcium Ion Homeostasis
0	GO:0034637	Cellular Carbohydrate Biosynthetic Process
0	GO:0044275	Cellular Carbohydrate Catabolic Process
0	GO:0030003	Cellular Cation Homeostasis
0	GO:0010927	Cellular Component Assembly Involved In Morphogenesis
0	GO:0071843	Cellular Component Biogenesis At Cellular Level
0	GO:0022411	Cellular Component Disassembly
0	GO:0071845	Cellular Component Disassembly At Cellular Level
0	GO:0006921	Cellular Component Disassembly Involved In Apoptotic Process
0	GO:0043954	Cellular Component Maintenance
0	GO:0006878	Cellular Copper Ion Homeostasis
0	GO:0006968	Cellular Defense Response
0	GO:0072503	Cellular Divalent Inorganic Cation Homeostasis
0	GO:0045123	Cellular Extravasation
0	GO:0006073	Cellular Glucan Metabolic Process
0	GO:0001678	Cellular Glucose Homeostasis
0	GO:0034754	Cellular Hormone Metabolic Process
0	GO:0006873	Cellular Ion Homeostasis
0	GO:0006879	Cellular Iron Ion Homeostasis
0	GO:0044242	Cellular Lipid Catabolic Process
0	GO:0034622	Cellular Macromolecular Complex Assembly
0	GO:0034623	Cellular Macromolecular Complex Disassembly
0	GO:0006944	Cellular Membrane Fusion
0	GO:0043094	Cellular Metabolic Compound Salvage
0	GO:0006875	Cellular Metal Ion Homeostasis
0	GO:0042398	Cellular Modified Amino Acid Biosynthetic Process
0	GO:0006575	Cellular Modified Amino Acid Metabolic Process
0	GO:0030004	Cellular Monovalent Inorganic Cation Homeostasis

0	GO:0033059	Cellular Pigmentation
0	GO:0033692	Cellular Polysaccharide Biosynthetic Process
0	GO:0044247	Cellular Polysaccharide Catabolic Process
0	GO:0044264	Cellular Polysaccharide Metabolic Process
1	GO:0071804	Cellular Potassium Ion Transport
0	GO:0048610	Cellular Process Involved In Reproduction
0	GO:0022412	Cellular Process Involved In Reproduction In Multicellular Organism
0	GO:0044257	Cellular Protein Catabolic Process
0	GO:0043623	Cellular Protein Complex Assembly
0	GO:0043624	Cellular Protein Complex Disassembly
0	GO:0045333	Cellular Respiration
0	GO:0071214	Cellular Response To Abiotic Stimulus
0	GO:0071229	Cellular Response To Acid
0	GO:0071418	Cellular Response To Amine Stimulus
0	GO:0071230	Cellular Response To Amino Acid Stimulus
0	GO:0071216	Cellular Response To Biotic Stimulus
0	GO:0071277	Cellular Response To Calcium Ion
0	GO:0071320	Cellular Response To Camp
0	GO:0071322	Cellular Response To Carbohydrate Stimulus
0	GO:0071384	Cellular Response To Corticosteroid Stimulus
0	GO:0071345	Cellular Response To Cytokine Stimulus
0	GO:0071549	Cellular Response To Dexamethasone Stimulus
0	GO:0035690	Cellular Response To Drug
0	GO:0071359	Cellular Response To Dsrna
0	GO:0071495	Cellular Response To Endogenous Stimulus
0	GO:0071391	Cellular Response To Estrogen Stimulus
0	GO:0071496	Cellular Response To External Stimulus
0	GO:0031668	Cellular Response To Extracellular Stimulus
0	GO:0044344	Cellular Response To Fibroblast Growth Factor Stimulus
0	GO:0071377	Cellular Response To Glucagon Stimulus
0	GO:0071385	Cellular Response To Glucocorticoid Stimulus
0	GO:0042149	Cellular Response To Glucose Starvation
0	GO:0071333	Cellular Response To Glucose Stimulus
0	GO:0071371	Cellular Response To Gonadotropin Stimulus
0	GO:0071363	Cellular Response To Growth Factor Stimulus
0	GO:0071378	Cellular Response To Growth Hormone Stimulus
0	GO:0034605	Cellular Response To Heat
0	GO:0071331	Cellular Response To Hexose Stimulus
0	GO:0032870	Cellular Response To Hormone Stimulus
0	GO:0070301	Cellular Response To Hydrogen Peroxide
0	GO:0071456	Cellular Response To Hypoxia
0	GO:0071241	Cellular Response To Inorganic Substance
0	GO:0032869	Cellular Response To Insulin Stimulus
0	GO:0071346	Cellular Response To Interferon-Gamma
0	GO:0071347	Cellular Response To Interleukin-1
0	GO:0071479	Cellular Response To Ionizing Radiation
0	GO:0071482	Cellular Response To Light Stimulus
0	GO:0071396	Cellular Response To Lipid
0	GO:0071222	Cellular Response To Lipopolysaccharide
0	GO:0071285	Cellular Response To Lithium Ion
0	GO:0071260	Cellular Response To Mechanical Stimulus
0	GO:0071248	Cellular Response To Metal Ion
0	GO:0071219	Cellular Response To Molecule Of Bacterial Origin
0	GO:0071326	Cellular Response To Monosaccharide Stimulus
0	GO:0031670	Cellular Response To Nutrient
0	GO:0031669	Cellular Response To Nutrient Levels

0	GO:0071407	Cellular Response To Organic Cyclic Compound
0	GO:0071417	Cellular Response To Organic Nitrogen
0	GO:0034599	Cellular Response To Oxidative Stress
0	GO:0071453	Cellular Response To Oxygen Levels
0	GO:0071450	Cellular Response To Oxygen Radical
0	GO:0071375	Cellular Response To Peptide Hormone Stimulus
0	GO:0071478	Cellular Response To Radiation
0	GO:0034614	Cellular Response To Reactive Oxygen Species
0	GO:0071300	Cellular Response To Retinoic Acid
0	GO:0009267	Cellular Response To Starvation
0	GO:0071383	Cellular Response To Steroid Hormone Stimulus
0	GO:0071451	Cellular Response To Superoxide
0	GO:0035967	Cellular Response To Topologically Incorrect Protein
0	GO:0071560	Cellular Response To Transforming Growth Factor Beta Stimulus
0	GO:0071356	Cellular Response To Tumor Necrosis Factor
0	GO:0071357	Cellular Response To Type I Interferon
0	GO:0034620	Cellular Response To Unfolded Protein
0	GO:0034644	Cellular Response To Uv
0	GO:0035924	Cellular Response To Vascular Endothelial Growth Factor Stimulus
0	GO:0071295	Cellular Response To Vitamin
0	GO:0071299	Cellular Response To Vitamin A
0	GO:0071305	Cellular Response To Vitamin D
0	GO:0071466	Cellular Response To Xenobiotic Stimulus
0	GO:0090398	Cellular Senescence
0	GO:0006882	Cellular Zinc Ion Homeostasis
0	GO:0034080	Cenh3-Containing Nucleosome Assembly At Centromere
1	GO:0022010	Central Nervous System Myelination
1	GO:0021955	Central Nervous System Neuron Axonogenesis
1	GO:0021954	Central Nervous System Neuron Development
1	GO:0021953	Central Nervous System Neuron Differentiation
1	GO:0021952	Central Nervous System Projection Neuron Axonogenesis
0	GO:0005814	Centriole
0	GO:0007099	Centriole Replication
0	GO:0034508	Centromere Complex Assembly
0	GO:0005721	Centromeric Heterochromatin
0	GO:0005813	Centrosome
0	GO:0007098	Centrosome Cycle
0	GO:0051298	Centrosome Duplication
0	GO:0051297	Centrosome Organization
0	GO:0046513	Ceramide Biosynthetic Process
0	GO:0006672	Ceramide Metabolic Process
1	GO:0021695	Cerebellar Cortex Development
1	GO:0021697	Cerebellar Cortex Formation
1	GO:0021696	Cerebellar Cortex Morphogenesis
1	GO:0021680	Cerebellar Purkinje Cell Layer Development
1	GO:0021549	Cerebellum Development
1	GO:0021587	Cerebellum Morphogenesis
1	GO:0021795	Cerebral Cortex Cell Migration
1	GO:0021987	Cerebral Cortex Development
1	GO:0021895	Cerebral Cortex Neuron Differentiation
1	GO:0021799	Cerebral Cortex Radially Oriented Cell Migration
0	GO:0030553	Cgmp Binding
0	GO:0006182	Cgmp Biosynthetic Process
0	GO:0046068	Cgmp Metabolic Process
0	GO:0019934	Cgmp-Mediated Signaling
1	GO:0015267	Channel Activity

1	GO:0016248	Channel Inhibitor Activity
1	GO:0016247	Channel Regulator Activity
0	GO:0051087	Chaperone Binding
0	GO:0051085	Chaperone Mediated Protein Folding Requiring Cofactor
0	GO:0051131	Chaperone-Mediated Protein Complex Assembly
0	GO:0061077	Chaperone-Mediated Protein Folding
0	GO:0042056	Chemoattractant Activity
0	GO:0008009	Chemokine Activity
0	GO:0042033	Chemokine Biosynthetic Process
0	GO:0050755	Chemokine Metabolic Process
0	GO:0032602	Chemokine Production
0	GO:0004950	Chemokine Receptor Activity
0	GO:0042379	Chemokine Receptor Binding
0	GO:0070098	Chemokine-Mediated Signaling Pathway
0	GO:0005254	Chloride Channel Activity
0	GO:0034707	Chloride Channel Complex
0	GO:0015108	Chloride Transmembrane Transporter Activity
0	GO:0006821	Chloride Transport
0	GO:0015485	Cholesterol Binding
0	GO:0006695	Cholesterol Biosynthetic Process
0	GO:0006707	Cholesterol Catabolic Process
0	GO:0033344	Cholesterol Efflux
0	GO:0034435	Cholesterol Esterification
0	GO:0042632	Cholesterol Homeostasis
0	GO:0008203	Cholesterol Metabolic Process
0	GO:0010878	Cholesterol Storage
0	GO:0030301	Cholesterol Transport
0	GO:0017127	Cholesterol Transporter Activity
0	GO:0002063	Chondrocyte Development
0	GO:0002062	Chondrocyte Differentiation
0	GO:0030204	Chondroitin Sulfate Metabolic Process
0	GO:0050650	Chondroitin Sulfate Proteoglycan Biosynthetic Process
0	GO:0050654	Chondroitin Sulfate Proteoglycan Metabolic Process
0	GO:0043009	Chordate Embryonic Development
0	GO:0000785	Chromatin
0	GO:0031497	Chromatin Assembly
0	GO:0006333	Chromatin Assembly Or Disassembly
0	GO:0003682	Chromatin Binding
0	GO:0031498	Chromatin Disassembly
0	GO:0031490	Chromatin Dna Binding
0	GO:0016568	Chromatin Modification
0	GO:0006325	Chromatin Organization
0	GO:0006338	Chromatin Remodeling
0	GO:0031055	Chromatin Remodeling At Centromere
0	GO:0016585	Chromatin Remodeling Complex
0	GO:0006342	Chromatin Silencing
0	GO:0044427	Chromosomal Part
0	GO:0030261	Chromosome Condensation
0	GO:0050000	Chromosome Localization
0	GO:0070192	Chromosome Organization Involved In Meiosis
0	GO:0007059	Chromosome Segregation
0	GO:0000775	Chromosome, Centromeric Region
0	GO:0000781	Chromosome, Telomeric Region
0	GO:0002544	Chronic Inflammatory Response
0	GO:0001539	Ciliary Or Flagellar Motility
0	GO:0035253	Ciliary Rootlet

0	GO:0005929	Cilium
0	GO:0042384	Cilium Assembly
0	GO:0035085	Cilium Axoneme
0	GO:0060271	Cilium Morphogenesis
0	GO:0044441	Cilium Part
1	GO:0048512	Circadian Behavior
1	GO:0007623	Circadian Rhythm
1	GO:0042745	Circadian Sleep/Wake Cycle
1	GO:0022410	Circadian Sleep/Wake Cycle Process
1	GO:0050802	Circadian Sleep/Wake Cycle, Sleep
1	GO:0003013	Circulatory System Process
0	GO:0005801	Cis-Golgi Network
0	GO:0016859	Cis-Trans Isomerase Activity
0	GO:0030131	Clathrin Adaptor Complex
0	GO:0030276	Clathrin Binding
0	GO:0030118	Clathrin Coat
0	GO:0030132	Clathrin Coat Of Coated Pit
0	GO:0030128	Clathrin Coat Of Endocytic Vesicle
0	GO:0030130	Clathrin Coat Of Trans-Golgi Network Vesicle
0	GO:0030665	Clathrin Coated Vesicle Membrane
0	GO:0060198	Clathrin Sculpted Vesicle
0	GO:0030125	Clathrin Vesicle Coat
0	GO:0045334	Clathrin-Coated Endocytic Vesicle
0	GO:0030669	Clathrin-Coated Endocytic Vesicle Membrane
0	GO:0030136	Clathrin-Coated Vesicle
0	GO:0032154	Cleavage Furrow
0	GO:0070410	Co-Smad Binding
0	GO:0016289	Coa Hydrolase Activity
0	GO:0050817	Coagulation
0	GO:0048475	Coated Membrane
0	GO:0005905	Coated Pit
0	GO:0030135	Coated Vesicle
0	GO:0030662	Coated Vesicle Membrane
0	GO:0090102	Cochlea Development
0	GO:0090103	Cochlea Morphogenesis
0	GO:0015936	Coenzyme A Metabolic Process
0	GO:0050662	Coenzyme Binding
0	GO:0009108	Coenzyme Biosynthetic Process
0	GO:0009109	Coenzyme Catabolic Process
0	GO:0006732	Coenzyme Metabolic Process
0	GO:0048037	Cofactor Binding
0	GO:0051188	Cofactor Biosynthetic Process
0	GO:0051187	Cofactor Catabolic Process
0	GO:0051186	Cofactor Metabolic Process
0	GO:0051181	Cofactor Transport
0	GO:0051184	Cofactor Transporter Activity
0	GO:0050890	Cognition
0	GO:0008278	Cohesin Complex
0	GO:0005581	Collagen
0	GO:0005518	Collagen Binding
0	GO:0032964	Collagen Biosynthetic Process
0	GO:0030574	Collagen Catabolic Process
0	GO:0030199	Collagen Fibril Organization
0	GO:0032963	Collagen Metabolic Process
0	GO:0002065	Columnar/Cuboidal Epithelial Cell Differentiation
1	GO:0043218	Compact Myelin

0	GO:0006956	Complement Activation
0	GO:0006957	Complement Activation, Alternative Pathway
0	GO:0006958	Complement Activation, Classical Pathway
0	GO:0000793	Condensed Chromosome
0	GO:0000777	Condensed Chromosome Kinetochore
0	GO:0000940	Condensed Chromosome Outer Kinetochore
0	GO:0000779	Condensed Chromosome, Centromeric Region
0	GO:0000794	Condensed Nuclear Chromosome
0	GO:0000780	Condensed Nuclear Chromosome, Centromeric Region
0	GO:0005922	Connexon Complex
0	GO:0043292	Contractile Fiber
0	GO:0044449	Contractile Fiber Part
0	GO:0060026	Convergent Extension
0	GO:0030663	Copi Coated Vesicle Membrane
0	GO:0048205	Copi Coating Of Golgi Vesicle
0	GO:0030126	Copi Vesicle Coat
0	GO:0030137	Copi-Coated Vesicle
0	GO:0035964	Copi-Coated Vesicle Budding
0	GO:0005507	Copper Ion Binding
0	GO:0055070	Copper Ion Homeostasis
0	GO:0006825	Copper Ion Transport
0	GO:0007620	Copulation
0	GO:0001047	Core Promoter Binding
0	GO:0001159	Core Promoter Proximal Region Dna Binding
0	GO:0000987	Core Promoter Proximal Region Sequence-Specific Dna Binding
0	GO:0001046	Core Promoter Sequence-Specific Dna Binding
0	GO:0015026	Coreceptor Activity
0	GO:0001533	Cornified Envelope
0	GO:0060976	Coronary Vasculature Development
0	GO:0030864	Cortical Actin Cytoskeleton
0	GO:0030866	Cortical Actin Cytoskeleton Organization
0	GO:0030863	Cortical Cytoskeleton
0	GO:0030865	Cortical Cytoskeleton Organization
0	GO:0031958	Corticosteroid Receptor Signaling Pathway
0	GO:0043034	Costamere
0	GO:0006613	Cotranslational Protein Targeting To Membrane
0	GO:0016569	Covalent Chromatin Modification
1	GO:0021545	Cranial Nerve Development
1	GO:0021602	Cranial Nerve Morphogenesis
1	GO:0060363	Cranial Suture Morphogenesis
0	GO:0097094	Craniofacial Suture Morphogenesis
0	GO:0080008	Cul4 Ring Ubiquitin Ligase Complex
0	GO:0031461	Cullin-Ring Ubiquitin Ligase Complex
0	GO:0009975	Cyclase Activity
0	GO:0030551	Cyclic Nucleotide Binding
0	GO:0009190	Cyclic Nucleotide Biosynthetic Process
0	GO:0009214	Cyclic Nucleotide Catabolic Process
0	GO:0009187	Cyclic Nucleotide Metabolic Process
0	GO:0004690	Cyclic Nucleotide-Dependent Protein Kinase Activity
0	GO:0004112	Cyclic-Nucleotide Phosphodiesterase Activity
0	GO:0019935	Cyclic-Nucleotide-Mediated Signaling
0	GO:0030332	Cyclin Binding
0	GO:0004693	Cyclin-Dependent Protein Kinase Activity
0	GO:0000307	Cyclin-Dependent Protein Kinase Holoenzyme Complex
0	GO:0004861	Cyclin-Dependent Protein Kinase Inhibitor Activity
0	GO:0016538	Cyclin-Dependent Protein Kinase Regulator Activity

0	GO:0008656	Cysteine-Type Endopeptidase Activator Activity Involved In Apoptotic Process
0	GO:0004197	Cysteine-Type Endopeptidase Activity
0	GO:0004869	Cysteine-Type Endopeptidase Inhibitor Activity
0	GO:0043027	Cysteine-Type Endopeptidase Inhibitor Activity Involved In Apoptotic Process
0	GO:0043028	Cysteine-Type Endopeptidase Regulator Activity Involved In Apoptotic Process
0	GO:0008234	Cysteine-Type Peptidase Activity
0	GO:0004129	Cytochrome-C Oxidase Activity
0	GO:0005125	Cytokine Activity
0	GO:0019955	Cytokine Binding
0	GO:0042089	Cytokine Biosynthetic Process
0	GO:0042107	Cytokine Metabolic Process
0	GO:0001816	Cytokine Production
0	GO:0002367	Cytokine Production Involved In Immune Response
0	GO:0004896	Cytokine Receptor Activity
0	GO:0005126	Cytokine Receptor Binding
0	GO:0050663	Cytokine Secretion
0	GO:0019221	Cytokine-Mediated Signaling Pathway
0	GO:0000910	Cytokinesis
0	GO:0019835	Cytolysis
0	GO:0005868	Cytoplasmic Dynein Complex
0	GO:0060205	Cytoplasmic Membrane-Bounded Vesicle Lumen
0	GO:0005881	Cytoplasmic Microtubule
0	GO:0031122	Cytoplasmic Microtubule Organization
0	GO:0000932	Cytoplasmic Mrna Processing Body
0	GO:0002753	Cytoplasmic Pattern Recognition Receptor Signaling Pathway
0	GO:0051220	Cytoplasmic Sequestering Of Protein
0	GO:0042994	Cytoplasmic Sequestering Of Transcription Factor
0	GO:0010494	Cytoplasmic Stress Granule
0	GO:0030659	Cytoplasmic Vesicle Membrane
0	GO:0044433	Cytoplasmic Vesicle Part
0	GO:0008093	Cytoskeletal Adaptor Activity
0	GO:0007016	Cytoskeletal Anchoring At Plasma Membrane
0	GO:0030705	Cytoskeleton-Dependent Intracellular Transport
0	GO:0051480	Cytosolic Calcium Ion Homeostasis
0	GO:0060401	Cytosolic Calcium Ion Transport
0	GO:0022625	Cytosolic Large Ribosomal Subunit
0	GO:0044445	Cytosolic Part
0	GO:0022626	Cytosolic Ribosome
0	GO:0022627	Cytosolic Small Ribosomal Subunit
0	GO:0003684	Damaged Dna Binding
0	GO:0019213	Deacetylase Activity
0	GO:0019239	Deaminase Activity
0	GO:0005035	Death Receptor Activity
0	GO:0005123	Death Receptor Binding
0	GO:0046697	Decidualization
0	GO:0042742	Defense Response To Bacterium
0	GO:0050832	Defense Response To Fungus
0	GO:0050829	Defense Response To Gram-Negative Bacterium
0	GO:0050830	Defense Response To Gram-Positive Bacterium
0	GO:0051607	Defense Response To Virus
0	GO:0060216	Definitive Hemopoiesis
0	GO:0005251	Delayed Rectifier Potassium Channel Activity
0	GO:0032451	Demethylase Activity
0	GO:0070988	Demethylation
1	GO:0030425	Dendrite
1	GO:0032839	Dendrite Cytoplasm

1	GO:0016358	Dendrite Development
1	GO:0048813	Dendrite Morphogenesis
1	GO:0002407	Dendritic Cell Chemotaxis
1	GO:0043198	Dendritic Shaft
1	GO:0043197	Dendritic Spine
1	GO:0060996	Dendritic Spine Development
1	GO:0044327	Dendritic Spine Head
1	GO:0060997	Dendritic Spine Morphogenesis
1	GO:0097061	Dendritic Spine Organization
0	GO:0004536	Deoxyribonuclease Activity
0	GO:0009263	Deoxyribonucleotide Biosynthetic Process
0	GO:0009264	Deoxyribonucleotide Catabolic Process
0	GO:0009262	Deoxyribonucleotide Metabolic Process
0	GO:0016311	Dephosphorylation
0	GO:0002029	Desensitization Of G-Protein Coupled Receptor Protein Signaling Pathway
0	GO:0030057	Desmosome
0	GO:0009582	Detection Of Abiotic Stimulus
0	GO:0016045	Detection Of Bacterium
0	GO:0009595	Detection Of Biotic Stimulus
0	GO:0009593	Detection Of Chemical Stimulus
0	GO:0050907	Detection Of Chemical Stimulus Involved In Sensory Perception
0	GO:0050911	Detection Of Chemical Stimulus Involved In Sensory Perception Of Smell
0	GO:0050912	Detection Of Chemical Stimulus Involved In Sensory Perception Of Taste
0	GO:0009581	Detection Of External Stimulus
0	GO:0009583	Detection Of Light Stimulus
0	GO:0050962	Detection Of Light Stimulus Involved In Sensory Perception
0	GO:0050908	Detection Of Light Stimulus Involved In Visual Perception
0	GO:0050982	Detection Of Mechanical Stimulus
0	GO:0050974	Detection Of Mechanical Stimulus Involved In Sensory Perception
0	GO:0051606	Detection Of Stimulus
0	GO:0050906	Detection Of Stimulus Involved In Sensory Perception
0	GO:0009584	Detection Of Visible Light
0	GO:0008340	Determination Of Adult Lifespan
0	GO:0009855	Determination Of Bilateral Symmetry
0	GO:0061371	Determination Of Heart Left/Right Asymmetry
0	GO:0007368	Determination Of Left/Right Symmetry
0	GO:0046545	Development Of Primary Female Sexual Characteristics
0	GO:0046546	Development Of Primary Male Sexual Characteristics
0	GO:0045137	Development Of Primary Sexual Characteristics
0	GO:0045136	Development Of Secondary Sexual Characteristics
0	GO:0048588	Developmental Cell Growth
0	GO:0048589	Developmental Growth
0	GO:0060560	Developmental Growth Involved In Morphogenesis
0	GO:0031128	Developmental Induction
0	GO:0021700	Developmental Maturation
0	GO:0048066	Developmental Pigmentation
0	GO:0003006	Developmental Process Involved In Reproduction
0	GO:0010623	Developmental Programmed Cell Death
0	GO:0004143	Diacylglycerol Kinase Activity
0	GO:0043648	Dicarboxylic Acid Metabolic Process
0	GO:0005310	Dicarboxylic Acid Transmembrane Transporter Activity
0	GO:0006835	Dicarboxylic Acid Transport
0	GO:0060600	Dichotomous Subdivision Of An Epithelial Terminal Unit
1	GO:0021536	Diencephalon Development
0	GO:0007586	Digestion
0	GO:0055123	Digestive System Development

0	GO:0022600	Digestive System Process
0	GO:0048565	Digestive Tract Development
0	GO:0048546	Digestive Tract Morphogenesis
0	GO:0034312	Diol Biosynthetic Process
0	GO:0034311	Diol Metabolic Process
0	GO:0051213	Dioxygenase Activity
0	GO:0016805	Dipeptidase Activity
0	GO:0008239	Dipeptidyl-Peptidase Activity
0	GO:0015036	Disulfide Oxidoreductase Activity
0	GO:0016101	Diterpenoid Metabolic Process
0	GO:0072507	Divalent Inorganic Cation Homeostasis
0	GO:0072509	Divalent Inorganic Cation Transmembrane Transporter Activity
0	GO:0072511	Divalent Inorganic Cation Transport
0	GO:0070838	Divalent Metal Ion Transport
0	GO:0006305	Dna Alkylation
0	GO:0008301	Dna Binding, Bending
0	GO:0071897	Dna Biosynthetic Process
0	GO:0006308	Dna Catabolic Process
0	GO:0000737	Dna Catabolic Process, Endonucleolytic
0	GO:0071103	Dna Conformation Change
0	GO:0000077	Dna Damage Checkpoint
0	GO:0030330	Dna Damage Response, Signal Transduction By P53 Class Mediator
0	GO:0006977	Dna Damage Response, Signal Transduction By P53 Class Mediator Resulting In Cell Cycle Arrest
0	GO:0042771	Dna Damage Response, Signal Transduction By P53 Class Mediator Resulting In Induction Of Apoptosis
0	GO:0006978	Dna Damage Response, Signal Transduction By P53 Class Mediator Resulting In Transcription Of P21 Class Mediator
0	GO:0008630	Dna Damage Response, Signal Transduction Resulting In Induction Of Apoptosis
0	GO:0042772	Dna Damage Response, Signal Transduction Resulting In Transcription
0	GO:0035510	Dna Dealkylation
0	GO:0080111	Dna Demethylation
0	GO:0032508	Dna Duplex Unwinding
0	GO:0044349	Dna Excision
0	GO:0032392	Dna Geometric Change
0	GO:0003678	Dna Helicase Activity
0	GO:0033202	Dna Helicase Complex
0	GO:0015074	Dna Integration
0	GO:0031570	Dna Integrity Checkpoint
0	GO:0006266	Dna Ligation
0	GO:0006306	Dna Methylation
0	GO:0043046	Dna Methylation Involved In Gamete Generation
0	GO:0006304	Dna Modification
0	GO:0019104	Dna N-Glycosylase Activity
0	GO:0006323	Dna Packaging
0	GO:0034061	Dna Polymerase Activity
0	GO:0042575	Dna Polymerase Complex
0	GO:0006310	Dna Recombination
0	GO:0006281	Dna Repair
0	GO:0006260	Dna Replication
0	GO:0000076	Dna Replication Checkpoint
0	GO:0006336	Dna Replication-Independent Nucleosome Assembly
0	GO:0034724	Dna Replication-Independent Nucleosome Organization
0	GO:0000217	Dna Secondary Structure Binding
0	GO:0022616	Dna Strand Elongation
0	GO:0006271	Dna Strand Elongation Involved In Dna Replication
0	GO:0003906	Dna-(Apurinic Or Apyrimidinic Site) Lyase Activity
0	GO:0008094	Dna-Dependent Atpase Activity
0	GO:0006261	Dna-Dependent Dna Replication

0	GO:0006270	Dna-Dependent Dna Replication Initiation
0	GO:0003887	Dna-Directed Dna Polymerase Activity
0	GO:0003899	Dna-Directed Rna Polymerase Activity
0	GO:0000428	Dna-Directed Rna Polymerase Complex
0	GO:0005665	Dna-Directed Rna Polymerase Ii, Core Complex
0	GO:0016591	Dna-Directed Rna Polymerase Ii, Holoenzyme
0	GO:0006488	Dolichol-Linked Oligosaccharide Biosynthetic Process
1	GO:0035240	Dopamine Binding
1	GO:0042417	Dopamine Metabolic Process
1	GO:0050780	Dopamine Receptor Binding
1	GO:0007212	Dopamine Receptor Signaling Pathway
1	GO:0014046	Dopamine Secretion
1	GO:0015872	Dopamine Transport
1	GO:0021516	Dorsal Spinal Cord Development
0	GO:0009950	Dorsal/Ventral Axis Specification
0	GO:0021904	Dorsal/Ventral Neural Tube Patterning
0	GO:0009953	Dorsal/Ventral Pattern Formation
0	GO:0006302	Double-Strand Break Repair
0	GO:0000724	Double-Strand Break Repair Via Homologous Recombination
0	GO:0006303	Double-Strand Break Repair Via Nonhomologous End Joining
0	GO:0003690	Double-Stranded Dna Binding
0	GO:0003725	Double-Stranded Rna Binding
0	GO:0008144	Drug Binding
0	GO:0042737	Drug Catabolic Process
0	GO:0017144	Drug Metabolic Process
0	GO:0015238	Drug Transmembrane Transporter Activity
0	GO:0015893	Drug Transport
0	GO:0031050	Dsrna Fragmentation
0	GO:0008831	Dtdp-4-Dehydrorhamnose Reductase Activity
0	GO:0045502	Dynein Binding
0	GO:0030286	Dynein Complex
0	GO:0016010	Dystrophin-Associated Glycoprotein Complex
0	GO:0070888	E-Box Binding
0	GO:0043583	Ear Development
0	GO:0042471	Ear Morphogenesis
0	GO:0005769	Early Endosome
0	GO:0031901	Early Endosome Membrane
0	GO:0045022	Early Endosome To Late Endosome Transport
0	GO:0042755	Eating Behavior
0	GO:0007398	Ectoderm Development
0	GO:0071696	Ectodermal Placode Development
0	GO:0060788	Ectodermal Placode Formation
0	GO:0071697	Ectodermal Placode Morphogenesis
0	GO:0009055	Electron Carrier Activity
0	GO:0022900	Electron Transport Chain
0	GO:0007204	Elevation Of Cytosolic Calcium Ion Concentration
0	GO:0051482	Elevation Of Cytosolic Calcium Ion Concentration Involved In Phospholipase C-Activating G-Protein Coupled Signaling Pathway
0	GO:0009792	Embryo Development Ending In Birth Or Egg Hatching
0	GO:0007566	Embryo Implantation
0	GO:0035113	Embryonic Appendage Morphogenesis
0	GO:0000578	Embryonic Axis Specification
0	GO:0031076	Embryonic Camera-Type Eye Development
0	GO:0048596	Embryonic Camera-Type Eye Morphogenesis
0	GO:0048701	Embryonic Cranial Skeleton Morphogenesis
0	GO:0048566	Embryonic Digestive Tract Development
0	GO:0048557	Embryonic Digestive Tract Morphogenesis

0	GO:0042733	Embryonic Digit Morphogenesis
0	GO:0001838	Embryonic Epithelial Tube Formation
0	GO:0048048	Embryonic Eye Morphogenesis
0	GO:0048617	Embryonic Foregut Morphogenesis
0	GO:0035115	Embryonic Forelimb Morphogenesis
0	GO:0035050	Embryonic Heart Tube Development
0	GO:0003143	Embryonic Heart Tube Morphogenesis
0	GO:0035162	Embryonic Hemopoiesis
0	GO:0035116	Embryonic Hindlimb Morphogenesis
0	GO:0030326	Embryonic Limb Morphogenesis
0	GO:0048598	Embryonic Morphogenesis
0	GO:0048568	Embryonic Organ Development
0	GO:0048562	Embryonic Organ Morphogenesis
0	GO:0009880	Embryonic Pattern Specification
0	GO:0001892	Embryonic Placenta Development
0	GO:0060669	Embryonic Placenta Morphogenesis
0	GO:0072498	Embryonic Skeletal Joint Development
0	GO:0048706	Embryonic Skeletal System Development
0	GO:0048704	Embryonic Skeletal System Morphogenesis
0	GO:0048703	Embryonic Viscerocranium Morphogenesis
0	GO:0003197	Endocardial Cushion Development
0	GO:0003203	Endocardial Cushion Morphogenesis
0	GO:0003416	Endochondral Bone Growth
0	GO:0060350	Endochondral Bone Morphogenesis
0	GO:0001958	Endochondral Ossification
0	GO:0060986	Endocrine Hormone Secretion
0	GO:0031018	Endocrine Pancreas Development
0	GO:0050886	Endocrine Process
0	GO:0035270	Endocrine System Development
0	GO:0032456	Endocytic Recycling
0	GO:0030139	Endocytic Vesicle
0	GO:0030666	Endocytic Vesicle Membrane
0	GO:0006897	Endocytosis
0	GO:0004520	Endodeoxyribonuclease Activity
0	GO:0016888	Endodeoxyribonuclease Activity, Producing 5'-Phosphomonoesters
0	GO:0007492	Endoderm Development
0	GO:0001706	Endoderm Formation
0	GO:0004519	Endonuclease Activity
0	GO:0016894	Endonuclease Activity, Active With Either Ribo- Or Deoxyribonucleic Acids And Producing 3'-Phosphomonoesters
0	GO:0016893	Endonuclease Activity, Active With Either Ribo- Or Deoxyribonucleic Acids And Producing 5'-Phosphomonoesters
0	GO:0004175	Endopeptidase Activity
0	GO:0004866	Endopeptidase Inhibitor Activity
0	GO:0061135	Endopeptidase Regulator Activity
0	GO:0032469	Endoplasmic Reticulum Calcium Ion Homeostasis
0	GO:0005788	Endoplasmic Reticulum Lumen
0	GO:0007029	Endoplasmic Reticulum Organization
0	GO:0030968	Endoplasmic Reticulum Unfolded Protein Response
0	GO:0005793	Endoplasmic Reticulum-Golgi Intermediate Compartment
0	GO:0033116	Endoplasmic Reticulum-Golgi Intermediate Compartment Membrane
0	GO:0004521	Endoribonuclease Activity
0	GO:0016891	Endoribonuclease Activity, Producing 5'-Phosphomonoesters
0	GO:0044440	Endosomal Part
0	GO:0016197	Endosomal Transport
0	GO:0005768	Endosome
0	GO:0010008	Endosome Membrane
0	GO:0007032	Endosome Organization

0	GO:0008333	Endosome To Lysosome Transport
0	GO:0001885	Endothelial Cell Development
0	GO:0045446	Endothelial Cell Differentiation
0	GO:0043542	Endothelial Cell Migration
0	GO:0001935	Endothelial Cell Proliferation
0	GO:0003158	Endothelium Development
0	GO:0015988	Energy Coupled Proton Transport, Against Electrochemical Gradient
0	GO:0015985	Energy Coupled Proton Transport, Down Electrochemical Gradient
0	GO:0015980	Energy Derivation By Oxidation Of Organic Compounds
0	GO:0006112	Energy Reserve Metabolic Process
0	GO:0035326	Enhancer Binding
0	GO:0001158	Enhancer Sequence-Specific Dna Binding
1	GO:0007272	Ensheathment Of Neurons
1	GO:0048484	Enteric Nervous System Development
0	GO:0051806	Entry Into Cell Of Other Organism Involved In Symbiotic Interaction
0	GO:0044409	Entry Into Host
0	GO:0030260	Entry Into Host Cell
0	GO:0051828	Entry Into Other Organism Involved In Symbiotic Interaction
0	GO:0008047	Enzyme Activator Activity
0	GO:0004857	Enzyme Inhibitor Activity
0	GO:0005003	Ephrin Receptor Activity
0	GO:0046875	Ephrin Receptor Binding
0	GO:0048013	Ephrin Receptor Signaling Pathway
0	GO:0009913	Epidermal Cell Differentiation
0	GO:0005154	Epidermal Growth Factor Receptor Binding
0	GO:0007173	Epidermal Growth Factor Receptor Signaling Pathway
0	GO:0008544	Epidermis Development
0	GO:0048730	Epidermis Morphogenesis
0	GO:0002064	Epithelial Cell Development
0	GO:0030855	Epithelial Cell Differentiation
0	GO:0035850	Epithelial Cell Differentiation Involved In Kidney Development
0	GO:0060742	Epithelial Cell Differentiation Involved In Prostate Gland Development
0	GO:0002070	Epithelial Cell Maturation
0	GO:0010631	Epithelial Cell Migration
0	GO:0003382	Epithelial Cell Morphogenesis
0	GO:0050673	Epithelial Cell Proliferation
0	GO:0060767	Epithelial Cell Proliferation Involved In Prostate Gland Development
0	GO:0090136	Epithelial Cell-Cell Adhesion
0	GO:0010669	Epithelial Structure Maintenance
0	GO:0001837	Epithelial To Mesenchymal Transition
0	GO:0060441	Epithelial Tube Branching Involved In Lung Morphogenesis
0	GO:0072175	Epithelial Tube Formation
0	GO:0060562	Epithelial Tube Morphogenesis
0	GO:0060429	Epithelium Development
0	GO:0090132	Epithelium Migration
0	GO:0030134	Er To Golgi Transport Vesicle
0	GO:0012507	Er To Golgi Transport Vesicle Membrane
0	GO:0006888	Er To Golgi Vesicle-Mediated Transport
0	GO:0030433	Er-Associated Protein Catabolic Process
0	GO:0006984	Er-Nucleus Signaling Pathway
0	GO:0070371	Erk1 And Erk2 Cascade
0	GO:0048821	Erythrocyte Development
0	GO:0030218	Erythrocyte Differentiation
0	GO:0034101	Erythrocyte Homeostasis
0	GO:0030010	Establishment Of Cell Polarity
0	GO:0051303	Establishment Of Chromosome Localization

0	GO:0032401	Establishment Of Melanosome Localization
0	GO:0051654	Establishment Of Mitochondrion Localization
0	GO:0040001	Establishment Of Mitotic Spindle Localization
0	GO:0000132	Establishment Of Mitotic Spindle Orientation
0	GO:0051656	Establishment Of Organelle Localization
0	GO:0051905	Establishment Of Pigment Granule Localization
0	GO:0001736	Establishment Of Planar Polarity
0	GO:0090177	Establishment Of Planar Polarity Involved In Neural Tube Closure
0	GO:0042249	Establishment Of Planar Polarity Of Embryonic Epithelium
0	GO:0090150	Establishment Of Protein Localization In Membrane
0	GO:0072655	Establishment Of Protein Localization In Mitochondrion
0	GO:0090002	Establishment Of Protein Localization In Plasma Membrane
0	GO:0072594	Establishment Of Protein Localization To Organelle
0	GO:0072663	Establishment Of Protein Localization To Peroxisome
0	GO:0051236	Establishment Of Rna Localization
0	GO:0051293	Establishment Of Spindle Localization
0	GO:0051294	Establishment Of Spindle Orientation
0	GO:0007164	Establishment Of Tissue Polarity
0	GO:0051650	Establishment Of Vesicle Localization
0	GO:0035088	Establishment Or Maintenance Of Apical/Basal Cell Polarity
0	GO:0061245	Establishment Or Maintenance Of Bipolar Cell Polarity
0	GO:0007163	Establishment Or Maintenance Of Cell Polarity
0	GO:0045197	Establishment Or Maintenance Of Epithelial Cell Apical/Basal Polarity
0	GO:0004303	Estradiol 17-Beta-Dehydrogenase Activity
0	GO:0008210	Estrogen Metabolic Process
0	GO:0030331	Estrogen Receptor Binding
0	GO:0042439	Ethanolamine-Containing Compound Metabolic Process
0	GO:0043499	Eukaryotic Cell Surface Binding
0	GO:0005852	Eukaryotic Translation Initiation Factor 3 Complex
0	GO:0005231	Excitatory Extracellular Ligand-Gated Ion Channel Activity
1	GO:0060076	Excitatory Synapse
0	GO:0007588	Excretion
0	GO:0010458	Exit From Mitosis
0	GO:0035272	Exocrine System Development
0	GO:0006887	Exocytosis
0	GO:0035145	Exon-Exon Junction Complex
0	GO:0004527	Exonuclease Activity
0	GO:0016796	Exonuclease Activity, Active With Either Ribo- Or Deoxyribonucleic Acids And Producing 5'-Phosphomonoesters
0	GO:0043928	Exonucleolytic Nuclear-Transcribed Mrna Catabolic Process Involved In Deadenylation-Dependent Decay
0	GO:0008238	Exopeptidase Activity
0	GO:0004532	Exoribonuclease Activity
0	GO:0016896	Exoribonuclease Activity, Producing 5'-Phosphomonoesters
0	GO:0000178	Exosome (Rnase Complex)
0	GO:0030312	External Encapsulating Structure
0	GO:0044462	External Encapsulating Structure Part
0	GO:0009897	External Side Of Plasma Membrane
0	GO:0005230	Extracellular Ligand-Gated Ion Channel Activity
0	GO:0031012	Extracellular Matrix
0	GO:0050840	Extracellular Matrix Binding
0	GO:0022617	Extracellular Matrix Disassembly
0	GO:0030198	Extracellular Matrix Organization
0	GO:0044420	Extracellular Matrix Part
0	GO:0005201	Extracellular Matrix Structural Constituent
0	GO:0045226	Extracellular Polysaccharide Biosynthetic Process
0	GO:0046379	Extracellular Polysaccharide Metabolic Process
0	GO:0043062	Extracellular Structure Organization

0	GO:0005234	Extracellular-Glutamate-Gated Ion Channel Activity
0	GO:0031234	Extrinsic To Internal Side Of Plasma Membrane
0	GO:0019898	Extrinsic To Membrane
0	GO:0019897	Extrinsic To Plasma Membrane
0	GO:0001654	Eye Development
0	GO:0048592	Eye Morphogenesis
0	GO:0042462	Eye Photoreceptor Cell Development
0	GO:0001754	Eye Photoreceptor Cell Differentiation
0	GO:0060324	Face Development
0	GO:0060325	Face Morphogenesis
0	GO:0043240	Fanconi Anaemia Nuclear Complex
0	GO:0005916	Fascia Adherens
0	GO:0045444	Fat Cell Differentiation
0	GO:0042362	Fat-Soluble Vitamin Biosynthetic Process
0	GO:0006775	Fat-Soluble Vitamin Metabolic Process
0	GO:0006635	Fatty Acid Beta-Oxidation
0	GO:0033540	Fatty Acid Beta-Oxidation Using Acyl-Coa Oxidase
0	GO:0005504	Fatty Acid Binding
0	GO:0006633	Fatty Acid Biosynthetic Process
0	GO:0009062	Fatty Acid Catabolic Process
0	GO:0015645	Fatty Acid Ligase Activity
0	GO:0006631	Fatty Acid Metabolic Process
0	GO:0019395	Fatty Acid Oxidation
0	GO:0015908	Fatty Acid Transport
0	GO:0000062	Fatty-Acyl-Coa Binding
0	GO:0046949	Fatty-Acyl-Coa Biosynthetic Process
0	GO:0035337	Fatty-Acyl-Coa Metabolic Process
1	GO:0042596	Fear Response
1	GO:0007631	Feeding Behavior
0	GO:0007292	Female Gamete Generation
0	GO:0008585	Female Gonad Development
0	GO:0007143	Female Meiosis
0	GO:0007565	Female Pregnancy
0	GO:0046660	Female Sex Differentiation
0	GO:0015682	Ferric Iron Transport
0	GO:0008198	Ferrous Iron Binding
0	GO:0015093	Ferrous Iron Transmembrane Transporter Activity
0	GO:0015684	Ferrous Iron Transport
0	GO:0009566	Fertilization
0	GO:0001660	Fever Generation
0	GO:0005583	Fibrillar Collagen
0	GO:0042730	Fibrinolysis
0	GO:0017134	Fibroblast Growth Factor Binding
0	GO:0005104	Fibroblast Growth Factor Receptor Binding
0	GO:0008543	Fibroblast Growth Factor Receptor Signaling Pathway
0	GO:0010761	Fibroblast Migration
0	GO:0048144	Fibroblast Proliferation
0	GO:0001968	Fibronectin Binding
0	GO:0031941	Filamentous Actin
0	GO:0030175	Filopodium
0	GO:0046847	Filopodium Assembly
0	GO:0031527	Filopodium Membrane
0	GO:0005528	Fk506 Binding
0	GO:0019861	Flagellum
0	GO:0044460	Flagellum Part
0	GO:0050660	Flavin Adenine Dinucleotide Binding

0	GO:0042044	Fluid Transport
0	GO:0010181	Fmn Binding
0	GO:0090077	Foam Cell Differentiation
0	GO:0005925	Focal Adhesion
0	GO:0048041	Focal Adhesion Assembly
0	GO:0005542	Folic Acid Binding
0	GO:0006760	Folic Acid-Containing Compound Metabolic Process
1	GO:0021885	Forebrain Cell Migration
1	GO:0030900	Forebrain Development
1	GO:0021872	Forebrain Generation Of Neurons
1	GO:0048853	Forebrain Morphogenesis
1	GO:0021879	Forebrain Neuron Differentiation
1	GO:0021871	Forebrain Regionalization
0	GO:0007440	Foregut Morphogenesis
0	GO:0035136	Forelimb Morphogenesis
0	GO:0001704	Formation Of Primary Germ Layer
0	GO:0009378	Four-Way Junction Helicase Activity
0	GO:0005109	Frizzled Binding
0	GO:0006000	Fructose Metabolic Process
0	GO:0006004	Fucose Metabolic Process
0	GO:0008417	Fucosyltransferase Activity
0	GO:0001965	G-Protein Alpha-Subunit Binding
0	GO:0031683	G-Protein Beta/Gamma-Subunit Complex Binding
0	GO:0007213	G-Protein Coupled Acetylcholine Receptor Signaling Pathway
0	GO:0008227	G-Protein Coupled Amine Receptor Activity
0	GO:0001637	G-Protein Coupled Chemoattractant Receptor Activity
0	GO:0007216	G-Protein Coupled Glutamate Receptor Signaling Pathway
0	GO:0001608	G-Protein Coupled Nucleotide Receptor Activity
0	GO:0008528	G-Protein Coupled Peptide Receptor Activity
0	GO:0045028	G-Protein Coupled Purinergic Nucleotide Receptor Activity
0	GO:0004930	G-Protein Coupled Receptor Activity
0	GO:0001664	G-Protein Coupled Receptor Binding
0	GO:0007187	G-Protein Coupled Receptor Signaling Pathway, Coupled To Cyclic Nucleotide Second Messenger
0	GO:0051318	G1 Phase
0	GO:0000080	G1 Phase Of Mitotic Cell Cycle
0	GO:0071779	G1/S Transition Checkpoint
0	GO:0000082	G1/S Transition Of Mitotic Cell Cycle
0	GO:0031576	G2/M Transition Checkpoint
0	GO:0031572	G2/M Transition Dna Damage Checkpoint
0	GO:0000086	G2/M Transition Of Mitotic Cell Cycle
1	GO:0016917	Gaba Receptor Activity
1	GO:0004890	Gaba-A Receptor Activity
0	GO:0008378	Galactosyltransferase Activity
0	GO:0007276	Gamete Generation
0	GO:0007214	Gamma-Aminobutyric Acid Signaling Pathway
0	GO:0015812	Gamma-Aminobutyric Acid Transport
0	GO:0045295	Gamma-Catenin Binding
0	GO:0043015	Gamma-Tubulin Binding
0	GO:0000930	Gamma-Tubulin Complex
0	GO:0001573	Ganglioside Metabolic Process
0	GO:0005921	Gap Junction
0	GO:0005243	Gap Junction Channel Activity
0	GO:0015669	Gas Transport
0	GO:0007369	Gastrulation
0	GO:0001702	Gastrulation With Mouth Forming Second
0	GO:0022836	Gated Channel Activity

0	GO:0019003	Gdp Binding
0	GO:0016458	Gene Silencing
0	GO:0035195	Gene Silencing By Mirna
0	GO:0031047	Gene Silencing By Rna
0	GO:0003001	Generation Of A Signal Involved In Cell-Cell Signaling
0	GO:0006091	Generation Of Precursor Metabolites And Energy
0	GO:0071514	Genetic Imprinting
0	GO:0048806	Genitalia Development
0	GO:0035112	Genitalia Morphogenesis
0	GO:0007281	Germ Cell Development
0	GO:0008354	Germ Cell Migration
0	GO:0043073	Germ Cell Nucleus
0	GO:0060293	Germ Plasm
0	GO:0002467	Germinal Center Formation
0	GO:0048732	Gland Development
0	GO:0022612	Gland Morphogenesis
1	GO:0021782	Glial Cell Development
1	GO:0010001	Glial Cell Differentiation
1	GO:0021781	Glial Cell Fate Commitment
1	GO:0014009	Glial Cell Proliferation
1	GO:0042063	Gliogenesis
0	GO:0032835	Glomerulus Development
0	GO:0072012	Glomerulus Vasculature Development
0	GO:0009250	Glucan Biosynthetic Process
0	GO:0009251	Glucan Catabolic Process
0	GO:0044042	Glucan Metabolic Process
0	GO:0006704	Glucocorticoid Biosynthetic Process
0	GO:0008211	Glucocorticoid Metabolic Process
0	GO:0006094	Gluconeogenesis
0	GO:0006041	Glucosamine Metabolic Process
0	GO:0006007	Glucose Catabolic Process
0	GO:0042593	Glucose Homeostasis
0	GO:0046323	Glucose Import
0	GO:0006006	Glucose Metabolic Process
0	GO:0005355	Glucose Transmembrane Transporter Activity
0	GO:0015758	Glucose Transport
0	GO:0015926	Glucosidase Activity
0	GO:0046527	Glucosyltransferase Activity
0	GO:0015020	Glucuronosyltransferase Activity
1	GO:0006536	Glutamate Metabolic Process
1	GO:0008066	Glutamate Receptor Activity
1	GO:0035254	Glutamate Receptor Binding
1	GO:0007215	Glutamate Receptor Signaling Pathway
1	GO:0014047	Glutamate Secretion
0	GO:0009084	Glutamine Family Amino Acid Biosynthetic Process
0	GO:0009065	Glutamine Family Amino Acid Catabolic Process
0	GO:0009064	Glutamine Family Amino Acid Metabolic Process
0	GO:0006541	Glutamine Metabolic Process
0	GO:0006750	Glutathione Biosynthetic Process
0	GO:0006749	Glutathione Metabolic Process
0	GO:0004602	Glutathione Peroxidase Activity
0	GO:0004364	Glutathione Transferase Activity
0	GO:0046504	Glycerol Ether Biosynthetic Process
0	GO:0044269	Glycerol Ether Catabolic Process
0	GO:0006662	Glycerol Ether Metabolic Process
0	GO:0006071	Glycerol Metabolic Process

0	GO:0045017	Glycerolipid Biosynthetic Process
0	GO:0046503	Glycerolipid Catabolic Process
0	GO:0046486	Glycerolipid Metabolic Process
0	GO:0046474	Glycerophospholipid Biosynthetic Process
0	GO:0006650	Glycerophospholipid Metabolic Process
0	GO:0016594	Glycine Binding
0	GO:0006544	Glycine Metabolic Process
0	GO:0005978	Glycogen Biosynthetic Process
0	GO:0005980	Glycogen Catabolic Process
0	GO:0005977	Glycogen Metabolic Process
0	GO:0051861	Glycolipid Binding
0	GO:0009247	Glycolipid Biosynthetic Process
0	GO:0006664	Glycolipid Metabolic Process
0	GO:0006096	Glycolysis
0	GO:0001948	Glycoprotein Binding
0	GO:0009101	Glycoprotein Biosynthetic Process
0	GO:0006516	Glycoprotein Catabolic Process
0	GO:0009100	Glycoprotein Metabolic Process
0	GO:0005539	Glycosaminoglycan Binding
0	GO:0006024	Glycosaminoglycan Biosynthetic Process
0	GO:0006027	Glycosaminoglycan Catabolic Process
0	GO:0030203	Glycosaminoglycan Metabolic Process
0	GO:0006688	Glycosphingolipid Biosynthetic Process
0	GO:0006687	Glycosphingolipid Metabolic Process
0	GO:0070085	Glycosylation
0	GO:0006677	Glycosylceramide Metabolic Process
0	GO:0019002	Gmp Binding
0	GO:0031985	Golgi Cisterna
0	GO:0032580	Golgi Cisterna Membrane
0	GO:0005796	Golgi Lumen
0	GO:0000139	Golgi Membrane
0	GO:0007030	Golgi Organization
0	GO:0005795	Golgi Stack
0	GO:0006895	Golgi To Endosome Transport
0	GO:0043001	Golgi To Plasma Membrane Protein Transport
0	GO:0006893	Golgi To Plasma Membrane Transport
0	GO:0017119	Golgi Transport Complex
0	GO:0048200	Golgi Transport Vesicle Coating
0	GO:0048194	Golgi Vesicle Budding
0	GO:0048193	Golgi Vesicle Transport
0	GO:0005798	Golgi-Associated Vesicle
0	GO:0030660	Golgi-Associated Vesicle Membrane
0	GO:0008406	Gonad Development
0	GO:0006506	Gpi Anchor Biosynthetic Process
0	GO:0006505	Gpi Anchor Metabolic Process
0	GO:0071621	Granulocyte Chemotaxis
0	GO:0030851	Granulocyte Differentiation
1	GO:0007625	Grooming Behavior
0	GO:0030426	Growth Cone
0	GO:0008083	Growth Factor Activity
0	GO:0019838	Growth Factor Binding
0	GO:0070851	Growth Factor Receptor Binding
0	GO:0060396	Growth Hormone Receptor Signaling Pathway
0	GO:0030252	Growth Hormone Secretion
0	GO:0044110	Growth Involved In Symbiotic Interaction
0	GO:0044117	Growth Of Symbiont In Host

0	GO:0044116	Growth Of Symbiont Involved In Interaction With Host
0	GO:0003417	Growth Plate Cartilage Development
0	GO:0005525	Gtp Binding
0	GO:0006184	Gtp Catabolic Process
0	GO:0046039	Gtp Metabolic Process
0	GO:0030742	Gtp-Dependent Protein Binding
0	GO:0005096	Gtpase Activator Activity
0	GO:0003924	Gtpase Activity
0	GO:0051020	Gtpase Binding
0	GO:0005095	Gtpase Inhibitor Activity
0	GO:0030695	Gtpase Regulator Activity
0	GO:0019001	Guanyl Nucleotide Binding
0	GO:0032561	Guanyl Ribonucleotide Binding
0	GO:0005085	Guanyl-Nucleotide Exchange Factor Activity
0	GO:0004385	Guanylate Kinase Activity
0	GO:0043189	H4/H2A Histone Acetyltransferase Complex
0	GO:0042633	Hair Cycle
0	GO:0022405	Hair Cycle Process
0	GO:0001942	Hair Follicle Development
0	GO:0048820	Hair Follicle Maturation
0	GO:0031069	Hair Follicle Morphogenesis
0	GO:0060322	Head Development
0	GO:0060323	Head Morphogenesis
0	GO:0060047	Heart Contraction
0	GO:0007507	Heart Development
0	GO:0060914	Heart Formation
0	GO:0060419	Heart Growth
0	GO:0001947	Heart Looping
0	GO:0003007	Heart Morphogenesis
0	GO:0003015	Heart Process
0	GO:0060347	Heart Trabecula Formation
0	GO:0061384	Heart Trabecula Morphogenesis
0	GO:0003170	Heart Valve Development
0	GO:0003179	Heart Valve Morphogenesis
0	GO:0031649	Heat Generation
0	GO:0031072	Heat Shock Protein Binding
0	GO:0008158	Hedgehog Receptor Activity
0	GO:0004386	Helicase Activity
0	GO:0020037	Heme Binding
0	GO:0006783	Heme Biosynthetic Process
0	GO:0042168	Heme Metabolic Process
0	GO:0015002	Heme-Copper Terminal Oxidase Activity
0	GO:0031581	Hemidesmosome Assembly
0	GO:0020027	Hemoglobin Metabolic Process
0	GO:0030097	Hemopoiesis
0	GO:0048534	Hemopoietic Or Lymphoid Organ Development
0	GO:0002244	Hemopoietic Progenitor Cell Differentiation
0	GO:0007599	Hemostasis
0	GO:0043395	Heparan Sulfate Proteoglycan Binding
0	GO:0015012	Heparan Sulfate Proteoglycan Biosynthetic Process
0	GO:0030201	Heparan Sulfate Proteoglycan Metabolic Process
0	GO:0034483	Heparan Sulfate Sulfotransferase Activity
0	GO:0008201	Heparin Binding
0	GO:0061008	Hepaticobiliary System Development
0	GO:0000792	Heterochromatin
0	GO:0018130	Heterocycle Biosynthetic Process

0	GO:0030530	Heterogeneous Nuclear Ribonucleoprotein Complex
0	GO:0007157	Heterophilic Cell-Cell Adhesion
1	GO:0005834	Heterotrimeric G-Protein Complex
0	GO:0015929	Hexosaminidase Activity
0	GO:0019319	Hexose Biosynthetic Process
0	GO:0019320	Hexose Catabolic Process
0	GO:0019318	Hexose Metabolic Process
0	GO:0015149	Hexose Transmembrane Transporter Activity
0	GO:0008645	Hexose Transport
0	GO:0034364	High-Density Lipoprotein Particle
0	GO:0034375	High-Density Lipoprotein Particle Remodeling
1	GO:0030902	Hindbrain Development
1	GO:0021575	Hindbrain Morphogenesis
0	GO:0035137	Hindlimb Morphogenesis
0	GO:0035329	Hippo Signaling Cascade
1	GO:0021766	Hippocampus Development
0	GO:0016573	Histone Acetylation
0	GO:0004402	Histone Acetyltransferase Activity
0	GO:0035035	Histone Acetyltransferase Binding
0	GO:0000123	Histone Acetyltransferase Complex
0	GO:0042393	Histone Binding
0	GO:0004407	Histone Deacetylase Activity
0	GO:0031078	Histone Deacetylase Activity (H3-K14 Specific)
0	GO:0032129	Histone Deacetylase Activity (H3-K9 Specific)
0	GO:0034739	Histone Deacetylase Activity (H4-K16 Specific)
0	GO:0042826	Histone Deacetylase Binding
0	GO:0000118	Histone Deacetylase Complex
0	GO:0016575	Histone Deacetylation
0	GO:0032452	Histone Demethylase Activity
0	GO:0016577	Histone Demethylation
0	GO:0016578	Histone Deubiquitination
0	GO:0043486	Histone Exchange
0	GO:0043968	Histone H2A Acetylation
0	GO:0033522	Histone H2A Ubiquitination
0	GO:0043966	Histone H3 Acetylation
0	GO:0051568	Histone H3-K4 Methylation
0	GO:0051567	Histone H3-K9 Methylation
0	GO:0043967	Histone H4 Acetylation
0	GO:0035173	Histone Kinase Activity
0	GO:0070076	Histone Lysine Demethylation
0	GO:0034968	Histone Lysine Methylation
0	GO:0016571	Histone Methylation
0	GO:0042054	Histone Methyltransferase Activity
0	GO:0042800	Histone Methyltransferase Activity (H3-K4 Specific)
0	GO:0035097	Histone Methyltransferase Complex
0	GO:0016570	Histone Modification
0	GO:0010390	Histone Monoubiquitination
0	GO:0008334	Histone Mrna Metabolic Process
0	GO:0016572	Histone Phosphorylation
0	GO:0016574	Histone Ubiquitination
0	GO:0018024	Histone-Lysine N-Methyltransferase Activity
0	GO:0071837	Hmg Box Domain Binding
0	GO:0048872	Homeostasis Of Number Of Cells
0	GO:0048873	Homeostasis Of Number Of Cells Within A Tissue
0	GO:0007156	Homophilic Cell Adhesion
0	GO:0034109	Homotypic Cell-Cell Adhesion

0	GO:0030897	Hops Complex
0	GO:0005179	Hormone Activity
0	GO:0042562	Hormone Binding
0	GO:0042446	Hormone Biosynthetic Process
0	GO:0042445	Hormone Metabolic Process
0	GO:0051427	Hormone Receptor Binding
0	GO:0046879	Hormone Secretion
0	GO:0009914	Hormone Transport
0	GO:0009755	Hormone-Mediated Signaling Pathway
0	GO:0030544	Hsp70 Protein Binding
0	GO:0051879	Hsp90 Protein Binding
0	GO:0006959	Humoral Immune Response
0	GO:0002455	Humoral Immune Response Mediated By Circulating Immunoglobulin
0	GO:0005540	Hyaluronic Acid Binding
0	GO:0016836	Hydro-Lyase Activity
0	GO:0015078	Hydrogen Ion Transmembrane Transporter Activity
0	GO:0046933	Hydrogen Ion Transporting Atp Synthase Activity, Rotational Mechanism
0	GO:0042744	Hydrogen Peroxide Catabolic Process
0	GO:0042743	Hydrogen Peroxide Metabolic Process
0	GO:0006818	Hydrogen Transport
0	GO:0016820	Hydrolase Activity, Acting On Acid Anhydrides, Catalyzing Transmembrane Movement Of Substances
0	GO:0016810	Hydrolase Activity, Acting On Carbon-Nitrogen (But Not Peptide) Bonds
0	GO:0016814	Hydrolase Activity, Acting On Carbon-Nitrogen (But Not Peptide) Bonds, In Cyclic Amidines
0	GO:0016811	Hydrolase Activity, Acting On Carbon-Nitrogen (But Not Peptide) Bonds, In Linear Amides
0	GO:0016813	Hydrolase Activity, Acting On Carbon-Nitrogen (But Not Peptide) Bonds, In Linear Amidines
0	GO:0016798	Hydrolase Activity, Acting On Glycosyl Bonds
0	GO:0016799	Hydrolase Activity, Hydrolyzing N-Glycosyl Compounds
0	GO:0004553	Hydrolase Activity, Hydrolyzing O-Glycosyl Compounds
0	GO:0006972	Hyperosmotic Response
1	GO:0021854	Hypothalamus Development
0	GO:0031674	I Band
0	GO:0007249	I-Kappab Kinase/Nf-Kappab Cascade
0	GO:0070411	I-Smad Binding
0	GO:0046456	Icosanoid Biosynthetic Process
0	GO:0006690	Icosanoid Metabolic Process
0	GO:0004953	Icosanoid Receptor Activity
0	GO:0032309	Icosanoid Secretion
0	GO:0071715	Icosanoid Transport
0	GO:0002252	Immune Effector Process
0	GO:0002429	Immune Response-Activating Cell Surface Receptor Signaling Pathway
0	GO:0002757	Immune Response-Activating Signal Transduction
0	GO:0002768	Immune Response-Regulating Cell Surface Receptor Signaling Pathway
0	GO:0002764	Immune Response-Regulating Signaling Pathway
0	GO:0019865	Immunoglobulin Binding
0	GO:0016064	Immunoglobulin Mediated Immune Response
0	GO:0002377	Immunoglobulin Production
0	GO:0002381	Immunoglobulin Production Involved In Immunoglobulin Mediated Immune Response
0	GO:0048305	Immunoglobulin Secretion
0	GO:0001772	Immunological Synapse
0	GO:0001701	In Utero Embryonic Development
0	GO:0000188	Inactivation Of Mapk Activity
0	GO:0016234	Inclusion Body
0	GO:0046218	Indolalkylamine Catabolic Process
0	GO:0006586	Indolalkylamine Metabolic Process
0	GO:0042436	Indole-Containing Compound Catabolic Process
0	GO:0042430	Indole-Containing Compound Metabolic Process

0	GO:0006917	Induction Of Apoptosis
0	GO:0008624	Induction Of Apoptosis By Extracellular Signals
0	GO:0008629	Induction Of Apoptosis By Intracellular Signals
0	GO:0008625	Induction Of Apoptosis Via Death Domain Receptors
0	GO:0050930	Induction Of Positive Chemotaxis
0	GO:0012502	Induction Of Programmed Cell Death
0	GO:0006954	Inflammatory Response
0	GO:0002437	Inflammatory Response To Antigenic Stimulus
0	GO:0019059	Initiation Of Viral Infection
0	GO:0045087	Innate Immune Response
0	GO:0002758	Innate Immune Response-Activating Signal Transduction
0	GO:0001833	Inner Cell Mass Cell Proliferation
0	GO:0048839	Inner Ear Development
0	GO:0042472	Inner Ear Morphogenesis
0	GO:0060119	Inner Ear Receptor Cell Development
0	GO:0060113	Inner Ear Receptor Cell Differentiation
0	GO:0060122	Inner Ear Receptor Stereocilium Organization
0	GO:0031011	Ino80 Complex
0	GO:0005452	Inorganic Anion Exchanger Activity
0	GO:0015103	Inorganic Anion Transmembrane Transporter Activity
0	GO:0015698	Inorganic Anion Transport
0	GO:0022890	Inorganic Cation Transmembrane Transporter Activity
0	GO:0048017	Inositol Lipid-Mediated Signaling
0	GO:0004428	Inositol Or Phosphatidylinositol Kinase Activity
0	GO:0004437	Inositol Or Phosphatidylinositol Phosphatase Activity
0	GO:0032958	Inositol Phosphate Biosynthetic Process
0	GO:0043647	Inositol Phosphate Metabolic Process
0	GO:0052745	Inositol Phosphate Phosphatase Activity
0	GO:0048016	Inositol Phosphate-Mediated Signaling
0	GO:0007320	Insemination
0	GO:0005158	Insulin Receptor Binding
0	GO:0008286	Insulin Receptor Signaling Pathway
0	GO:0043560	Insulin Receptor Substrate Binding
0	GO:0030073	Insulin Secretion
0	GO:0035773	Insulin Secretion Involved In Cellular Response To Glucose Stimulus
0	GO:0005520	Insulin-Like Growth Factor Binding
0	GO:0005159	Insulin-Like Growth Factor Receptor Binding
0	GO:0048009	Insulin-Like Growth Factor Receptor Signaling Pathway
0	GO:0030176	Integral To Endoplasmic Reticulum Membrane
0	GO:0030173	Integral To Golgi Membrane
0	GO:0000299	Integral To Membrane Of Membrane Fraction
0	GO:0032592	Integral To Mitochondrial Membrane
0	GO:0031301	Integral To Organelle Membrane
0	GO:0005779	Integral To Peroxisomal Membrane
0	GO:0032039	Integrator Complex
0	GO:0005178	Integrin Binding
0	GO:0008305	Integrin Complex
0	GO:0007229	Integrin-Mediated Signaling Pathway
0	GO:0051701	Interaction With Host
0	GO:0051702	Interaction With Symbiont
0	GO:0014704	Intercalated Disc
0	GO:0032607	Interferon-Alpha Production
0	GO:0032608	Interferon-Beta Production
0	GO:0042095	Interferon-Gamma Biosynthetic Process
0	GO:0032609	Interferon-Gamma Production
0	GO:0060333	Interferon-Gamma-Mediated Signaling Pathway

0	GO:0032611	Interleukin-1 Beta Production
0	GO:0050702	Interleukin-1 Beta Secretion
0	GO:0032612	Interleukin-1 Production
0	GO:0005149	Interleukin-1 Receptor Binding
0	GO:0050701	Interleukin-1 Secretion
0	GO:0070498	Interleukin-1-Mediated Signaling Pathway
0	GO:0032613	Interleukin-10 Production
0	GO:0032615	Interleukin-12 Production
0	GO:0032616	Interleukin-13 Production
0	GO:0032620	Interleukin-17 Production
0	GO:0042094	Interleukin-2 Biosynthetic Process
0	GO:0032623	Interleukin-2 Production
0	GO:0032633	Interleukin-4 Production
0	GO:0042226	Interleukin-6 Biosynthetic Process
0	GO:0032635	Interleukin-6 Production
0	GO:0042228	Interleukin-8 Biosynthetic Process
0	GO:0032637	Interleukin-8 Production
0	GO:0005882	Intermediate Filament
0	GO:0045111	Intermediate Filament Cytoskeleton
0	GO:0045104	Intermediate Filament Cytoskeleton Organization
0	GO:0045109	Intermediate Filament Organization
0	GO:0045103	Intermediate Filament-Based Process
0	GO:0018393	Internal Peptidyl-Lysine Acetylation
0	GO:0006475	Internal Protein Amino Acid Acetylation
0	GO:0009898	Internal Side Of Plasma Membrane
0	GO:0051325	Interphase
0	GO:0051329	Interphase Of Mitotic Cell Cycle
0	GO:0044419	Interspecies Interaction Between Organisms
0	GO:0005614	Interstitial Matrix
0	GO:0050892	Intestinal Absorption
0	GO:0030299	Intestinal Cholesterol Absorption
0	GO:0006891	Intra-Golgi Vesicle-Mediated Transport
0	GO:0030520	Intracellular Estrogen Receptor Signaling Pathway
0	GO:0005217	Intracellular Ligand-Gated Ion Channel Activity
0	GO:0032365	Intracellular Lipid Transport
0	GO:0051452	Intracellular Ph Reduction
0	GO:0030522	Intracellular Receptor Mediated Signaling Pathway
0	GO:0030518	Intracellular Steroid Hormone Receptor Signaling Pathway
0	GO:0016860	Intramolecular Oxidoreductase Activity
0	GO:0016861	Intramolecular Oxidoreductase Activity, Interconverting Aldoses And Ketoses
0	GO:0016862	Intramolecular Oxidoreductase Activity, Interconverting Keto- And Enol-Groups
0	GO:0016863	Intramolecular Oxidoreductase Activity, Transposing C=C Bonds
0	GO:0016866	Intramolecular Transferase Activity
0	GO:0070059	Intrinsic Apoptotic Signaling Pathway In Response To Endoplasmic Reticulum Stress
0	GO:0031227	Intrinsic To Endoplasmic Reticulum Membrane
0	GO:0031233	Intrinsic To External Side Of Plasma Membrane
0	GO:0031228	Intrinsic To Golgi Membrane
0	GO:0031235	Intrinsic To Internal Side Of Plasma Membrane
0	GO:0031300	Intrinsic To Organelle Membrane
0	GO:0031231	Intrinsic To Peroxisomal Membrane
0	GO:0005242	Inward Rectifier Potassium Channel Activity
0	GO:0005216	Ion Channel Activity
0	GO:0034702	Ion Channel Complex
0	GO:0008200	Ion Channel Inhibitor Activity
0	GO:0022839	Ion Gated Channel Activity
0	GO:0034220	Ion Transmembrane Transport

1	GO:0004970	Ionotropic Glutamate Receptor Activity
1	GO:0035255	Ionotropic Glutamate Receptor Binding
1	GO:0008328	Ionotropic Glutamate Receptor Complex
1	GO:0035235	Ionotropic Glutamate Receptor Signaling Pathway
0	GO:0005506	Iron Ion Binding
0	GO:0055072	Iron Ion Homeostasis
0	GO:0005381	Iron Ion Transmembrane Transporter Activity
0	GO:0006826	Iron Ion Transport
0	GO:0016226	Iron-Sulfur Cluster Assembly
0	GO:0051536	Iron-Sulfur Cluster Binding
0	GO:0016853	Isomerase Activity
0	GO:0019840	Isoprenoid Binding
0	GO:0008299	Isoprenoid Biosynthetic Process
0	GO:0006720	Isoprenoid Metabolic Process
0	GO:0045190	Isotype Switching
0	GO:0048291	Isotype Switching To Igg Isotypes
0	GO:0007259	Jak-Stat Cascade
0	GO:0007254	Jnk Cascade
0	GO:0045095	Keratin Filament
0	GO:0031424	Keratinization
0	GO:0030216	Keratinocyte Differentiation
0	GO:0043616	Keratinocyte Proliferation
0	GO:0001822	Kidney Development
0	GO:0072073	Kidney Epithelium Development
0	GO:0072074	Kidney Mesenchyme Development
0	GO:0060993	Kidney Morphogenesis
0	GO:0031640	Killing Of Cells Of Other Organism
0	GO:0019209	Kinase Activator Activity
0	GO:0019900	Kinase Binding
0	GO:0019210	Kinase Inhibitor Activity
0	GO:0019207	Kinase Regulator Activity
0	GO:0019894	Kinesin Binding
0	GO:0005871	Kinesin Complex
0	GO:0000776	Kinetochore
0	GO:0043092	L-Amino Acid Import
0	GO:0015179	L-Amino Acid Transmembrane Transporter Activity
0	GO:0015807	L-Amino Acid Transport
0	GO:0031418	L-Ascorbic Acid Binding
0	GO:0042354	L-Fucose Metabolic Process
0	GO:0005313	L-Glutamate Transmembrane Transporter Activity
0	GO:0015813	L-Glutamate Transport
0	GO:0060716	Labyrinthine Layer Blood Vessel Development
0	GO:0060711	Labyrinthine Layer Development
0	GO:0060713	Labyrinthine Layer Morphogenesis
0	GO:0007595	Lactation
0	GO:0030027	Lamellipodium
0	GO:0030032	Lamellipodium Assembly
0	GO:0031258	Lamellipodium Membrane
0	GO:0043236	Laminin Binding
0	GO:0043256	Laminin Complex
0	GO:0015934	Large Ribosomal Subunit
0	GO:0005770	Late Endosome
0	GO:0031902	Late Endosome Membrane
0	GO:0048368	Lateral Mesoderm Development
0	GO:0016328	Lateral Plasma Membrane
0	GO:0060601	Lateral Sprouting From An Epithelium

0	GO:0031256	Leading Edge Membrane
1	GO:0007612	Learning
1	GO:0007611	Learning Or Memory
0	GO:0002088	Lens Development In Camera-Type Eye
0	GO:0070307	Lens Fiber Cell Development
0	GO:0070306	Lens Fiber Cell Differentiation
0	GO:0002089	Lens Morphogenesis In Camera-Type Eye
0	GO:0045321	Leukocyte Activation
0	GO:0002366	Leukocyte Activation Involved In Immune Response
0	GO:0071887	Leukocyte Apoptotic Process
0	GO:0007159	Leukocyte Cell-Cell Adhesion
0	GO:0030595	Leukocyte Chemotaxis
0	GO:0043299	Leukocyte Degranulation
0	GO:0002521	Leukocyte Differentiation
0	GO:0001776	Leukocyte Homeostasis
0	GO:0001909	Leukocyte Mediated Cytotoxicity
0	GO:0002443	Leukocyte Mediated Immunity
0	GO:0050900	Leukocyte Migration
0	GO:0070661	Leukocyte Proliferation
0	GO:0019370	Leukotriene Biosynthetic Process
0	GO:0006691	Leukotriene Metabolic Process
0	GO:0033327	Leydig Cell Differentiation
0	GO:0004879	Ligand-Activated Sequence-Specific Dna Binding Rna Polymerase Ii Transcription Factor Activity
0	GO:0016922	Ligand-Dependent Nuclear Receptor Binding
0	GO:0030374	Ligand-Dependent Nuclear Receptor Transcription Coactivator Activity
0	GO:0022834	Ligand-Gated Channel Activity
0	GO:0015276	Ligand-Gated Ion Channel Activity
0	GO:0003706	Ligand-Regulated Transcription Factor Activity
0	GO:0016874	Ligase Activity
0	GO:0016876	Ligase Activity, Forming Aminoacyl-Trna And Related Compounds
0	GO:0016879	Ligase Activity, Forming Carbon-Nitrogen Bonds
0	GO:0016875	Ligase Activity, Forming Carbon-Oxygen Bonds
0	GO:0016877	Ligase Activity, Forming Carbon-Sulfur Bonds
0	GO:0060174	Limb Bud Formation
0	GO:0060173	Limb Development
0	GO:0035108	Limb Morphogenesis
1	GO:0021761	Limbic System Development
0	GO:0016298	Lipase Activity
0	GO:0055102	Lipase Inhibitor Activity
0	GO:0008289	Lipid Binding
0	GO:0008610	Lipid Biosynthetic Process
0	GO:0016042	Lipid Catabolic Process
0	GO:0044241	Lipid Digestion
0	GO:0030259	Lipid Glycosylation
0	GO:0055088	Lipid Homeostasis
0	GO:0001727	Lipid Kinase Activity
0	GO:0010876	Lipid Localization
0	GO:0030258	Lipid Modification
0	GO:0034440	Lipid Oxidation
0	GO:0005811	Lipid Particle
0	GO:0046834	Lipid Phosphorylation
0	GO:0019915	Lipid Storage
0	GO:0006869	Lipid Transport
0	GO:0005319	Lipid Transporter Activity
0	GO:0001530	Lipopolysaccharide Binding
0	GO:0009103	Lipopolysaccharide Biosynthetic Process

0	GO:0008653	Lipopolysaccharide Metabolic Process
0	GO:0031663	Lipopolysaccharide-Mediated Signaling Pathway
0	GO:0042158	Lipoprotein Biosynthetic Process
0	GO:0042157	Lipoprotein Metabolic Process
0	GO:0071813	Lipoprotein Particle Binding
0	GO:0030228	Lipoprotein Particle Receptor Activity
0	GO:0070325	Lipoprotein Particle Receptor Binding
0	GO:0042953	Lipoprotein Transport
0	GO:0001889	Liver Development
0	GO:0051668	Localization Within Membrane
1	GO:0007626	Locomotory Behavior
0	GO:0001676	Long-Chain Fatty Acid Metabolic Process
0	GO:0015909	Long-Chain Fatty Acid Transport
0	GO:0004467	Long-Chain Fatty Acid-Coa Ligase Activity
0	GO:0035338	Long-Chain Fatty-Acyl-Coa Biosynthetic Process
0	GO:0035336	Long-Chain Fatty-Acyl-Coa Metabolic Process
1	GO:0007616	Long-Term Memory
0	GO:0060291	Long-Term Synaptic Potentiation
0	GO:0034362	Low-Density Lipoprotein Particle
0	GO:0030169	Low-Density Lipoprotein Particle Binding
0	GO:0034383	Low-Density Lipoprotein Particle Clearance
0	GO:0050750	Low-Density Lipoprotein Particle Receptor Binding
0	GO:0034374	Low-Density Lipoprotein Particle Remodeling
0	GO:0005041	Low-Density Lipoprotein Receptor Activity
0	GO:0032799	Low-Density Lipoprotein Receptor Particle Metabolic Process
0	GO:0030275	Lrr Domain Binding
0	GO:0048286	Lung Alveolus Development
0	GO:0060479	Lung Cell Differentiation
0	GO:0030324	Lung Development
0	GO:0060487	Lung Epithelial Cell Differentiation
0	GO:0060428	Lung Epithelium Development
0	GO:0060425	Lung Morphogenesis
0	GO:0016829	Lyase Activity
0	GO:0048535	Lymph Node Development
0	GO:0001945	Lymph Vessel Development
0	GO:0046649	Lymphocyte Activation
0	GO:0002285	Lymphocyte Activation Involved In Immune Response
0	GO:0070227	Lymphocyte Apoptotic Process
0	GO:0048247	Lymphocyte Chemotaxis
0	GO:0031294	Lymphocyte Costimulation
0	GO:0030098	Lymphocyte Differentiation
0	GO:0002260	Lymphocyte Homeostasis
0	GO:0002449	Lymphocyte Mediated Immunity
0	GO:0072676	Lymphocyte Migration
0	GO:0046651	Lymphocyte Proliferation
0	GO:0002320	Lymphoid Progenitor Cell Differentiation
0	GO:0016278	Lysine N-Methyltransferase Activity
0	GO:0004622	Lysophospholipase Activity
0	GO:0043202	Lysosomal Lumen
0	GO:0005765	Lysosomal Membrane
0	GO:0007041	Lysosomal Transport
0	GO:0005764	Lysosome
0	GO:0007040	Lysosome Organization
0	GO:0001619	Lysosphingolipid And Lysophosphatidic Acid Receptor Activity
0	GO:0000323	Lytic Vacuole
0	GO:0000279	M Phase

0	GO:0051327	M Phase Of Meiotic Cell Cycle
0	GO:0000087	M Phase Of Mitotic Cell Cycle
0	GO:0000216	M/G1 Transition Of Mitotic Cell Cycle
0	GO:0016236	Macroautophagy
0	GO:0005527	Macrolide Binding
0	GO:0032984	Macromolecular Complex Disassembly
0	GO:0034367	Macromolecular Complex Remodeling
0	GO:0043413	Macromolecule Glycosylation
0	GO:0043414	Macromolecule Methylation
0	GO:0022884	Macromolecule Transmembrane Transporter Activity
0	GO:0042116	Macrophage Activation
0	GO:0048246	Macrophage Chemotaxis
0	GO:0010742	Macrophage Derived Foam Cell Differentiation
0	GO:0030225	Macrophage Differentiation
0	GO:0000287	Magnesium Ion Binding
1	GO:0044304	Main Axon
0	GO:0045005	Maintenance Of Fidelity Involved In Dna-Dependent Dna Replication
0	GO:0051235	Maintenance Of Location
0	GO:0051651	Maintenance Of Location In Cell
0	GO:0072595	Maintenance Of Protein Localization To Organelle
0	GO:0045185	Maintenance Of Protein Location
0	GO:0032507	Maintenance Of Protein Location In Cell
0	GO:0051457	Maintenance Of Protein Location In Nucleus
0	GO:0048232	Male Gamete Generation
0	GO:0030539	Male Genitalia Development
0	GO:0001673	Male Germ Cell Nucleus
0	GO:0008584	Male Gonad Development
0	GO:0007140	Male Meiosis
0	GO:0007141	Male Meiosis I
0	GO:0030238	Male Sex Determination
0	GO:0046661	Male Sex Differentiation
0	GO:0060749	Mammary Gland Alveolus Development
0	GO:0030879	Mammary Gland Development
0	GO:0060603	Mammary Gland Duct Morphogenesis
0	GO:0060644	Mammary Gland Epithelial Cell Differentiation
0	GO:0033598	Mammary Gland Epithelial Cell Proliferation
0	GO:0061180	Mammary Gland Epithelium Development
0	GO:0060056	Mammary Gland Involution
0	GO:0061377	Mammary Gland Lobule Development
0	GO:0060443	Mammary Gland Morphogenesis
0	GO:0030145	Manganese Ion Binding
0	GO:0005537	Mannose Binding
0	GO:0006013	Mannose Metabolic Process
0	GO:0015923	Mannosidase Activity
0	GO:0015924	Mannosyl-Oligosaccharide Mannosidase Activity
0	GO:0000030	Mannosyltransferase Activity
0	GO:0004707	Map Kinase Activity
0	GO:0004708	Map Kinase Kinase Activity
0	GO:0004709	Map Kinase Kinase Kinase Activity
0	GO:0033549	Map Kinase Phosphatase Activity
0	GO:0017017	Map Kinase Tyrosine/Serine/Threonine Phosphatase Activity
0	GO:0000165	Mapk Cascade
0	GO:0045576	Mast Cell Activation
0	GO:0002279	Mast Cell Activation Involved In Immune Response
0	GO:0043303	Mast Cell Degranulation
0	GO:0002448	Mast Cell Mediated Immunity

0	GO:0001893	Maternal Placenta Development
0	GO:0060135	Maternal Process Involved In Female Pregnancy
0	GO:0007618	Mating
1	GO:0007617	Mating Behavior
0	GO:0000460	Maturation Of 5.8S Rrna
0	GO:0042490	Mechanoreceptor Differentiation
0	GO:0016592	Mediator Complex
0	GO:0030219	Megakaryocyte Differentiation
0	GO:0007126	Meiosis
0	GO:0007127	Meiosis I
0	GO:0051321	Meiotic Cell Cycle
0	GO:0045132	Meiotic Chromosome Segregation
0	GO:0007128	Meiotic Prophase I
0	GO:0006582	Melanin Metabolic Process
0	GO:0030318	Melanocyte Differentiation
0	GO:0042470	Melanosome
0	GO:0032400	Melanosome Localization
0	GO:0032438	Melanosome Organization
0	GO:0006900	Membrane Budding
0	GO:0030117	Membrane Coat
0	GO:0051899	Membrane Depolarization
0	GO:0022406	Membrane Docking
0	GO:0061025	Membrane Fusion
0	GO:0060081	Membrane Hyperpolarization
0	GO:0010324	Membrane Invagination
0	GO:0046467	Membrane Lipid Biosynthetic Process
0	GO:0046466	Membrane Lipid Catabolic Process
0	GO:0006643	Membrane Lipid Metabolic Process
0	GO:0006509	Membrane Protein Ectodomain Proteolysis
0	GO:0031293	Membrane Protein Intracellular Domain Proteolysis
0	GO:0033619	Membrane Protein Proteolysis
0	GO:0045121	Membrane Raft
1	GO:0007613	Memory
0	GO:0014031	Mesenchymal Cell Development
0	GO:0048762	Mesenchymal Cell Differentiation
0	GO:0010463	Mesenchymal Cell Proliferation
0	GO:0060231	Mesenchymal To Epithelial Transition
0	GO:0003337	Mesenchymal To Epithelial Transition Involved In Metanephros Morphogenesis
0	GO:0060485	Mesenchyme Development
0	GO:0072132	Mesenchyme Morphogenesis
0	GO:0007498	Mesoderm Development
0	GO:0001707	Mesoderm Formation
0	GO:0048332	Mesoderm Morphogenesis
0	GO:0048333	Mesodermal Cell Differentiation
0	GO:0001710	Mesodermal Cell Fate Commitment
0	GO:0007501	Mesodermal Cell Fate Specification
0	GO:0072163	Mesonephric Epithelium Development
0	GO:0072164	Mesonephric Tubule Development
0	GO:0001823	Mesonephros Development
0	GO:0051540	Metal Cluster Binding
0	GO:0055065	Metal Ion Homeostasis
0	GO:0046873	Metal Ion Transmembrane Transporter Activity
0	GO:0031163	Metallo-Sulfur Cluster Assembly
0	GO:0004181	Metallocarboxypeptidase Activity
0	GO:0004222	Metalloendopeptidase Activity
0	GO:0008191	Metalloendopeptidase Inhibitor Activity

0	GO:0048551	Metalloenzyme Inhibitor Activity
0	GO:0010576	Metalloenzyme Regulator Activity
0	GO:0008235	Metalloexopeptidase Activity
0	GO:0008237	Metallopeptidase Activity
0	GO:0072207	Metanephric Epithelium Development
0	GO:0072224	Metanephric Glomerulus Development
0	GO:0072075	Metanephric Mesenchyme Development
0	GO:0072210	Metanephric Nephron Development
0	GO:0072243	Metanephric Nephron Epithelium Development
0	GO:0072273	Metanephric Nephron Morphogenesis
0	GO:0072234	Metanephric Nephron Tubule Development
0	GO:0072283	Metanephric Renal Vesicle Morphogenesis
0	GO:0072170	Metanephric Tubule Development
0	GO:0001656	Metanephros Development
0	GO:0003338	Metanephros Morphogenesis
0	GO:0051310	Metaphase Plate Congression
1	GO:0022037	Metencephalon Development
0	GO:0009086	Methionine Biosynthetic Process
0	GO:0006555	Methionine Metabolic Process
0	GO:0035064	Methylated Histone Residue Binding
0	GO:0032259	Methylation
0	GO:0008168	Methyltransferase Activity
0	GO:0034708	Methyltransferase Complex
0	GO:0042288	Mhc Class I Protein Binding
0	GO:0042612	Mhc Class I Protein Complex
0	GO:0032393	Mhc Class I Receptor Activity
0	GO:0045342	Mhc Class Ii Biosynthetic Process
0	GO:0042613	Mhc Class Ii Protein Complex
0	GO:0042287	Mhc Protein Binding
0	GO:0042611	Mhc Protein Complex
0	GO:0042579	Microbody
0	GO:0031907	Microbody Lumen
0	GO:0031903	Microbody Membrane
0	GO:0044438	Microbody Part
0	GO:0000146	Microfilament Motor Activity
0	GO:0001774	Microglial Cell Activation
0	GO:0005792	Microsome
0	GO:0005874	Microtubule
0	GO:0034453	Microtubule Anchoring
0	GO:0005875	Microtubule Associated Complex
0	GO:0005932	Microtubule Basal Body
0	GO:0008017	Microtubule Binding
0	GO:0001578	Microtubule Bundle Formation
0	GO:0000226	Microtubule Cytoskeleton Organization
0	GO:0007019	Microtubule Depolymerization
0	GO:0003777	Microtubule Motor Activity
0	GO:0007020	Microtubule Nucleation
0	GO:0005815	Microtubule Organizing Center
0	GO:0031023	Microtubule Organizing Center Organization
0	GO:0044450	Microtubule Organizing Center Part
0	GO:0051010	Microtubule Plus-End Binding
0	GO:0046785	Microtubule Polymerization
0	GO:0031109	Microtubule Polymerization Or Depolymerization
0	GO:0009434	Microtubule-Based Flagellum
0	GO:0044442	Microtubule-Based Flagellum Part
0	GO:0007018	Microtubule-Based Movement

0	GO:0007017	Microtubule-Based Process
0	GO:0010970	Microtubule-Based Transport
0	GO:0005902	Microvillus
0	GO:0031528	Microvillus Membrane
0	GO:0030496	Midbody
1	GO:0030901	Midbrain Development
1	GO:0030917	Midbrain-Hindbrain Boundary Development
0	GO:0042474	Middle Ear Morphogenesis
0	GO:0007494	Midgut Development
0	GO:0008212	Mineralocorticoid Metabolic Process
0	GO:0006298	Mismatch Repair
0	GO:0030983	Mismatched Dna Binding
0	GO:0042775	Mitochondrial Atp Synthesis Coupled Electron Transport
0	GO:0042776	Mitochondrial Atp Synthesis Coupled Proton Transport
0	GO:0051882	Mitochondrial Depolarization
0	GO:0006120	Mitochondrial Electron Transport, Nadh To Ubiquinone
0	GO:0005740	Mitochondrial Envelope
0	GO:0000266	Mitochondrial Fission
0	GO:0000002	Mitochondrial Genome Maintenance
0	GO:0005743	Mitochondrial Inner Membrane
0	GO:0005758	Mitochondrial Intermembrane Space
0	GO:0005762	Mitochondrial Large Ribosomal Subunit
0	GO:0005759	Mitochondrial Matrix
0	GO:0031966	Mitochondrial Membrane
0	GO:0007006	Mitochondrial Membrane Organization
0	GO:0044455	Mitochondrial Membrane Part
0	GO:0042645	Mitochondrial Nucleoid
0	GO:0005741	Mitochondrial Outer Membrane
0	GO:0005753	Mitochondrial Proton-Transporting Atp Synthase Complex
0	GO:0005746	Mitochondrial Respiratory Chain
0	GO:0033108	Mitochondrial Respiratory Chain Complex Assembly
0	GO:0005747	Mitochondrial Respiratory Chain Complex I
0	GO:0032981	Mitochondrial Respiratory Chain Complex I Assembly
0	GO:0097031	Mitochondrial Respiratory Chain Complex I Biogenesis
0	GO:0005761	Mitochondrial Ribosome
0	GO:0000959	Mitochondrial Rna Metabolic Process
0	GO:0005763	Mitochondrial Small Ribosomal Subunit
0	GO:0032543	Mitochondrial Translation
0	GO:0006839	Mitochondrial Transport
0	GO:0051646	Mitochondrion Localization
0	GO:0007005	Mitochondrion Organization
0	GO:0051019	Mitogen-Activated Protein Kinase Binding
0	GO:0031434	Mitogen-Activated Protein Kinase Kinase Binding
0	GO:0031435	Mitogen-Activated Protein Kinase Kinase Kinase Binding
0	GO:0007067	Mitosis
0	GO:0000090	Mitotic Anaphase
0	GO:0007093	Mitotic Cell Cycle Checkpoint
0	GO:0031575	Mitotic Cell Cycle G1/S Transition Checkpoint
0	GO:0031571	Mitotic Cell Cycle G1/S Transition Dna Damage Checkpoint
0	GO:0007094	Mitotic Cell Cycle Spindle Assembly Checkpoint
0	GO:0071174	Mitotic Cell Cycle Spindle Checkpoint
0	GO:0007076	Mitotic Chromosome Condensation
0	GO:0007080	Mitotic Metaphase Plate Congression
0	GO:0007091	Mitotic Metaphase/Anaphase Transition
0	GO:0000236	Mitotic Prometaphase
0	GO:0006312	Mitotic Recombination

0	GO:0000070	Mitotic Sister Chromatid Segregation
0	GO:0007052	Mitotic Spindle Organization
0	GO:0071339	Mll1 Complex
0	GO:0051851	Modification By Host Of Symbiont Morphology Or Physiology
0	GO:0044003	Modification By Symbiont Of Host Morphology Or Physiology
0	GO:0035821	Modification Of Morphology Or Physiology Of Other Organism
0	GO:0051817	Modification Of Morphology Or Physiology Of Other Organism Involved In Symbiotic Interaction
0	GO:0043632	Modification-Dependent Macromolecule Catabolic Process
0	GO:0019941	Modification-Dependent Protein Catabolic Process
0	GO:0072341	Modified Amino Acid Binding
0	GO:0052472	Modulation By Host Of Symbiont Transcription
0	GO:0043921	Modulation By Host Of Viral Transcription
0	GO:0044144	Modulation Of Growth Of Symbiont Involved In Interaction With Host
0	GO:0052312	Modulation Of Transcription In Other Organism Involved In Symbiotic Interaction
0	GO:0042303	Molting Cycle
0	GO:0022404	Molting Cycle Process
0	GO:0015844	Monoamine Transport
0	GO:0033293	Monocarboxylic Acid Binding
0	GO:0072329	Monocarboxylic Acid Catabolic Process
0	GO:0032787	Monocarboxylic Acid Metabolic Process
0	GO:0008028	Monocarboxylic Acid Transmembrane Transporter Activity
0	GO:0015718	Monocarboxylic Acid Transport
0	GO:0002548	Monocyte Chemotaxis
0	GO:0030224	Monocyte Differentiation
0	GO:0071674	Mononuclear Cell Migration
0	GO:0032943	Mononuclear Cell Proliferation
0	GO:0004497	Monooxygenase Activity
0	GO:0048029	Monosaccharide Binding
0	GO:0046364	Monosaccharide Biosynthetic Process
0	GO:0046365	Monosaccharide Catabolic Process
0	GO:0005996	Monosaccharide Metabolic Process
0	GO:0015145	Monosaccharide Transmembrane Transporter Activity
0	GO:0015749	Monosaccharide Transport
0	GO:0055067	Monovalent Inorganic Cation Homeostasis
0	GO:0015077	Monovalent Inorganic Cation Transmembrane Transporter Activity
0	GO:0015672	Monovalent Inorganic Cation Transport
0	GO:0061138	Morphogenesis Of A Branching Epithelium
0	GO:0001763	Morphogenesis Of A Branching Structure
0	GO:0001738	Morphogenesis Of A Polarized Epithelium
0	GO:0060572	Morphogenesis Of An Epithelial Bud
0	GO:0060571	Morphogenesis Of An Epithelial Fold
0	GO:0002011	Morphogenesis Of An Epithelial Sheet
0	GO:0002009	Morphogenesis Of An Epithelium
0	GO:0016331	Morphogenesis Of Embryonic Epithelium
0	GO:0031514	Motile Cilium
0	GO:0003774	Motor Activity
1	GO:0008045	Motor Axon Guidance
0	GO:0052192	Movement In Environment Of Other Organism Involved In Symbiotic Interaction
0	GO:0052126	Movement In Host Environment
0	GO:0031124	Mrna 3'-End Processing
0	GO:0003730	Mrna 3'-Utr Binding
0	GO:0003729	Mrna Binding
0	GO:0006370	Mrna Capping
0	GO:0006402	Mrna Catabolic Process
0	GO:0006379	Mrna Cleavage
0	GO:0005849	Mrna Cleavage Factor Complex

0	GO:0006406	Mrna Export From Nucleus
0	GO:0006378	Mrna Polyadenylation
0	GO:0006397	Mrna Processing
0	GO:0006376	Mrna Splice Site Selection
0	GO:0048255	Mrna Stabilization
0	GO:0051028	Mrna Transport
0	GO:0035264	Multicellular Organism Growth
0	GO:0010259	Multicellular Organismal Aging
0	GO:0044243	Multicellular Organismal Catabolic Process
0	GO:0048871	Multicellular Organismal Homeostasis
0	GO:0044259	Multicellular Organismal Macromolecule Metabolic Process
0	GO:0044236	Multicellular Organismal Metabolic Process
0	GO:0050879	Multicellular Organismal Movement
0	GO:0033057	Multicellular Organismal Reproductive Behavior
0	GO:0033555	Multicellular Organismal Response To Stress
0	GO:0050891	Multicellular Organismal Water Homeostasis
0	GO:0005771	Multivesicular Body
0	GO:0043500	Muscle Adaptation
0	GO:0010657	Muscle Cell Apoptotic Process
0	GO:0055001	Muscle Cell Development
0	GO:0042692	Muscle Cell Differentiation
0	GO:0042693	Muscle Cell Fate Commitment
0	GO:0046716	Muscle Cell Homeostasis
0	GO:0014812	Muscle Cell Migration
0	GO:0033002	Muscle Cell Proliferation
0	GO:0006936	Muscle Contraction
0	GO:0048747	Muscle Fiber Development
0	GO:0030049	Muscle Filament Sliding
0	GO:0014896	Muscle Hypertrophy
0	GO:0005859	Muscle Myosin Complex
0	GO:0007517	Muscle Organ Development
0	GO:0048644	Muscle Organ Morphogenesis
0	GO:0061061	Muscle Structure Development
0	GO:0003012	Muscle System Process
0	GO:0060537	Muscle Tissue Development
0	GO:0060415	Muscle Tissue Morphogenesis
0	GO:0050881	Musculoskeletal Movement
0	GO:0002755	Myd88-Dependent Toll-Like Receptor Signaling Pathway
0	GO:0002756	Myd88-Independent Toll-Like Receptor Signaling Pathway
1	GO:0032288	Myelin Assembly
1	GO:0043209	Myelin Sheath
1	GO:0042552	Myelination
1	GO:0022011	Myelination In Peripheral Nervous System
0	GO:0002275	Myeloid Cell Activation Involved In Immune Response
0	GO:0033028	Myeloid Cell Apoptotic Process
0	GO:0030099	Myeloid Cell Differentiation
0	GO:0002262	Myeloid Cell Homeostasis
0	GO:0001773	Myeloid Dendritic Cell Activation
0	GO:0043011	Myeloid Dendritic Cell Differentiation
0	GO:0002274	Myeloid Leukocyte Activation
0	GO:0061082	Myeloid Leukocyte Cytokine Production
0	GO:0002573	Myeloid Leukocyte Differentiation
0	GO:0002444	Myeloid Leukocyte Mediated Immunity
0	GO:0045445	Myoblast Differentiation
0	GO:0007520	Myoblast Fusion
0	GO:0030016	Myofibril

0	GO:0030239	Myofibril Assembly
0	GO:0017022	Myosin Binding
0	GO:0016459	Myosin Complex
0	GO:0032982	Myosin Filament
0	GO:0016460	Myosin Ii Complex
0	GO:0014902	Myotube Differentiation
0	GO:0006044	N-Acetylglucosamine Metabolic Process
0	GO:0008080	N-Acetyltransferase Activity
0	GO:0016410	N-Acyltransferase Activity
0	GO:0008170	N-Methyltransferase Activity
0	GO:0031365	N-Terminal Protein Amino Acid Modification
0	GO:0051287	Nad Binding
0	GO:0009435	Nad Biosynthetic Process
0	GO:0019674	Nad Metabolic Process
0	GO:0017136	Nad-Dependent Histone Deacetylase Activity
0	GO:0032041	Nad-Dependent Histone Deacetylase Activity (H3-K14 Specific)
0	GO:0046969	Nad-Dependent Histone Deacetylase Activity (H3-K9 Specific)
0	GO:0046970	Nad-Dependent Histone Deacetylase Activity (H4-K16 Specific)
0	GO:0034979	Nad-Dependent Protein Deacetylase Activity
0	GO:0003950	Nad+ Adp-Ribosyltransferase Activity
0	GO:0070403	Nad+ Binding
0	GO:0050136	Nadh Dehydrogenase (Quinone) Activity
0	GO:0008137	Nadh Dehydrogenase (Ubiquinone) Activity
0	GO:0003954	Nadh Dehydrogenase Activity
0	GO:0030964	Nadh Dehydrogenase Complex
0	GO:0010257	Nadh Dehydrogenase Complex Assembly
0	GO:0050661	Nadp Binding
0	GO:0006739	Nadp Metabolic Process
0	GO:0006740	Nadph Regeneration
0	GO:0030101	Natural Killer Cell Activation
0	GO:0001779	Natural Killer Cell Differentiation
0	GO:0042267	Natural Killer Cell Mediated Cytotoxicity
0	GO:0002228	Natural Killer Cell Mediated Immunity
1	GO:0071565	Nbaf Complex
0	GO:0034661	Ncrna Catabolic Process
0	GO:0034660	Ncrna Metabolic Process
0	GO:0034470	Ncrna Processing
0	GO:0070265	Necrotic Cell Death
0	GO:0022401	Negative Adaptation Of Signaling Pathway
0	GO:0050919	Negative Chemotaxis
0	GO:0030835	Negative Regulation Of Actin Filament Depolymerization
0	GO:0030837	Negative Regulation Of Actin Filament Polymerization
0	GO:0002820	Negative Regulation Of Adaptive Immune Response
0	GO:0002823	Negative Regulation Of Adaptive Immune Response Based On Somatic Recombination Of Immune Receptors Built From Immunoglobulin Superfamily Domains
0	GO:0007194	Negative Regulation Of Adenylate Cyclase Activity
0	GO:0046636	Negative Regulation Of Alpha-Beta T Cell Activation
0	GO:0046639	Negative Regulation Of Alpha-Beta T Cell Differentiation
0	GO:0051953	Negative Regulation Of Amine Transport
0	GO:0060766	Negative Regulation Of Androgen Receptor Signaling Pathway
0	GO:0016525	Negative Regulation Of Angiogenesis
0	GO:0050858	Negative Regulation Of Antigen Receptor-Mediated Signaling Pathway
0	GO:0048712	Negative Regulation Of Astrocyte Differentiation
1	GO:0030517	Negative Regulation Of Axon Extension
1	GO:0050771	Negative Regulation Of Axonogenesis
0	GO:0050869	Negative Regulation Of B Cell Activation
0	GO:0030889	Negative Regulation Of B Cell Proliferation

1	GO:0048521	Negative Regulation Of Behavior
0	GO:0051100	Negative Regulation Of Binding
0	GO:0070168	Negative Regulation Of Biomineral Tissue Development
0	GO:0030195	Negative Regulation Of Blood Coagulation
0	GO:0045776	Negative Regulation Of Blood Pressure
0	GO:0030514	Negative Regulation Of Bmp Signaling Pathway
0	GO:0030502	Negative Regulation Of Bone Mineralization
0	GO:0046851	Negative Regulation Of Bone Remodeling
0	GO:0051926	Negative Regulation Of Calcium Ion Transport
0	GO:0030818	Negative Regulation Of Camp Biosynthetic Process
0	GO:0030815	Negative Regulation Of Camp Metabolic Process
0	GO:0090090	Negative Regulation Of Canonical Wnt Receptor Signaling Pathway
0	GO:0045912	Negative Regulation Of Carbohydrate Metabolic Process
0	GO:0009895	Negative Regulation Of Catabolic Process
0	GO:0043086	Negative Regulation Of Catalytic Activity
0	GO:0050866	Negative Regulation Of Cell Activation
0	GO:0007162	Negative Regulation Of Cell Adhesion
0	GO:0045786	Negative Regulation Of Cell Cycle
0	GO:0010948	Negative Regulation Of Cell Cycle Process
0	GO:0010721	Negative Regulation Of Cell Development
0	GO:0045596	Negative Regulation Of Cell Differentiation
0	GO:0030308	Negative Regulation Of Cell Growth
0	GO:0030336	Negative Regulation Of Cell Migration
0	GO:0010771	Negative Regulation Of Cell Morphogenesis Involved In Differentiation
0	GO:2000146	Negative Regulation Of Cell Motility
0	GO:0031345	Negative Regulation Of Cell Projection Organization
0	GO:0008285	Negative Regulation Of Cell Proliferation
0	GO:0022408	Negative Regulation Of Cell-Cell Adhesion
0	GO:0001953	Negative Regulation Of Cell-Matrix Adhesion
0	GO:0010812	Negative Regulation Of Cell-Substrate Adhesion
0	GO:0010677	Negative Regulation Of Cellular Carbohydrate Metabolic Process
0	GO:0031330	Negative Regulation Of Cellular Catabolic Process
0	GO:0051271	Negative Regulation Of Cellular Component Movement
0	GO:0051129	Negative Regulation Of Cellular Component Organization
0	GO:0032269	Negative Regulation Of Cellular Protein Metabolic Process
0	GO:0050922	Negative Regulation Of Chemotaxis
0	GO:0032331	Negative Regulation Of Chondrocyte Differentiation
0	GO:2001251	Negative Regulation Of Chromosome Organization
0	GO:0050819	Negative Regulation Of Coagulation
0	GO:0031280	Negative Regulation Of Cyclase Activity
0	GO:0030803	Negative Regulation Of Cyclic Nucleotide Biosynthetic Process
0	GO:0030800	Negative Regulation Of Cyclic Nucleotide Metabolic Process
0	GO:0045736	Negative Regulation Of Cyclin-Dependent Protein Kinase Activity
0	GO:2000117	Negative Regulation Of Cysteine-Type Endopeptidase Activity
0	GO:0043154	Negative Regulation Of Cysteine-Type Endopeptidase Activity Involved In Apoptotic Process
0	GO:0042036	Negative Regulation Of Cytokine Biosynthetic Process
0	GO:0001818	Negative Regulation Of Cytokine Production
0	GO:0050710	Negative Regulation Of Cytokine Secretion
0	GO:0001960	Negative Regulation Of Cytokine-Mediated Signaling Pathway
0	GO:0051494	Negative Regulation Of Cytoskeleton Organization
0	GO:0031348	Negative Regulation Of Defense Response
0	GO:0048640	Negative Regulation Of Developmental Growth
0	GO:0051093	Negative Regulation Of Developmental Process
0	GO:0043392	Negative Regulation Of Dna Binding
0	GO:0051053	Negative Regulation Of Dna Metabolic Process
0	GO:0045910	Negative Regulation Of Dna Recombination

0	GO:0008156	Negative Regulation Of Dna Replication
0	GO:2000104	Negative Regulation Of Dna-Dependent Dna Replication
0	GO:0045806	Negative Regulation Of Endocytosis
0	GO:0010951	Negative Regulation Of Endopeptidase Activity
0	GO:0010596	Negative Regulation Of Endothelial Cell Migration
0	GO:0001937	Negative Regulation Of Endothelial Cell Proliferation
0	GO:0042059	Negative Regulation Of Epidermal Growth Factor Receptor Signaling Pathway
0	GO:0030857	Negative Regulation Of Epithelial Cell Differentiation
0	GO:0050680	Negative Regulation Of Epithelial Cell Proliferation
0	GO:0010719	Negative Regulation Of Epithelial To Mesenchymal Transition
0	GO:0070373	Negative Regulation Of Erk1 And Erk2 Cascade
0	GO:0045920	Negative Regulation Of Exocytosis
0	GO:0045599	Negative Regulation Of Fat Cell Differentiation
0	GO:0045922	Negative Regulation Of Fatty Acid Metabolic Process
0	GO:0051918	Negative Regulation Of Fibrinolysis
0	GO:0040037	Negative Regulation Of Fibroblast Growth Factor Receptor Signaling Pathway
0	GO:0048147	Negative Regulation Of Fibroblast Proliferation
1	GO:0045744	Negative Regulation Of G-Protein Coupled Receptor Protein Signaling Pathway
0	GO:0010972	Negative Regulation Of G2/M Transition Of Mitotic Cell Cycle
0	GO:0045814	Negative Regulation Of Gene Expression, Epigenetic
1	GO:0045686	Negative Regulation Of Glial Cell Differentiation
1	GO:0014014	Negative Regulation Of Gliogenesis
0	GO:0045926	Negative Regulation Of Growth
0	GO:0044130	Negative Regulation Of Growth Of Symbiont In Host
0	GO:0044146	Negative Regulation Of Growth Of Symbiont Involved In Interaction With Host
0	GO:0045822	Negative Regulation Of Heart Contraction
0	GO:0031057	Negative Regulation Of Histone Modification
0	GO:0032845	Negative Regulation Of Homeostatic Process
0	GO:0046888	Negative Regulation Of Hormone Secretion
0	GO:0051346	Negative Regulation Of Hydrolase Activity
0	GO:0043124	Negative Regulation Of I-Kappab Kinase/Nf-Kappab Cascade
0	GO:0002698	Negative Regulation Of Immune Effector Process
0	GO:0050777	Negative Regulation Of Immune Response
0	GO:0002683	Negative Regulation Of Immune System Process
0	GO:0050728	Negative Regulation Of Inflammatory Response
0	GO:0046627	Negative Regulation Of Insulin Receptor Signaling Pathway
0	GO:0046676	Negative Regulation Of Insulin Secretion
0	GO:0032689	Negative Regulation Of Interferon-Gamma Production
0	GO:0032703	Negative Regulation Of Interleukin-2 Production
0	GO:0032715	Negative Regulation Of Interleukin-6 Production
0	GO:0010741	Negative Regulation Of Intracellular Protein Kinase Cascade
0	GO:0090317	Negative Regulation Of Intracellular Protein Transport
0	GO:0033144	Negative Regulation Of Intracellular Steroid Hormone Receptor Signaling Pathway
0	GO:0032387	Negative Regulation Of Intracellular Transport
0	GO:0032413	Negative Regulation Of Ion Transmembrane Transporter Activity
0	GO:0043271	Negative Regulation Of Ion Transport
0	GO:0046426	Negative Regulation Of Jak-Stat Cascade
0	GO:0046329	Negative Regulation Of Jnk Cascade
0	GO:0043508	Negative Regulation Of Jun Kinase Activity
0	GO:0033673	Negative Regulation Of Kinase Activity
0	GO:0002695	Negative Regulation Of Leukocyte Activation
0	GO:2000107	Negative Regulation Of Leukocyte Apoptotic Process
0	GO:0002704	Negative Regulation Of Leukocyte Mediated Immunity
0	GO:0070664	Negative Regulation Of Leukocyte Proliferation
0	GO:0051352	Negative Regulation Of Ligase Activity
0	GO:0051055	Negative Regulation Of Lipid Biosynthetic Process

0	GO:0050995	Negative Regulation Of Lipid Catabolic Process
0	GO:0045833	Negative Regulation Of Lipid Metabolic Process
0	GO:0010888	Negative Regulation Of Lipid Storage
0	GO:0032369	Negative Regulation Of Lipid Transport
0	GO:0040013	Negative Regulation Of Locomotion
0	GO:0051350	Negative Regulation Of Lyase Activity
0	GO:0051250	Negative Regulation Of Lymphocyte Activation
0	GO:0070229	Negative Regulation Of Lymphocyte Apoptotic Process
0	GO:0045620	Negative Regulation Of Lymphocyte Differentiation
0	GO:0002707	Negative Regulation Of Lymphocyte Mediated Immunity
0	GO:0050672	Negative Regulation Of Lymphocyte Proliferation
0	GO:0010745	Negative Regulation Of Macrophage Derived Foam Cell Differentiation
0	GO:0043407	Negative Regulation Of Map Kinase Activity
0	GO:0043409	Negative Regulation Of Mapk Cascade
0	GO:0007026	Negative Regulation Of Microtubule Depolymerization
0	GO:0031111	Negative Regulation Of Microtubule Polymerization Or Depolymerization
0	GO:0045839	Negative Regulation Of Mitosis
0	GO:0045930	Negative Regulation Of Mitotic Cell Cycle
0	GO:0045841	Negative Regulation Of Mitotic Metaphase/Anaphase Transition
0	GO:0032945	Negative Regulation Of Mononuclear Cell Proliferation
0	GO:0032769	Negative Regulation Of Monooxygenase Activity
0	GO:0050686	Negative Regulation Of Mrna Processing
0	GO:0043901	Negative Regulation Of Multi-Organism Process
0	GO:0051241	Negative Regulation Of Multicellular Organismal Process
0	GO:0010656	Negative Regulation Of Muscle Cell Apoptotic Process
0	GO:0051148	Negative Regulation Of Muscle Cell Differentiation
0	GO:0045932	Negative Regulation Of Muscle Contraction
0	GO:0048635	Negative Regulation Of Muscle Organ Development
0	GO:0045638	Negative Regulation Of Myeloid Cell Differentiation
0	GO:0002762	Negative Regulation Of Myeloid Leukocyte Differentiation
1	GO:2000178	Negative Regulation Of Neural Precursor Cell Proliferation
1	GO:0050768	Negative Regulation Of Neurogenesis
1	GO:0031645	Negative Regulation Of Neurological System Process
1	GO:0043524	Negative Regulation Of Neuron Apoptotic Process
1	GO:0045665	Negative Regulation Of Neuron Differentiation
1	GO:0010977	Negative Regulation Of Neuron Projection Development
0	GO:0042347	Negative Regulation Of Nf-Kappab Import Into Nucleus
0	GO:0032088	Negative Regulation Of Nf-Kappab Transcription Factor Activity
0	GO:0045746	Negative Regulation Of Notch Signaling Pathway
0	GO:0051784	Negative Regulation Of Nuclear Division
0	GO:0046823	Negative Regulation Of Nucleocytoplasmic Transport
0	GO:0030809	Negative Regulation Of Nucleotide Biosynthetic Process
0	GO:0045980	Negative Regulation Of Nucleotide Metabolic Process
1	GO:0048715	Negative Regulation Of Oligodendrocyte Differentiation
0	GO:0010639	Negative Regulation Of Organelle Organization
0	GO:0030279	Negative Regulation Of Ossification
0	GO:0045668	Negative Regulation Of Osteoblast Differentiation
0	GO:0045671	Negative Regulation Of Osteoclast Differentiation
0	GO:0051354	Negative Regulation Of Oxidoreductase Activity
0	GO:0010466	Negative Regulation Of Peptidase Activity
0	GO:0090278	Negative Regulation Of Peptide Hormone Secretion
0	GO:0002792	Negative Regulation Of Peptide Secretion
0	GO:0033137	Negative Regulation Of Peptidyl-Serine Phosphorylation
0	GO:0050732	Negative Regulation Of Peptidyl-Tyrosine Phosphorylation
0	GO:0045936	Negative Regulation Of Phosphate Metabolic Process
0	GO:0010563	Negative Regulation Of Phosphorus Metabolic Process

0	GO:0042326	Negative Regulation Of Phosphorylation
0	GO:0032435	Negative Regulation Of Proteasomal Ubiquitin-Dependent Protein Catabolic Process
0	GO:0032091	Negative Regulation Of Protein Binding
0	GO:0042177	Negative Regulation Of Protein Catabolic Process
0	GO:0031333	Negative Regulation Of Protein Complex Assembly
0	GO:0043242	Negative Regulation Of Protein Complex Disassembly
0	GO:0042308	Negative Regulation Of Protein Import Into Nucleus
0	GO:0006469	Negative Regulation Of Protein Kinase Activity
0	GO:0051898	Negative Regulation Of Protein Kinase B Signaling Cascade
0	GO:0051248	Negative Regulation Of Protein Metabolic Process
0	GO:0031400	Negative Regulation Of Protein Modification Process
0	GO:0001933	Negative Regulation Of Protein Phosphorylation
0	GO:0032272	Negative Regulation Of Protein Polymerization
0	GO:0050709	Negative Regulation Of Protein Secretion
0	GO:0071901	Negative Regulation Of Protein Serine/Threonine Kinase Activity
0	GO:0051224	Negative Regulation Of Protein Transport
0	GO:0061099	Negative Regulation Of Protein Tyrosine Kinase Activity
0	GO:0031397	Negative Regulation Of Protein Ubiquitination
0	GO:0045861	Negative Regulation Of Proteolysis
0	GO:0046580	Negative Regulation Of Ras Protein Signal Transduction
0	GO:2000242	Negative Regulation Of Reproductive Process
0	GO:0002832	Negative Regulation Of Response To Biotic Stimulus
0	GO:0060761	Negative Regulation Of Response To Cytokine Stimulus
0	GO:2001021	Negative Regulation Of Response To Dna Damage Stimulus
0	GO:0032102	Negative Regulation Of Response To External Stimulus
0	GO:0032105	Negative Regulation Of Response To Extracellular Stimulus
0	GO:0032108	Negative Regulation Of Response To Nutrient Levels
0	GO:0033119	Negative Regulation Of Rna Splicing
0	GO:0045749	Negative Regulation Of S Phase Of Mitotic Cell Cycle
0	GO:0051048	Negative Regulation Of Secretion
0	GO:0043433	Negative Regulation Of Sequence-Specific Dna Binding Transcription Factor Activity
0	GO:0051283	Negative Regulation Of Sequestering Of Calcium Ion
0	GO:0009968	Negative Regulation Of Signal Transduction
0	GO:0051058	Negative Regulation Of Small Gtpase Mediated Signal Transduction
0	GO:0048662	Negative Regulation Of Smooth Muscle Cell Proliferation
0	GO:0045879	Negative Regulation Of Smoothened Signaling Pathway
0	GO:0010894	Negative Regulation Of Steroid Biosynthetic Process
0	GO:0045939	Negative Regulation Of Steroid Metabolic Process
0	GO:0070303	Negative Regulation Of Stress-Activated Protein Kinase Signaling Cascade
0	GO:0045843	Negative Regulation Of Striated Muscle Tissue Development
1	GO:0050805	Negative Regulation Of Synaptic Transmission
0	GO:0003085	Negative Regulation Of Systemic Arterial Blood Pressure
0	GO:0050868	Negative Regulation Of T Cell Activation
0	GO:0045581	Negative Regulation Of T Cell Differentiation
0	GO:0042130	Negative Regulation Of T Cell Proliferation
0	GO:0050860	Negative Regulation Of T Cell Receptor Signaling Pathway
0	GO:0034104	Negative Regulation Of Tissue Remodeling
0	GO:0032007	Negative Regulation Of Tor Signaling Cascade
0	GO:0042992	Negative Regulation Of Transcription Factor Import Into Nucleus
0	GO:0000122	Negative Regulation Of Transcription From Rna Polymerase Ii Promoter
0	GO:0051348	Negative Regulation Of Transferase Activity
0	GO:0030512	Negative Regulation Of Transforming Growth Factor Beta Receptor Signaling Pathway
0	GO:0017148	Negative Regulation Of Translation
0	GO:0045947	Negative Regulation Of Translational Initiation
0	GO:0090101	Negative Regulation Of Transmembrane Receptor Protein Serine/Threonine Kinase Signaling Pathway
0	GO:0034763	Negative Regulation Of Transmembrane Transport

0	GO:0051970	Negative Regulation Of Transmission Of Nerve Impulse
0	GO:0051051	Negative Regulation Of Transport
0	GO:0032410	Negative Regulation Of Transporter Activity
0	GO:0032720	Negative Regulation Of Tumor Necrosis Factor Production
0	GO:0032480	Negative Regulation Of Type I Interferon Production
0	GO:0051444	Negative Regulation Of Ubiquitin-Protein Ligase Activity
0	GO:0051436	Negative Regulation Of Ubiquitin-Protein Ligase Activity Involved In Mitotic Cell Cycle
0	GO:0045071	Negative Regulation Of Viral Genome Replication
0	GO:0048525	Negative Regulation Of Viral Reproduction
0	GO:0032897	Negative Regulation Of Viral Transcription
0	GO:0030178	Negative Regulation Of Wnt Receptor Signaling Pathway
0	GO:0043383	Negative T Cell Selection
0	GO:0045060	Negative Thymic T Cell Selection
0	GO:0072006	Nephron Development
0	GO:0072009	Nephron Epithelium Development
0	GO:0072088	Nephron Epithelium Morphogenesis
0	GO:0072028	Nephron Morphogenesis
0	GO:0072080	Nephron Tubule Development
0	GO:0072160	Nephron Tubule Epithelial Cell Differentiation
0	GO:0072079	Nephron Tubule Formation
0	GO:0072078	Nephron Tubule Morphogenesis
1	GO:0021675	Nerve Development
1	GO:0048011	Nerve Growth Factor Receptor Signaling Pathway
1	GO:0014032	Neural Crest Cell Development
1	GO:0014033	Neural Crest Cell Differentiation
1	GO:0001755	Neural Crest Cell Migration
1	GO:0001840	Neural Plate Development
1	GO:0060896	Neural Plate Pattern Specification
1	GO:0061351	Neural Precursor Cell Proliferation
1	GO:0003407	Neural Retina Development
1	GO:0001843	Neural Tube Closure
1	GO:0021915	Neural Tube Development
1	GO:0001841	Neural Tube Formation
1	GO:0021532	Neural Tube Patterning
1	GO:0007405	Neuroblast Proliferation
1	GO:0060053	Neurofilament Cytoskeleton
1	GO:0001976	Neurological System Process Involved In Regulation Of Systemic Arterial Blood Pressure
0	GO:0031594	Neuromuscular Junction
0	GO:0007528	Neuromuscular Junction Development
0	GO:0050905	Neuromuscular Process
0	GO:0050885	Neuromuscular Process Controlling Balance
0	GO:0050884	Neuromuscular Process Controlling Posture
0	GO:0007274	Neuromuscular Synaptic Transmission
1	GO:0051402	Neuron Apoptotic Process
1	GO:0007158	Neuron Cell-Cell Adhesion
1	GO:0070997	Neuron Death
1	GO:0048663	Neuron Fate Commitment
1	GO:0048665	Neuron Fate Specification
1	GO:0042551	Neuron Maturation
1	GO:0001764	Neuron Migration
1	GO:0032589	Neuron Projection Membrane
1	GO:0031102	Neuron Projection Regeneration
1	GO:0044306	Neuron Projection Terminus
1	GO:0008038	Neuron Recognition
1	GO:0044309	Neuron Spine
1	GO:0007270	Neuron-Neuron Synaptic Transmission

1	GO:0043025	Neuronal Cell Body
1	GO:0005184	Neuropeptide Hormone Activity
1	GO:0008188	Neuropeptide Receptor Activity
1	GO:0071855	Neuropeptide Receptor Binding
1	GO:0007218	Neuropeptide Signaling Pathway
1	GO:0043526	Neuroprotection
1	GO:0042165	Neurotransmitter Binding
1	GO:0042136	Neurotransmitter Biosynthetic Process
1	GO:0042133	Neurotransmitter Metabolic Process
1	GO:0030594	Neurotransmitter Receptor Activity
1	GO:0007269	Neurotransmitter Secretion
1	GO:0006836	Neurotransmitter Transport
1	GO:0005326	Neurotransmitter Transporter Activity
1	GO:0001504	Neurotransmitter Uptake
1	GO:0005328	Neurotransmitter:Sodium Symporter Activity
0	GO:0015175	Neutral Amino Acid Transmembrane Transporter Activity
0	GO:0015804	Neutral Amino Acid Transport
0	GO:0046460	Neutral Lipid Biosynthetic Process
0	GO:0046461	Neutral Lipid Catabolic Process
0	GO:0006638	Neutral Lipid Metabolic Process
0	GO:0042119	Neutrophil Activation
0	GO:0030593	Neutrophil Chemotaxis
0	GO:0002446	Neutrophil Mediated Immunity
0	GO:0051059	Nf-Kappab Binding
0	GO:0042348	Nf-Kappab Import Into Nucleus
0	GO:0019359	Nicotinamide Nucleotide Biosynthetic Process
0	GO:0046496	Nicotinamide Nucleotide Metabolic Process
0	GO:0006809	Nitric Oxide Biosynthetic Process
0	GO:0007263	Nitric Oxide Mediated Signal Transduction
0	GO:0046209	Nitric Oxide Metabolic Process
0	GO:0071705	Nitrogen Compound Transport
0	GO:0071941	Nitrogen Cycle Metabolic Process
0	GO:0006607	Nls-Bearing Substrate Import Into Nucleus
0	GO:0035567	Non-Canonical Wnt Receptor Signaling Pathway
0	GO:0004715	Non-Membrane Spanning Protein Tyrosine Kinase Activity
0	GO:0000726	Non-Recombinational Repair
0	GO:0031513	Nonmotile Primary Cilium
1	GO:0048243	Norepinephrine Secretion
1	GO:0015874	Norepinephrine Transport
0	GO:0043584	Nose Development
0	GO:0005112	Notch Binding
0	GO:0007220	Notch Receptor Processing
0	GO:0007219	Notch Signaling Pathway
0	GO:0030903	Notochord Development
1	GO:0071564	Npbaf Complex
0	GO:0035267	Nua4 Histone Acetyltransferase Complex
0	GO:0016604	Nuclear Body
0	GO:0000790	Nuclear Chromatin
0	GO:0000228	Nuclear Chromosome
0	GO:0044454	Nuclear Chromosome Part
0	GO:0000784	Nuclear Chromosome, Telomeric Region
0	GO:0000280	Nuclear Division
0	GO:0055029	Nuclear Dna-Directed Rna Polymerase Complex
0	GO:0005635	Nuclear Envelope
0	GO:0006998	Nuclear Envelope Organization
0	GO:0051168	Nuclear Export

0	GO:0005720	Nuclear Heterochromatin
0	GO:0035257	Nuclear Hormone Receptor Binding
0	GO:0051170	Nuclear Import
0	GO:0005637	Nuclear Inner Membrane
0	GO:0016363	Nuclear Matrix
0	GO:0031965	Nuclear Membrane
0	GO:0000398	Nuclear Mrna Splicing, Via Spliceosome
0	GO:0005640	Nuclear Outer Membrane
0	GO:0034399	Nuclear Periphery
0	GO:0005643	Nuclear Pore
0	GO:0043596	Nuclear Replication Fork
0	GO:0043601	Nuclear Replisome
0	GO:0016607	Nuclear Speck
0	GO:0000783	Nuclear Telomere Cap Complex
0	GO:0051169	Nuclear Transport
0	GO:0000152	Nuclear Ubiquitin Ligase Complex
0	GO:0000956	Nuclear-Transcribed Mrna Catabolic Process
0	GO:0000288	Nuclear-Transcribed Mrna Catabolic Process, Deadenylation-Dependent Decay
0	GO:0000291	Nuclear-Transcribed Mrna Catabolic Process, Exonucleolytic
0	GO:0000184	Nuclear-Transcribed Mrna Catabolic Process, Nonsense-Mediated Decay
0	GO:0000289	Nuclear-Transcribed Mrna Poly(A) Tail Shortening
0	GO:0004518	Nuclease Activity
0	GO:0090305	Nucleic Acid Phosphodiester Bond Hydrolysis
0	GO:0050657	Nucleic Acid Transport
0	GO:0046112	Nucleobase Biosynthetic Process
0	GO:0009112	Nucleobase Metabolic Process
0	GO:0015851	Nucleobase Transport
0	GO:0034654	Nucleobase-Containing Compound Biosynthetic Process
0	GO:0019205	Nucleobase-Containing Compound Kinase Activity
0	GO:0015932	Nucleobase-Containing Compound Transmembrane Transporter Activity
0	GO:0015931	Nucleobase-Containing Compound Transport
0	GO:0015949	Nucleobase-Containing Small Molecule Interconversion
0	GO:0006913	Nucleocytoplasmic Transport
0	GO:0005487	Nucleocytoplasmic Transporter Activity
0	GO:0009295	Nucleoid
0	GO:0044452	Nucleolar Part
0	GO:0005730	Nucleolus
0	GO:0001882	Nucleoside Binding
0	GO:0009163	Nucleoside Biosynthetic Process
0	GO:0033865	Nucleoside Bisphosphate Metabolic Process
0	GO:0009164	Nucleoside Catabolic Process
0	GO:0009132	Nucleoside Diphosphate Metabolic Process
0	GO:0019206	Nucleoside Kinase Activity
0	GO:0009116	Nucleoside Metabolic Process
0	GO:0009124	Nucleoside Monophosphate Biosynthetic Process
0	GO:0009125	Nucleoside Monophosphate Catabolic Process
0	GO:0009123	Nucleoside Monophosphate Metabolic Process
0	GO:0043174	Nucleoside Salvage
0	GO:0009142	Nucleoside Triphosphate Biosynthetic Process
0	GO:0060589	Nucleoside-Triphosphatase Regulator Activity
0	GO:0000786	Nucleosome
0	GO:0006334	Nucleosome Assembly
0	GO:0006337	Nucleosome Disassembly
0	GO:0034728	Nucleosome Organization
0	GO:0008252	Nucleotidase Activity
0	GO:0009165	Nucleotide Biosynthetic Process

0	GO:0019201	Nucleotide Kinase Activity
0	GO:0046939	Nucleotide Phosphorylation
0	GO:0016502	Nucleotide Receptor Activity
0	GO:0035872	Nucleotide-Binding Domain, Leucine Rich Repeat Containing Receptor Signaling Pathway
0	GO:0070423	Nucleotide-Binding Oligomerization Domain Containing Signaling Pathway
0	GO:0006289	Nucleotide-Excision Repair
0	GO:0000718	Nucleotide-Excision Repair, Dna Damage Removal
0	GO:0006297	Nucleotide-Excision Repair, Dna Gap Filling
0	GO:0009225	Nucleotide-Sugar Metabolic Process
0	GO:0016779	Nucleotidyltransferase Activity
0	GO:0051647	Nucleus Localization
0	GO:0006997	Nucleus Organization
0	GO:0031080	Nup107-160 Complex
0	GO:0016581	Nurd Complex
0	GO:0008374	O-Acyltransferase Activity
0	GO:0008171	O-Methyltransferase Activity
0	GO:0070160	Occluding Junction
0	GO:0042476	Odontogenesis
0	GO:0042475	Odontogenesis Of Dentin-Containing Tooth
0	GO:0021772	Olfactory Bulb Development
0	GO:0021889	Olfactory Bulb Interneuron Differentiation
0	GO:0021988	Olfactory Lobe Development
0	GO:0004984	Olfactory Receptor Activity
0	GO:0014003	Oligodendrocyte Development
0	GO:0048709	Oligodendrocyte Differentiation
0	GO:0009312	Oligosaccharide Biosynthetic Process
0	GO:0009311	Oligosaccharide Metabolic Process
0	GO:0004576	Oligosaccharyl Transferase Activity
0	GO:0008250	Oligosaccharyltransferase Complex
0	GO:0008242	Omega Peptidase Activity
0	GO:0006730	One-Carbon Metabolic Process
0	GO:0048599	Oocyte Development
0	GO:0009994	Oocyte Differentiation
0	GO:0001556	Oocyte Maturation
0	GO:0048477	Oogenesis
0	GO:0048645	Organ Formation
0	GO:0035265	Organ Growth
0	GO:0001759	Organ Induction
0	GO:0031100	Organ Regeneration
0	GO:0000315	Organellar Large Ribosomal Subunit
0	GO:0000313	Organellar Ribosome
0	GO:0000314	Organellar Small Ribosomal Subunit
0	GO:0070925	Organelle Assembly
0	GO:0031970	Organelle Envelope Lumen
0	GO:0048285	Organelle Fission
0	GO:0048284	Organelle Fusion
0	GO:0019866	Organelle Inner Membrane
0	GO:0051640	Organelle Localization
0	GO:0031968	Organelle Outer Membrane
0	GO:0031984	Organelle Subcompartment
0	GO:0072384	Organelle Transport Along Microtubule
0	GO:0016053	Organic Acid Biosynthetic Process
0	GO:0016054	Organic Acid Catabolic Process
0	GO:0005342	Organic Acid Transmembrane Transporter Activity
0	GO:0015849	Organic Acid Transport
0	GO:0005343	Organic Acid:Sodium Symporter Activity

0	GO:0015850	Organic Alcohol Transport
0	GO:0008514	Organic Anion Transmembrane Transporter Activity
0	GO:0015711	Organic Anion Transport
0	GO:0015101	Organic Cation Transmembrane Transporter Activity
0	GO:0015695	Organic Cation Transport
0	GO:0018904	Organic Ether Metabolic Process
0	GO:0071702	Organic Substance Transport
0	GO:0090407	Organophosphate Biosynthetic Process
0	GO:0046434	Organophosphate Catabolic Process
0	GO:0019637	Organophosphate Metabolic Process
0	GO:0001503	Ossification
0	GO:0002076	Osteoblast Development
0	GO:0001649	Osteoblast Differentiation
0	GO:0033687	Osteoblast Proliferation
0	GO:0030316	Osteoclast Differentiation
0	GO:0071599	Otic Vesicle Development
0	GO:0030916	Otic Vesicle Formation
0	GO:0071600	Otic Vesicle Morphogenesis
0	GO:0019867	Outer Membrane
0	GO:0030288	Outer Membrane-Bounded Periplasmic Space
0	GO:0003151	Outflow Tract Morphogenesis
0	GO:0001541	Ovarian Follicle Development
0	GO:0030728	Ovulation
0	GO:0042698	Ovulation Cycle
0	GO:0022602	Ovulation Cycle Process
0	GO:0001542	Ovulation From Ovarian Follicle
0	GO:0061039	Ovum-Producing Ovary Development
0	GO:0006107	Oxaloacetate Metabolic Process
0	GO:0006119	Oxidative Phosphorylation
0	GO:0016675	Oxidoreductase Activity, Acting On A Heme Group Of Donors
0	GO:0016676	Oxidoreductase Activity, Acting On A Heme Group Of Donors, Oxygen As Acceptor
0	GO:0016667	Oxidoreductase Activity, Acting On A Sulfur Group Of Donors
0	GO:0016725	Oxidoreductase Activity, Acting On Ch Or Ch2 Groups
0	GO:0016614	Oxidoreductase Activity, Acting On Ch-Oh Group Of Donors
0	GO:0016651	Oxidoreductase Activity, Acting On Nadh Or Nadph
0	GO:0050664	Oxidoreductase Activity, Acting On Nadh Or Nadph, Oxygen As Acceptor
0	GO:0016655	Oxidoreductase Activity, Acting On Nadh Or Nadph, Quinone Or Similar Compound As Acceptor
0	GO:0016705	Oxidoreductase Activity, Acting On Paired Donors, With Incorporation Or Reduction Of Molecular Oxygen
0	GO:0016706	Oxidoreductase Activity, Acting On Paired Donors, With Incorporation Or Reduction Of Molecular Oxygen, 2-Oxoglutarate As One Donor, And Incorporation Of One Atom Each Of Oxygen Into Both Donors
0	GO:0016709	Oxidoreductase Activity, Acting On Paired Donors, With Incorporation Or Reduction Of Molecular Oxygen, Nadh Or Nadph As One Donor, And Incorporation Of One Atom Of Oxygen
0	GO:0016712	Oxidoreductase Activity, Acting On Paired Donors, With Incorporation Or Reduction Of Molecular Oxygen, Reduced Flavin Or Flavoprotein As One Donor, And Incorporation Of One Atom Of Oxygen
0	GO:0016684	Oxidoreductase Activity, Acting On Peroxide As Acceptor
0	GO:0016701	Oxidoreductase Activity, Acting On Single Donors With Incorporation Of Molecular Oxygen
0	GO:0016702	Oxidoreductase Activity, Acting On Single Donors With Incorporation Of Molecular Oxygen, Incorporation Of Two Atoms Of Oxygen
0	GO:0016903	Oxidoreductase Activity, Acting On The Aldehyde Or Oxo Group Of Donors
0	GO:0016624	Oxidoreductase Activity, Acting On The Aldehyde Or Oxo Group Of Donors, Disulfide As Acceptor
0	GO:0016620	Oxidoreductase Activity, Acting On The Aldehyde Or Oxo Group Of Donors, Nad Or Nadp As Acceptor
0	GO:0016627	Oxidoreductase Activity, Acting On The Ch-Ch Group Of Donors
0	GO:0016628	Oxidoreductase Activity, Acting On The Ch-Ch Group Of Donors, Nad Or Nadp As Acceptor
0	GO:0016634	Oxidoreductase Activity, Acting On The Ch-Ch Group Of Donors, Oxygen As Acceptor
0	GO:0016645	Oxidoreductase Activity, Acting On The Ch-Nh Group Of Donors
0	GO:0016646	Oxidoreductase Activity, Acting On The Ch-Nh Group Of Donors, Nad Or Nadp As Acceptor
0	GO:0016638	Oxidoreductase Activity, Acting On The Ch-Nh2 Group Of Donors
0	GO:0016641	Oxidoreductase Activity, Acting On The Ch-Nh2 Group Of Donors, Oxygen As Acceptor
0	GO:0016616	Oxidoreductase Activity, Acting On The Ch-Oh Group Of Donors, Nad Or Nadp As Acceptor
0	GO:0006733	Oxidoreduction Coenzyme Metabolic Process

0	GO:0019825	Oxygen Binding
0	GO:0043186	P Granule
0	GO:0015450	P-P-Bond-Hydrolysis-Driven Protein Transmembrane Transporter Activity
0	GO:0015405	P-P-Bond-Hydrolysis-Driven Transmembrane Transporter Activity
0	GO:0002039	P53 Binding
0	GO:0060021	Palate Development
1	GO:0021543	Pallium Development
0	GO:0016409	Palmitoyltransferase Activity
0	GO:0031016	Pancreas Development
0	GO:0015939	Pantothenate Metabolic Process
0	GO:0048486	Parasympathetic Nervous System Development
0	GO:0048339	Paraxial Mesoderm Development
0	GO:0007567	Parturition
0	GO:0022803	Passive Transmembrane Transporter Activity
0	GO:0060389	Pathway-Restricted Smad Protein Phosphorylation
0	GO:0001871	Pattern Binding
0	GO:0008329	Pattern Recognition Receptor Activity
0	GO:0002221	Pattern Recognition Receptor Signaling Pathway
0	GO:0007389	Pattern Specification Process
0	GO:0001569	Patterning Of Blood Vessels
0	GO:0031519	Pcg Protein Complex
0	GO:0030165	Pdz Domain Binding
0	GO:0043084	Penile Erection
0	GO:0019321	Pentose Metabolic Process
0	GO:0006098	Pentose-Phosphate Shunt
0	GO:0016504	Peptidase Activator Activity
0	GO:0030414	Peptidase Inhibitor Activity
0	GO:0061134	Peptidase Regulator Activity
0	GO:0042605	Peptide Antigen Binding
0	GO:0042277	Peptide Binding
0	GO:0043043	Peptide Biosynthetic Process
0	GO:0018149	Peptide Cross-Linking
0	GO:0017046	Peptide Hormone Binding
0	GO:0016486	Peptide Hormone Processing
0	GO:0051428	Peptide Hormone Receptor Binding
0	GO:0030072	Peptide Hormone Secretion
0	GO:0006518	Peptide Metabolic Process
0	GO:0001653	Peptide Receptor Activity
0	GO:0002790	Peptide Secretion
0	GO:0015833	Peptide Transport
0	GO:0018195	Peptidyl-Arginine Modification
0	GO:0018196	Peptidyl-Asparagine Modification
0	GO:0018198	Peptidyl-Cysteine Modification
0	GO:0017187	Peptidyl-Glutamic Acid Carboxylation
0	GO:0018200	Peptidyl-Glutamic Acid Modification
0	GO:0018202	Peptidyl-Histidine Modification
0	GO:0018394	Peptidyl-Lysine Acetylation
0	GO:0018022	Peptidyl-Lysine Methylation
0	GO:0018205	Peptidyl-Lysine Modification
0	GO:0018208	Peptidyl-Proline Modification
0	GO:0003755	Peptidyl-Prolyl Cis-Trans Isomerase Activity
0	GO:0018209	Peptidyl-Serine Modification
0	GO:0018105	Peptidyl-Serine Phosphorylation
0	GO:0018210	Peptidyl-Threonine Modification
0	GO:0018107	Peptidyl-Threonine Phosphorylation
0	GO:0035335	Peptidyl-Tyrosine Dephosphorylation

0	GO:0018212	Peptidyl-Tyrosine Modification
0	GO:0018108	Peptidyl-Tyrosine Phosphorylation
0	GO:0060039	Pericardium Development
0	GO:0000242	Pericentriolar Material
0	GO:0043204	Perikaryon
0	GO:0048471	Perinuclear Region Of Cytoplasm
1	GO:0032292	Peripheral Nervous System Axon Ensheathment
1	GO:0007422	Peripheral Nervous System Development
1	GO:0048935	Peripheral Nervous System Neuron Development
1	GO:0048934	Peripheral Nervous System Neuron Differentiation
0	GO:0042597	Periplasmic Space
0	GO:0004601	Peroxidase Activity
0	GO:0005782	Peroxisomal Matrix
0	GO:0005778	Peroxisomal Membrane
0	GO:0044439	Peroxisomal Part
0	GO:0043574	Peroxisomal Transport
0	GO:0005777	Peroxisome
0	GO:0007031	Peroxisome Organization
0	GO:0045851	Ph Reduction
0	GO:0001891	Phagocytic Cup
0	GO:0045335	Phagocytic Vesicle
0	GO:0030670	Phagocytic Vesicle Membrane
0	GO:0006909	Phagocytosis
0	GO:0006911	Phagocytosis, Engulfment
0	GO:0060037	Pharyngeal System Development
0	GO:0014821	Phasic Smooth Muscle Contraction
0	GO:0018958	Phenol-Containing Compound Metabolic Process
0	GO:0016791	Phosphatase Activity
0	GO:0019902	Phosphatase Binding
0	GO:0019212	Phosphatase Inhibitor Activity
0	GO:0019208	Phosphatase Regulator Activity
0	GO:0042301	Phosphate Ion Binding
0	GO:0055062	Phosphate Ion Homeostasis
0	GO:0015114	Phosphate Ion Transmembrane Transporter Activity
0	GO:0006817	Phosphate Ion Transport
0	GO:0008195	Phosphatidate Phosphatase Activity
0	GO:0006656	Phosphatidylcholine Biosynthetic Process
0	GO:0046470	Phosphatidylcholine Metabolic Process
0	GO:0035004	Phosphatidylinositol 3-Kinase Activity
0	GO:0043548	Phosphatidylinositol 3-Kinase Binding
0	GO:0014065	Phosphatidylinositol 3-Kinase Cascade
0	GO:0005942	Phosphatidylinositol 3-Kinase Complex
0	GO:0035091	Phosphatidylinositol Binding
0	GO:0006661	Phosphatidylinositol Biosynthetic Process
0	GO:0034593	Phosphatidylinositol Bisphosphate Phosphatase Activity
0	GO:0052742	Phosphatidylinositol Kinase Activity
0	GO:0046488	Phosphatidylinositol Metabolic Process
0	GO:0016307	Phosphatidylinositol Phosphate Kinase Activity
0	GO:0004435	Phosphatidylinositol Phospholipase C Activity
0	GO:0046854	Phosphatidylinositol Phosphorylation
0	GO:0032266	Phosphatidylinositol-3-Phosphate Binding
0	GO:0043325	Phosphatidylinositol-3,4-Bisphosphate Binding
0	GO:0005547	Phosphatidylinositol-3,4,5-Trisphosphate Binding
0	GO:0080025	Phosphatidylinositol-3,5-Bisphosphate Binding
0	GO:0005546	Phosphatidylinositol-4,5-Bisphosphate Binding
0	GO:0048015	Phosphatidylinositol-Mediated Signaling

0	GO:0001786	Phosphatidylserine Binding
0	GO:0004623	Phospholipase A2 Activity
0	GO:0004620	Phospholipase Activity
0	GO:0043274	Phospholipase Binding
0	GO:0004629	Phospholipase C Activity
0	GO:0007200	Phospholipase C-Activating G-Protein Coupled Receptor Signaling Pathway
0	GO:0004859	Phospholipase Inhibitor Activity
0	GO:0005543	Phospholipid Binding
0	GO:0008654	Phospholipid Biosynthetic Process
0	GO:0009395	Phospholipid Catabolic Process
0	GO:0046839	Phospholipid Dephosphorylation
0	GO:0006644	Phospholipid Metabolic Process
0	GO:0015914	Phospholipid Transport
0	GO:0005548	Phospholipid Transporter Activity
0	GO:0004012	Phospholipid-Translocating Atpase Activity
0	GO:0051219	Phosphoprotein Binding
0	GO:0004721	Phosphoprotein Phosphatase Activity
0	GO:0008081	Phosphoric Diester Hydrolase Activity
0	GO:0042578	Phosphoric Ester Hydrolase Activity
0	GO:0016849	Phosphorus-Oxygen Lyase Activity
0	GO:0016780	Phosphotransferase Activity, For Other Substituted Phosphate Groups
0	GO:0016775	Phosphotransferase Activity, Nitrogenous Group As Acceptor
0	GO:0016776	Phosphotransferase Activity, Phosphate Group As Acceptor
0	GO:0001784	Phosphotyrosine Binding
0	GO:0009881	Photoreceptor Activity
0	GO:0042461	Photoreceptor Cell Development
0	GO:0046530	Photoreceptor Cell Differentiation
0	GO:0045494	Photoreceptor Cell Maintenance
0	GO:0032391	Photoreceptor Connecting Cilium
0	GO:0001917	Photoreceptor Inner Segment
0	GO:0001750	Photoreceptor Outer Segment
0	GO:0007602	Phototransduction
0	GO:0007603	Phototransduction, Visible Light
0	GO:0046148	Pigment Biosynthetic Process
0	GO:0050931	Pigment Cell Differentiation
0	GO:0048770	Pigment Granule
0	GO:0051875	Pigment Granule Localization
0	GO:0048753	Pigment Granule Organization
0	GO:0051904	Pigment Granule Transport
0	GO:0042440	Pigment Metabolic Process
0	GO:0043473	Pigmentation
1	GO:0021983	Pituitary Gland Development
0	GO:0060674	Placenta Blood Vessel Development
0	GO:0001890	Placenta Development
0	GO:0090179	Planar Cell Polarity Pathway Involved In Neural Tube Closure
0	GO:0034358	Plasma Lipoprotein Particle
0	GO:0034377	Plasma Lipoprotein Particle Assembly
0	GO:0034381	Plasma Lipoprotein Particle Clearance
0	GO:0071827	Plasma Lipoprotein Particle Organization
0	GO:0034369	Plasma Lipoprotein Particle Remodeling
0	GO:0045026	Plasma Membrane Fusion
0	GO:0007009	Plasma Membrane Organization
0	GO:0030168	Platelet Activation
0	GO:0031091	Platelet Alpha Granule
0	GO:0031093	Platelet Alpha Granule Lumen
0	GO:0002576	Platelet Degranulation

0	GO:0048407	Platelet-Derived Growth Factor Binding
0	GO:0005161	Platelet-Derived Growth Factor Receptor Binding
0	GO:0048008	Platelet-Derived Growth Factor Receptor Signaling Pathway
0	GO:0016605	Pml Body
0	GO:0045495	Pole Plasm
0	GO:0070717	Poly-Purine Tract Binding
0	GO:0006595	Polyamine Metabolic Process
0	GO:0019751	Polyol Metabolic Process
0	GO:0004653	Polypeptide N-Acetylgalactosaminyltransferase Activity
0	GO:0030247	Polysaccharide Binding
0	GO:0000271	Polysaccharide Biosynthetic Process
0	GO:0000272	Polysaccharide Catabolic Process
0	GO:0005976	Polysaccharide Metabolic Process
0	GO:0005844	Polysome
0	GO:0031593	Polyubiquitin Binding
0	GO:0046930	Pore Complex
0	GO:0006779	Porphyrin-Containing Compound Biosynthetic Process
0	GO:0006778	Porphyrin-Containing Compound Metabolic Process
0	GO:0050918	Positive Chemotaxis
0	GO:0032233	Positive Regulation Of Actin Filament Bundle Assembly
0	GO:0030838	Positive Regulation Of Actin Filament Polymerization
0	GO:0042104	Positive Regulation Of Activated T Cell Proliferation
0	GO:0002675	Positive Regulation Of Acute Inflammatory Response
0	GO:0002821	Positive Regulation Of Adaptive Immune Response
0	GO:0002824	Positive Regulation Of Adaptive Immune Response Based On Somatic Recombination Of Immune Receptors Built From Immunoglobulin Superfamily Domains
0	GO:0045762	Positive Regulation Of Adenylate Cyclase Activity
0	GO:0010579	Positive Regulation Of Adenylate Cyclase Activity Involved In G-Protein Coupled Receptor Signaling Pathway
0	GO:0046635	Positive Regulation Of Alpha-Beta T Cell Activation
0	GO:0046638	Positive Regulation Of Alpha-Beta T Cell Differentiation
0	GO:0046641	Positive Regulation Of Alpha-Beta T Cell Proliferation
0	GO:0051954	Positive Regulation Of Amine Transport
0	GO:0045766	Positive Regulation Of Angiogenesis
0	GO:0045768	Positive Regulation Of Anti-Apoptosis
0	GO:0002579	Positive Regulation Of Antigen Processing And Presentation
0	GO:0032781	Positive Regulation Of Atpase Activity
1	GO:0045773	Positive Regulation Of Axon Extension
1	GO:0050772	Positive Regulation Of Axonogenesis
0	GO:0050871	Positive Regulation Of B Cell Activation
0	GO:0002714	Positive Regulation Of B Cell Mediated Immunity
0	GO:0030890	Positive Regulation Of B Cell Proliferation
1	GO:0048520	Positive Regulation Of Behavior
0	GO:0051099	Positive Regulation Of Binding
0	GO:0070169	Positive Regulation Of Biomineral Tissue Development
0	GO:0030194	Positive Regulation Of Blood Coagulation
0	GO:0045777	Positive Regulation Of Blood Pressure
0	GO:0043536	Positive Regulation Of Blood Vessel Endothelial Cell Migration
0	GO:0030513	Positive Regulation Of Bmp Signaling Pathway
0	GO:0030501	Positive Regulation Of Bone Mineralization
0	GO:0046852	Positive Regulation Of Bone Remodeling
0	GO:0045780	Positive Regulation Of Bone Resorption
0	GO:0090190	Positive Regulation Of Branching Involved In Ureteric Bud Morphogenesis
0	GO:0051928	Positive Regulation Of Calcium Ion Transport
0	GO:0010524	Positive Regulation Of Calcium Ion Transport Into Cytosol
0	GO:0050850	Positive Regulation Of Calcium-Mediated Signaling
0	GO:0030819	Positive Regulation Of Camp Biosynthetic Process
0	GO:0030816	Positive Regulation Of Camp Metabolic Process

0	GO:0090263	Positive Regulation Of Canonical Wnt Receptor Signaling Pathway
0	GO:0045913	Positive Regulation Of Carbohydrate Metabolic Process
0	GO:0060045	Positive Regulation Of Cardiac Muscle Cell Proliferation
0	GO:0061036	Positive Regulation Of Cartilage Development
0	GO:0009896	Positive Regulation Of Catabolic Process
0	GO:0033605	Positive Regulation Of Catecholamine Secretion
0	GO:2000516	Positive Regulation Of Cd4-Positive, Alpha-Beta T Cell Activation
0	GO:0043372	Positive Regulation Of Cd4-Positive, Alpha-Beta T Cell Differentiation
0	GO:0050867	Positive Regulation Of Cell Activation
0	GO:0045785	Positive Regulation Of Cell Adhesion
0	GO:0033630	Positive Regulation Of Cell Adhesion Mediated By Integrin
0	GO:0045787	Positive Regulation Of Cell Cycle
0	GO:0071158	Positive Regulation Of Cell Cycle Arrest
0	GO:0090068	Positive Regulation Of Cell Cycle Process
0	GO:0010720	Positive Regulation Of Cell Development
0	GO:0045597	Positive Regulation Of Cell Differentiation
0	GO:0051781	Positive Regulation Of Cell Division
0	GO:0030307	Positive Regulation Of Cell Growth
0	GO:0031343	Positive Regulation Of Cell Killing
0	GO:0030335	Positive Regulation Of Cell Migration
0	GO:0010770	Positive Regulation Of Cell Morphogenesis Involved In Differentiation
0	GO:2000147	Positive Regulation Of Cell Motility
0	GO:0031346	Positive Regulation Of Cell Projection Organization
0	GO:0022409	Positive Regulation Of Cell-Cell Adhesion
0	GO:0001954	Positive Regulation Of Cell-Matrix Adhesion
0	GO:0010811	Positive Regulation Of Cell-Substrate Adhesion
0	GO:0010676	Positive Regulation Of Cellular Carbohydrate Metabolic Process
0	GO:0031331	Positive Regulation Of Cellular Catabolic Process
0	GO:0044089	Positive Regulation Of Cellular Component Biogenesis
0	GO:0051272	Positive Regulation Of Cellular Component Movement
0	GO:0051130	Positive Regulation Of Cellular Component Organization
0	GO:0032270	Positive Regulation Of Cellular Protein Metabolic Process
0	GO:0045080	Positive Regulation Of Chemokine Biosynthetic Process
0	GO:0032722	Positive Regulation Of Chemokine Production
0	GO:0050921	Positive Regulation Of Chemotaxis
0	GO:0032376	Positive Regulation Of Cholesterol Transport
0	GO:0032332	Positive Regulation Of Chondrocyte Differentiation
0	GO:2001252	Positive Regulation Of Chromosome Organization
1	GO:0042753	Positive Regulation Of Circadian Rhythm
0	GO:0050820	Positive Regulation Of Coagulation
0	GO:0032967	Positive Regulation Of Collagen Biosynthetic Process
0	GO:0010714	Positive Regulation Of Collagen Metabolic Process
0	GO:0031281	Positive Regulation Of Cyclase Activity
0	GO:0030804	Positive Regulation Of Cyclic Nucleotide Biosynthetic Process
0	GO:0030801	Positive Regulation Of Cyclic Nucleotide Metabolic Process
0	GO:0045737	Positive Regulation Of Cyclin-Dependent Protein Kinase Activity
0	GO:2001056	Positive Regulation Of Cysteine-Type Endopeptidase Activity
0	GO:0043280	Positive Regulation Of Cysteine-Type Endopeptidase Activity Involved In Apoptotic Process
0	GO:0042108	Positive Regulation Of Cytokine Biosynthetic Process
0	GO:0001819	Positive Regulation Of Cytokine Production
0	GO:0002720	Positive Regulation Of Cytokine Production Involved In Immune Response
0	GO:0050715	Positive Regulation Of Cytokine Secretion
0	GO:0001961	Positive Regulation Of Cytokine-Mediated Signaling Pathway
0	GO:0032467	Positive Regulation Of Cytokinesis
0	GO:0051495	Positive Regulation Of Cytoskeleton Organization
0	GO:0031349	Positive Regulation Of Defense Response

0	GO:0002230	Positive Regulation Of Defense Response To Virus By Host
1	GO:0050775	Positive Regulation Of Dendrite Morphogenesis
0	GO:0048639	Positive Regulation Of Developmental Growth
0	GO:0043388	Positive Regulation Of Dna Binding
0	GO:0051054	Positive Regulation Of Dna Metabolic Process
0	GO:0045911	Positive Regulation Of Dna Recombination
0	GO:0045739	Positive Regulation Of Dna Repair
0	GO:0045740	Positive Regulation Of Dna Replication
0	GO:0045807	Positive Regulation Of Endocytosis
0	GO:0010950	Positive Regulation Of Endopeptidase Activity
0	GO:0010595	Positive Regulation Of Endothelial Cell Migration
0	GO:0001938	Positive Regulation Of Endothelial Cell Proliferation
0	GO:0045742	Positive Regulation Of Epidermal Growth Factor Receptor Signaling Pathway
0	GO:0045684	Positive Regulation Of Epidermis Development
0	GO:0030858	Positive Regulation Of Epithelial Cell Differentiation
0	GO:0010634	Positive Regulation Of Epithelial Cell Migration
0	GO:0050679	Positive Regulation Of Epithelial Cell Proliferation
0	GO:0010718	Positive Regulation Of Epithelial To Mesenchymal Transition
0	GO:0070374	Positive Regulation Of Erk1 And Erk2 Cascade
0	GO:0045648	Positive Regulation Of Erythrocyte Differentiation
0	GO:0090004	Positive Regulation Of Establishment Of Protein Localization In Plasma Membrane
0	GO:0045921	Positive Regulation Of Exocytosis
0	GO:0045600	Positive Regulation Of Fat Cell Differentiation
0	GO:0045723	Positive Regulation Of Fatty Acid Biosynthetic Process
0	GO:0045923	Positive Regulation Of Fatty Acid Metabolic Process
0	GO:0048146	Positive Regulation Of Fibroblast Proliferation
0	GO:0051491	Positive Regulation Of Filopodium Assembly
0	GO:0045745	Positive Regulation Of G-Protein Coupled Receptor Protein Signaling Pathway
0	GO:0045815	Positive Regulation Of Gene Expression, Epigenetic
1	GO:0045687	Positive Regulation Of Glial Cell Differentiation
1	GO:0014015	Positive Regulation Of Gliogenesis
0	GO:0046326	Positive Regulation Of Glucose Import
0	GO:0010907	Positive Regulation Of Glucose Metabolic Process
0	GO:0010828	Positive Regulation Of Glucose Transport
0	GO:0045725	Positive Regulation Of Glycogen Biosynthetic Process
0	GO:0070875	Positive Regulation Of Glycogen Metabolic Process
0	GO:0045821	Positive Regulation Of Glycolysis
0	GO:0045927	Positive Regulation Of Growth
0	GO:0043547	Positive Regulation Of Gtpase Activity
0	GO:0045823	Positive Regulation Of Heart Contraction
0	GO:0010460	Positive Regulation Of Heart Rate
0	GO:0031652	Positive Regulation Of Heat Generation
0	GO:0035066	Positive Regulation Of Histone Acetylation
0	GO:0031058	Positive Regulation Of Histone Modification
0	GO:0032846	Positive Regulation Of Homeostatic Process
0	GO:0046886	Positive Regulation Of Hormone Biosynthetic Process
0	GO:0032352	Positive Regulation Of Hormone Metabolic Process
0	GO:0046887	Positive Regulation Of Hormone Secretion
0	GO:0002922	Positive Regulation Of Humoral Immune Response
0	GO:0051345	Positive Regulation Of Hydrolase Activity
0	GO:0043123	Positive Regulation Of I-Kappab Kinase/Nf-Kappab Cascade
0	GO:0002699	Positive Regulation Of Immune Effector Process
0	GO:0050778	Positive Regulation Of Immune Response
0	GO:0002684	Positive Regulation Of Immune System Process
0	GO:0002891	Positive Regulation Of Immunoglobulin Mediated Immune Response
0	GO:0050729	Positive Regulation Of Inflammatory Response

0	GO:0045089	Positive Regulation Of Innate Immune Response
0	GO:0032024	Positive Regulation Of Insulin Secretion
0	GO:0043568	Positive Regulation Of Insulin-Like Growth Factor Receptor Signaling Pathway
0	GO:0032728	Positive Regulation Of Interferon-Beta Production
0	GO:0045078	Positive Regulation Of Interferon-Gamma Biosynthetic Process
0	GO:0032729	Positive Regulation Of Interferon-Gamma Production
0	GO:0032731	Positive Regulation Of Interleukin-1 Beta Production
0	GO:0050718	Positive Regulation Of Interleukin-1 Beta Secretion
0	GO:0032732	Positive Regulation Of Interleukin-1 Production
0	GO:0050716	Positive Regulation Of Interleukin-1 Secretion
0	GO:0032733	Positive Regulation Of Interleukin-10 Production
0	GO:0032735	Positive Regulation Of Interleukin-12 Production
0	GO:0032740	Positive Regulation Of Interleukin-17 Production
0	GO:0045086	Positive Regulation Of Interleukin-2 Biosynthetic Process
0	GO:0032755	Positive Regulation Of Interleukin-6 Production
0	GO:0032757	Positive Regulation Of Interleukin-8 Production
0	GO:0010740	Positive Regulation Of Intracellular Protein Kinase Cascade
0	GO:0090316	Positive Regulation Of Intracellular Protein Transport
0	GO:0032388	Positive Regulation Of Intracellular Transport
0	GO:0032414	Positive Regulation Of Ion Transmembrane Transporter Activity
0	GO:0043270	Positive Regulation Of Ion Transport
0	GO:0045830	Positive Regulation Of Isotype Switching
0	GO:0046427	Positive Regulation Of Jak-Stat Cascade
0	GO:0046330	Positive Regulation Of Jnk Cascade
0	GO:0043507	Positive Regulation Of Jun Kinase Activity
0	GO:0090184	Positive Regulation Of Kidney Development
0	GO:0033674	Positive Regulation Of Kinase Activity
0	GO:0002696	Positive Regulation Of Leukocyte Activation
0	GO:2000108	Positive Regulation Of Leukocyte Apoptotic Process
0	GO:0002690	Positive Regulation Of Leukocyte Chemotaxis
0	GO:0001912	Positive Regulation Of Leukocyte Mediated Cytotoxicity
0	GO:0002705	Positive Regulation Of Leukocyte Mediated Immunity
0	GO:0002687	Positive Regulation Of Leukocyte Migration
0	GO:0070665	Positive Regulation Of Leukocyte Proliferation
0	GO:0051351	Positive Regulation Of Ligase Activity
0	GO:0060193	Positive Regulation Of Lipase Activity
0	GO:0046889	Positive Regulation Of Lipid Biosynthetic Process
0	GO:0050996	Positive Regulation Of Lipid Catabolic Process
0	GO:0090218	Positive Regulation Of Lipid Kinase Activity
0	GO:0045834	Positive Regulation Of Lipid Metabolic Process
0	GO:0010884	Positive Regulation Of Lipid Storage
0	GO:0032370	Positive Regulation Of Lipid Transport
0	GO:0040017	Positive Regulation Of Locomotion
0	GO:0051349	Positive Regulation Of Lyase Activity
0	GO:0051251	Positive Regulation Of Lymphocyte Activation
0	GO:0045621	Positive Regulation Of Lymphocyte Differentiation
0	GO:0002708	Positive Regulation Of Lymphocyte Mediated Immunity
0	GO:0050671	Positive Regulation Of Lymphocyte Proliferation
0	GO:0010744	Positive Regulation Of Macrophage Derived Foam Cell Differentiation
0	GO:0043406	Positive Regulation Of Map Kinase Activity
0	GO:0043410	Positive Regulation Of Mapk Cascade
0	GO:0033005	Positive Regulation Of Mast Cell Activation
0	GO:0051044	Positive Regulation Of Membrane Protein Ectodomain Proteolysis
0	GO:0002053	Positive Regulation Of Mesenchymal Cell Proliferation
0	GO:0031116	Positive Regulation Of Microtubule Polymerization
0	GO:0031112	Positive Regulation Of Microtubule Polymerization Or Depolymerization

0	GO:0010822	Positive Regulation Of Mitochondrion Organization
0	GO:0045840	Positive Regulation Of Mitosis
0	GO:0045931	Positive Regulation Of Mitotic Cell Cycle
0	GO:0032946	Positive Regulation Of Mononuclear Cell Proliferation
0	GO:0032770	Positive Regulation Of Monooxygenase Activity
0	GO:0040018	Positive Regulation Of Multicellular Organism Growth
0	GO:0044253	Positive Regulation Of Multicellular Organismal Metabolic Process
0	GO:0051240	Positive Regulation Of Multicellular Organismal Process
0	GO:0051149	Positive Regulation Of Muscle Cell Differentiation
0	GO:0045933	Positive Regulation Of Muscle Contraction
0	GO:0048636	Positive Regulation Of Muscle Organ Development
0	GO:0045639	Positive Regulation Of Myeloid Cell Differentiation
0	GO:0002763	Positive Regulation Of Myeloid Leukocyte Differentiation
0	GO:0032816	Positive Regulation Of Natural Killer Cell Activation
0	GO:0045954	Positive Regulation Of Natural Killer Cell Mediated Cytotoxicity
0	GO:0002717	Positive Regulation Of Natural Killer Cell Mediated Immunity
1	GO:0051962	Positive Regulation Of Nervous System Development
1	GO:2000179	Positive Regulation Of Neural Precursor Cell Proliferation
1	GO:0002052	Positive Regulation Of Neuroblast Proliferation
1	GO:0050769	Positive Regulation Of Neurogenesis
1	GO:0031646	Positive Regulation Of Neurological System Process
1	GO:0043525	Positive Regulation Of Neuron Apoptotic Process
1	GO:0045666	Positive Regulation Of Neuron Differentiation
1	GO:0010976	Positive Regulation Of Neuron Projection Development
0	GO:0090023	Positive Regulation Of Neutrophil Chemotaxis
0	GO:0042346	Positive Regulation Of Nf-Kappab Import Into Nucleus
0	GO:0051092	Positive Regulation Of Nf-Kappab Transcription Factor Activity
0	GO:0045429	Positive Regulation Of Nitric Oxide Biosynthetic Process
0	GO:0051000	Positive Regulation Of Nitric-Oxide Synthase Activity
0	GO:0045747	Positive Regulation Of Notch Signaling Pathway
0	GO:0051785	Positive Regulation Of Nuclear Division
0	GO:0046824	Positive Regulation Of Nucleocytoplasmic Transport
0	GO:0030810	Positive Regulation Of Nucleotide Biosynthetic Process
0	GO:0045981	Positive Regulation Of Nucleotide Metabolic Process
0	GO:0046622	Positive Regulation Of Organ Growth
0	GO:0010638	Positive Regulation Of Organelle Organization
0	GO:0032892	Positive Regulation Of Organic Acid Transport
0	GO:0045778	Positive Regulation Of Ossification
0	GO:0045669	Positive Regulation Of Osteoblast Differentiation
0	GO:0045672	Positive Regulation Of Osteoclast Differentiation
0	GO:0051353	Positive Regulation Of Oxidoreductase Activity
0	GO:0010862	Positive Regulation Of Pathway-Restricted Smad Protein Phosphorylation
0	GO:0010952	Positive Regulation Of Peptidase Activity
0	GO:0090277	Positive Regulation Of Peptide Hormone Secretion
0	GO:0002793	Positive Regulation Of Peptide Secretion
0	GO:2000758	Positive Regulation Of Peptidyl-Lysine Acetylation
0	GO:0033138	Positive Regulation Of Peptidyl-Serine Phosphorylation
0	GO:0010800	Positive Regulation Of Peptidyl-Threonine Phosphorylation
0	GO:0050731	Positive Regulation Of Peptidyl-Tyrosine Phosphorylation
0	GO:0050766	Positive Regulation Of Phagocytosis
0	GO:0010922	Positive Regulation Of Phosphatase Activity
0	GO:0045937	Positive Regulation Of Phosphate Metabolic Process
0	GO:0043552	Positive Regulation Of Phosphatidylinositol 3-Kinase Activity
0	GO:0014068	Positive Regulation Of Phosphatidylinositol 3-Kinase Cascade
0	GO:0010518	Positive Regulation Of Phospholipase Activity
0	GO:0010863	Positive Regulation Of Phospholipase C Activity

0	GO:0010562	Positive Regulation Of Phosphorus Metabolic Process
0	GO:0042327	Positive Regulation Of Phosphorylation
0	GO:0050927	Positive Regulation Of Positive Chemotaxis
0	GO:0002702	Positive Regulation Of Production Of Molecular Mediator Of Immune Response
0	GO:0032436	Positive Regulation Of Proteasomal Ubiquitin-Dependent Protein Catabolic Process
0	GO:0031954	Positive Regulation Of Protein Autophosphorylation
0	GO:0032092	Positive Regulation Of Protein Binding
0	GO:0045732	Positive Regulation Of Protein Catabolic Process
0	GO:0031334	Positive Regulation Of Protein Complex Assembly
0	GO:0043243	Positive Regulation Of Protein Complex Disassembly
0	GO:0090312	Positive Regulation Of Protein Deacetylation
0	GO:0042307	Positive Regulation Of Protein Import Into Nucleus
0	GO:0045860	Positive Regulation Of Protein Kinase Activity
0	GO:0051897	Positive Regulation Of Protein Kinase B Signaling Cascade
0	GO:0051247	Positive Regulation Of Protein Metabolic Process
0	GO:0031401	Positive Regulation Of Protein Modification Process
0	GO:0032461	Positive Regulation Of Protein Oligomerization
0	GO:0001934	Positive Regulation Of Protein Phosphorylation
0	GO:0032273	Positive Regulation Of Protein Polymerization
0	GO:0050714	Positive Regulation Of Protein Secretion
0	GO:0071902	Positive Regulation Of Protein Serine/Threonine Kinase Activity
0	GO:0051222	Positive Regulation Of Protein Transport
0	GO:0061098	Positive Regulation Of Protein Tyrosine Kinase Activity
0	GO:0031398	Positive Regulation Of Protein Ubiquitination
0	GO:0045862	Positive Regulation Of Proteolysis
0	GO:0032855	Positive Regulation Of Rac Gtpase Activity
0	GO:0032320	Positive Regulation Of Ras Gtpase Activity
0	GO:0046579	Positive Regulation Of Ras Protein Signal Transduction
0	GO:2000379	Positive Regulation Of Reactive Oxygen Species Metabolic Process
0	GO:2000273	Positive Regulation Of Receptor Activity
0	GO:0048260	Positive Regulation Of Receptor-Mediated Endocytosis
0	GO:0090200	Positive Regulation Of Release Of Cytochrome C From Mitochondria
0	GO:0051281	Positive Regulation Of Release Of Sequestered Calcium Ion Into Cytosol
0	GO:0035815	Positive Regulation Of Renal Sodium Excretion
0	GO:2000243	Positive Regulation Of Reproductive Process
0	GO:0060760	Positive Regulation Of Response To Cytokine Stimulus
0	GO:2001022	Positive Regulation Of Response To Dna Damage Stimulus
0	GO:0032103	Positive Regulation Of Response To External Stimulus
0	GO:0032321	Positive Regulation Of Rho Gtpase Activity
0	GO:0051047	Positive Regulation Of Secretion
0	GO:0051091	Positive Regulation Of Sequence-Specific Dna Binding Transcription Factor Activity
0	GO:0048643	Positive Regulation Of Skeletal Muscle Tissue Development
0	GO:0051057	Positive Regulation Of Small Gtpase Mediated Signal Transduction
0	GO:0014911	Positive Regulation Of Smooth Muscle Cell Migration
0	GO:0048661	Positive Regulation Of Smooth Muscle Cell Proliferation
0	GO:0045987	Positive Regulation Of Smooth Muscle Contraction
0	GO:0045880	Positive Regulation Of Smoothened Signaling Pathway
0	GO:0010765	Positive Regulation Of Sodium Ion Transport
0	GO:0010893	Positive Regulation Of Steroid Biosynthetic Process
0	GO:0045940	Positive Regulation Of Steroid Metabolic Process
0	GO:0032373	Positive Regulation Of Sterol Transport
0	GO:0051496	Positive Regulation Of Stress Fiber Assembly
0	GO:0032874	Positive Regulation Of Stress-Activated Mapk Cascade
0	GO:0070304	Positive Regulation Of Stress-Activated Protein Kinase Signaling Cascade
0	GO:0051155	Positive Regulation Of Striated Muscle Cell Differentiation
0	GO:0045844	Positive Regulation Of Striated Muscle Tissue Development

0	GO:0045885	Positive Regulation Of Survival Gene Product Expression
1	GO:0051965	Positive Regulation Of Synapse Assembly
1	GO:0050806	Positive Regulation Of Synaptic Transmission
0	GO:0003084	Positive Regulation Of Systemic Arterial Blood Pressure
0	GO:0050870	Positive Regulation Of T Cell Activation
0	GO:0045582	Positive Regulation Of T Cell Differentiation
0	GO:0001916	Positive Regulation Of T Cell Mediated Cytotoxicity
0	GO:0002711	Positive Regulation Of T Cell Mediated Immunity
0	GO:0042102	Positive Regulation Of T Cell Proliferation
0	GO:0002827	Positive Regulation Of T-Helper 1 Type Immune Response
0	GO:0045624	Positive Regulation Of T-Helper Cell Differentiation
0	GO:0034105	Positive Regulation Of Tissue Remodeling
0	GO:0032008	Positive Regulation Of Tor Signaling Cascade
0	GO:0042993	Positive Regulation Of Transcription Factor Import Into Nucleus
0	GO:0051347	Positive Regulation Of Transferase Activity
0	GO:0071636	Positive Regulation Of Transforming Growth Factor Beta Production
0	GO:0030511	Positive Regulation Of Transforming Growth Factor Beta Receptor Signaling Pathway
0	GO:0045727	Positive Regulation Of Translation
0	GO:0090100	Positive Regulation Of Transmembrane Receptor Protein Serine/Threonine Kinase Signaling Pathway
0	GO:0034764	Positive Regulation Of Transmembrane Transport
0	GO:0051971	Positive Regulation Of Transmission Of Nerve Impulse
0	GO:0051050	Positive Regulation Of Transport
0	GO:0032411	Positive Regulation Of Transporter Activity
0	GO:0032760	Positive Regulation Of Tumor Necrosis Factor Production
0	GO:0032481	Positive Regulation Of Type I Interferon Production
0	GO:0042531	Positive Regulation Of Tyrosine Phosphorylation Of Stat Protein
0	GO:0042517	Positive Regulation Of Tyrosine Phosphorylation Of Stat3 Protein
0	GO:0042523	Positive Regulation Of Tyrosine Phosphorylation Of Stat5 Protein
0	GO:0051443	Positive Regulation Of Ubiquitin-Protein Ligase Activity
0	GO:0051437	Positive Regulation Of Ubiquitin-Protein Ligase Activity Involved In Mitotic Cell Cycle
0	GO:0030949	Positive Regulation Of Vascular Endothelial Growth Factor Receptor Signaling Pathway
0	GO:0045907	Positive Regulation Of Vasoconstriction
0	GO:0045909	Positive Regulation Of Vasodilation
0	GO:0045070	Positive Regulation Of Viral Genome Replication
0	GO:0048524	Positive Regulation Of Viral Reproduction
0	GO:0050434	Positive Regulation Of Viral Transcription
0	GO:0030177	Positive Regulation Of Wnt Receptor Signaling Pathway
0	GO:0010575	Positive Regulation Vascular Endothelial Growth Factor Production
0	GO:0043368	Positive T Cell Selection
0	GO:0009791	Post-Embryonic Development
0	GO:0009886	Post-Embryonic Morphogenesis
0	GO:0048569	Post-Embryonic Organ Development
0	GO:0006892	Post-Golgi Vesicle-Mediated Transport
0	GO:0043687	Post-Translational Protein Modification
0	GO:0006301	Postreplication Repair
1	GO:0014069	Postsynaptic Density
1	GO:0045211	Postsynaptic Membrane
0	GO:0016441	Posttranscriptional Gene Silencing
0	GO:0035194	Posttranscriptional Gene Silencing By Rna
0	GO:0010608	Posttranscriptional Regulation Of Gene Expression
1	GO:0005267	Potassium Channel Activity
1	GO:0034705	Potassium Channel Complex
1	GO:0015459	Potassium Channel Regulator Activity
1	GO:0071805	Potassium Ion Transmembrane Transport
1	GO:0015079	Potassium Ion Transmembrane Transporter Activity
1	GO:0006813	Potassium Ion Transport

0	GO:0008556	Potassium-Transporting Atpase Activity
0	GO:0035102	Prc1 Complex
0	GO:0000407	Pre-Autophagosomal Structure
0	GO:0016254	Preassembly Of Gpi Anchor In Er Membrane
0	GO:0016272	Prefoldin Complex
0	GO:0004659	Prenyltransferase Activity
0	GO:0060134	Prepulse Inhibition
0	GO:0030684	Preribosome
1	GO:0042734	Presynaptic Membrane
0	GO:0015399	Primary Active Transmembrane Transporter Activity
0	GO:0072372	Primary Cilium
1	GO:0014020	Primary Neural Tube Formation
0	GO:0090009	Primitive Streak Formation
0	GO:0035196	Production Of Mirnas Involved In Gene Silencing By Mirna
0	GO:0002532	Production Of Molecular Mediator Involved In Inflammatory Response
0	GO:0002440	Production Of Molecular Mediator Of Immune Response
0	GO:0070918	Production Of Small Rna Involved In Gene Silencing By Rna
0	GO:0070064	Proline-Rich Region Binding
0	GO:0045120	Pronucleus
0	GO:0051324	Prophase
0	GO:0001516	Prostaglandin Biosynthetic Process
0	GO:0006693	Prostaglandin Metabolic Process
0	GO:0046457	Prostanoid Biosynthetic Process
0	GO:0006692	Prostanoid Metabolic Process
0	GO:0004954	Prostanoid Receptor Activity
0	GO:0030850	Prostate Gland Development
0	GO:0060740	Prostate Gland Epithelium Morphogenesis
0	GO:0060736	Prostate Gland Growth
0	GO:0060512	Prostate Gland Morphogenesis
0	GO:0060525	Prostate Glandular Acinus Development
0	GO:0002020	Protease Binding
0	GO:0010498	Proteasomal Protein Catabolic Process
0	GO:0043161	Proteasomal Ubiquitin-Dependent Protein Catabolic Process
0	GO:0022624	Proteasome Accessory Complex
0	GO:0000502	Proteasome Complex
0	GO:0005839	Proteasome Core Complex
0	GO:0006473	Protein Acetylation
0	GO:0072376	Protein Activation Cascade
0	GO:0043543	Protein Acylation
0	GO:0006471	Protein Adp-Ribosylation
0	GO:0008213	Protein Alkylation
0	GO:0046777	Protein Autophosphorylation
0	GO:0016540	Protein Autoprocessing
0	GO:0051865	Protein Autoubiquitination
0	GO:0000988	Protein Binding Transcription Factor Activity
0	GO:0030674	Protein Binding, Bridging
0	GO:0008022	Protein C-Terminus Binding
0	GO:0018214	Protein Carboxylation
0	GO:0030163	Protein Catabolic Process
0	GO:0032403	Protein Complex Binding
0	GO:0043241	Protein Complex Disassembly
0	GO:0032947	Protein Complex Scaffold
0	GO:0033558	Protein Deacetylase Activity
0	GO:0006476	Protein Deacetylation
0	GO:0035601	Protein Deacylation
0	GO:0008214	Protein Dealkylation

0	GO:0006482	Protein Demethylation
0	GO:0006470	Protein Dephosphorylation
0	GO:0051261	Protein Depolymerization
0	GO:0031648	Protein Destabilization
0	GO:0016579	Protein Deubiquitination
0	GO:0015035	Protein Disulfide Oxidoreductase Activity
0	GO:0006611	Protein Export From Nucleus
0	GO:0006457	Protein Folding
0	GO:0006486	Protein Glycosylation
0	GO:0046982	Protein Heterodimerization Activity
0	GO:0051291	Protein Heterooligomerization
0	GO:0004673	Protein Histidine Kinase Activity
0	GO:0042803	Protein Homodimerization Activity
0	GO:0051260	Protein Homooligomerization
0	GO:0051289	Protein Homotetramerization
0	GO:0070207	Protein Homotrimerization
0	GO:0017038	Protein Import
0	GO:0006606	Protein Import Into Nucleus
0	GO:0000060	Protein Import Into Nucleus, Translocation
0	GO:0016558	Protein Import Into Peroxisome Matrix
0	GO:0051205	Protein Insertion Into Membrane
0	GO:0070979	Protein K11-Linked Ubiquitination
0	GO:0071108	Protein K48-Linked Deubiquitination
0	GO:0070936	Protein K48-Linked Ubiquitination
0	GO:0070536	Protein K63-Linked Deubiquitination
0	GO:0070534	Protein K63-Linked Ubiquitination
0	GO:0051018	Protein Kinase A Binding
0	GO:0010737	Protein Kinase A Signaling Cascade
0	GO:0030295	Protein Kinase Activator Activity
0	GO:0043491	Protein Kinase B Signaling Cascade
0	GO:0019901	Protein Kinase Binding
0	GO:0004697	Protein Kinase C Activity
0	GO:0005080	Protein Kinase C Binding
0	GO:0070528	Protein Kinase C Signaling Cascade
0	GO:0007205	Protein Kinase C-Activating G-Protein Coupled Receptor Signaling Pathway
0	GO:0004860	Protein Kinase Inhibitor Activity
0	GO:0019887	Protein Kinase Regulator Activity
0	GO:0006497	Protein Lipidation
0	GO:0034394	Protein Localization At Cell Surface
0	GO:0070972	Protein Localization In Endoplasmic Reticulum
0	GO:0034067	Protein Localization In Golgi Apparatus
0	GO:0072657	Protein Localization In Membrane
0	GO:0070585	Protein Localization In Mitochondrion
0	GO:0072659	Protein Localization In Plasma Membrane
0	GO:0034502	Protein Localization To Chromosome
0	GO:0034504	Protein Localization To Nucleus
0	GO:0033365	Protein Localization To Organelle
0	GO:0072662	Protein Localization To Peroxisome
0	GO:0051604	Protein Maturation
0	GO:0006479	Protein Methylation
0	GO:0008276	Protein Methyltransferase Activity
0	GO:0032446	Protein Modification By Small Protein Conjugation
0	GO:0070647	Protein Modification By Small Protein Conjugation Or Removal
0	GO:0070646	Protein Modification By Small Protein Removal
0	GO:0006513	Protein Monoubiquitination
0	GO:0006487	Protein N-Linked Glycosylation

0	GO:0018279	Protein N-Linked Glycosylation Via Asparagine
0	GO:0047485	Protein N-Terminus Binding
0	GO:0006493	Protein O-Linked Glycosylation
0	GO:0051259	Protein Oligomerization
0	GO:0018345	Protein Palmitoylation
0	GO:0000413	Protein Peptidyl-Prolyl Isomerization
0	GO:0051721	Protein Phosphatase 2A Binding
0	GO:0019903	Protein Phosphatase Binding
0	GO:0004864	Protein Phosphatase Inhibitor Activity
0	GO:0019888	Protein Phosphatase Regulator Activity
0	GO:0000159	Protein Phosphatase Type 2A Complex
0	GO:0008601	Protein Phosphatase Type 2A Regulator Activity
0	GO:0045309	Protein Phosphorylated Amino Acid Binding
0	GO:0051258	Protein Polymerization
0	GO:0000209	Protein Polyubiquitination
0	GO:0016485	Protein Processing
0	GO:0042026	Protein Refolding
0	GO:0009306	Protein Secretion
0	GO:0043621	Protein Self-Association
0	GO:0030291	Protein Serine/Threonine Kinase Inhibitor Activity
0	GO:0004722	Protein Serine/Threonine Phosphatase Activity
0	GO:0008287	Protein Serine/Threonine Phosphatase Complex
0	GO:0004712	Protein Serine/Threonine/Tyrosine Kinase Activity
0	GO:0050821	Protein Stabilization
0	GO:0016925	Protein Sumoylation
0	GO:0006605	Protein Targeting
0	GO:0006612	Protein Targeting To Membrane
0	GO:0006626	Protein Targeting To Mitochondrion
0	GO:0006625	Protein Targeting To Peroxisome
0	GO:0051262	Protein Tetramerization
0	GO:0008320	Protein Transmembrane Transporter Activity
0	GO:0008565	Protein Transporter Activity
0	GO:0070206	Protein Trimerization
0	GO:0030296	Protein Tyrosine Kinase Activator Activity
0	GO:0004713	Protein Tyrosine Kinase Activity
0	GO:0004725	Protein Tyrosine Phosphatase Activity
0	GO:0008138	Protein Tyrosine/Serine/Threonine Phosphatase Activity
0	GO:0016567	Protein Ubiquitination
0	GO:0042787	Protein Ubiquitination Involved In Ubiquitin-Dependent Protein Catabolic Process
0	GO:0018298	Protein-Chromophore Linkage
0	GO:0032993	Protein-Dna Complex
0	GO:0065004	Protein-Dna Complex Assembly
0	GO:0032986	Protein-Dna Complex Disassembly
0	GO:0071824	Protein-Dna Complex Subunit Organization
0	GO:0016500	Protein-Hormone Receptor Activity
0	GO:0032994	Protein-Lipid Complex
0	GO:0065005	Protein-Lipid Complex Assembly
0	GO:0071814	Protein-Lipid Complex Binding
0	GO:0034368	Protein-Lipid Complex Remodeling
0	GO:0071825	Protein-Lipid Complex Subunit Organization
0	GO:0016279	Protein-Lysine N-Methyltransferase Activity
0	GO:0005578	Proteinaceous Extracellular Matrix
0	GO:0043394	Proteoglycan Binding
0	GO:0030166	Proteoglycan Biosynthetic Process
0	GO:0006029	Proteoglycan Metabolic Process
0	GO:0051603	Proteolysis Involved In Cellular Protein Catabolic Process

0	GO:0015992	Proton Transport
0	GO:0045259	Proton-Transporting Atp Synthase Complex
0	GO:0045263	Proton-Transporting Atp Synthase Complex, Coupling Factor F(O)
0	GO:0046961	Proton-Transporting Atpase Activity, Rotational Mechanism
0	GO:0016469	Proton-Transporting Two-Sector Atpase Complex
0	GO:0033178	Proton-Transporting Two-Sector Atpase Complex, Catalytic Domain
0	GO:0033177	Proton-Transporting Two-Sector Atpase Complex, Proton-Transporting Domain
0	GO:0033176	Proton-Transporting V-Type Atpase Complex
0	GO:0033180	Proton-Transporting V-Type Atpase, V1 Domain
0	GO:0009954	Proximal/Distal Pattern Formation
0	GO:0031143	Pseudopodium
0	GO:0031269	Pseudopodium Assembly
0	GO:0031268	Pseudopodium Organization
0	GO:0009982	Pseudouridine Synthase Activity
0	GO:0001522	Pseudouridine Synthesis
0	GO:0042559	Pteridine-Containing Compound Biosynthetic Process
0	GO:0042558	Pteridine-Containing Compound Metabolic Process
0	GO:0009113	Purine Base Biosynthetic Process
0	GO:0006144	Purine Base Metabolic Process
0	GO:0070035	Purine Ntp-Dependent Helicase Activity
0	GO:0042451	Purine Nucleoside Biosynthetic Process
0	GO:0034032	Purine Nucleoside Bisphosphate Metabolic Process
0	GO:0042278	Purine Nucleoside Metabolic Process
0	GO:0009127	Purine Nucleoside Monophosphate Biosynthetic Process
0	GO:0009126	Purine Nucleoside Monophosphate Metabolic Process
0	GO:0009145	Purine Nucleoside Triphosphate Biosynthetic Process
0	GO:0006164	Purine Nucleotide Biosynthetic Process
0	GO:0046129	Purine Ribonucleoside Biosynthetic Process
0	GO:0034035	Purine Ribonucleoside Bisphosphate Metabolic Process
0	GO:0046128	Purine Ribonucleoside Metabolic Process
0	GO:0009168	Purine Ribonucleoside Monophosphate Biosynthetic Process
0	GO:0009167	Purine Ribonucleoside Monophosphate Metabolic Process
0	GO:0009206	Purine Ribonucleoside Triphosphate Biosynthetic Process
0	GO:0009152	Purine Ribonucleotide Biosynthetic Process
0	GO:0072522	Purine-Containing Compound Biosynthetic Process
0	GO:0043101	Purine-Containing Compound Salvage
0	GO:0072530	Purine-Containing Compound Transmembrane Transport
1	GO:0001614	Purinergic Nucleotide Receptor Activity
1	GO:0035586	Purinergic Receptor Activity
1	GO:0035587	Purinergic Receptor Signaling Pathway
0	GO:0019363	Pyridine Nucleotide Biosynthetic Process
0	GO:0019362	Pyridine Nucleotide Metabolic Process
0	GO:0072525	Pyridine-Containing Compound Biosynthetic Process
0	GO:0072524	Pyridine-Containing Compound Metabolic Process
0	GO:0030170	Pyridoxal Phosphate Binding
0	GO:0006206	Pyrimidine Base Metabolic Process
0	GO:0009219	Pyrimidine Deoxyribonucleotide Metabolic Process
0	GO:0046134	Pyrimidine Nucleoside Biosynthetic Process
0	GO:0046135	Pyrimidine Nucleoside Catabolic Process
0	GO:0006213	Pyrimidine Nucleoside Metabolic Process
0	GO:0009148	Pyrimidine Nucleoside Triphosphate Biosynthetic Process
0	GO:0009147	Pyrimidine Nucleoside Triphosphate Metabolic Process
0	GO:0006221	Pyrimidine Nucleotide Biosynthetic Process
0	GO:0006220	Pyrimidine Nucleotide Metabolic Process
0	GO:0046131	Pyrimidine Ribonucleoside Metabolic Process
0	GO:0009220	Pyrimidine Ribonucleotide Biosynthetic Process

0	GO:0009218	Pyrimidine Ribonucleotide Metabolic Process
0	GO:0072528	Pyrimidine-Containing Compound Biosynthetic Process
0	GO:0072529	Pyrimidine-Containing Compound Catabolic Process
0	GO:0072527	Pyrimidine-Containing Compound Metabolic Process
0	GO:0072531	Pyrimidine-Containing Compound Transmembrane Transport
0	GO:0006090	Pyruvate Metabolic Process
0	GO:0050997	Quaternary Ammonium Group Binding
0	GO:0015697	Quaternary Ammonium Group Transport
0	GO:0048038	Quinone Binding
0	GO:0042375	Quinone Cofactor Metabolic Process
0	GO:0070412	R-Smad Binding
0	GO:0005097	Rab Gtpase Activator Activity
0	GO:0017137	Rab Gtpase Binding
0	GO:0030675	Rac Gtpase Activator Activity
0	GO:0048365	Rac Gtpase Binding
0	GO:0016601	Rac Protein Signal Transduction
0	GO:0016854	Racemase And Epimerase Activity
0	GO:0008536	Ran Gtpase Binding
0	GO:0005099	Ras Gtpase Activator Activity
0	GO:0017016	Ras Gtpase Binding
0	GO:0005088	Ras Guanyl-Nucleotide Exchange Factor Activity
0	GO:0007265	Ras Protein Signal Transduction
0	GO:0072593	Reactive Oxygen Species Metabolic Process
0	GO:0030546	Receptor Activator Activity
0	GO:0048019	Receptor Antagonist Activity
0	GO:0032800	Receptor Biosynthetic Process
0	GO:0043113	Receptor Clustering
0	GO:0043235	Receptor Complex
0	GO:0007168	Receptor Guanylyl Cyclase Signaling Pathway
0	GO:0030547	Receptor Inhibitor Activity
0	GO:0031623	Receptor Internalization
0	GO:0043112	Receptor Metabolic Process
0	GO:0001881	Receptor Recycling
0	GO:0030545	Receptor Regulator Activity
0	GO:0030159	Receptor Signaling Complex Scaffold Activity
0	GO:0005057	Receptor Signaling Protein Activity
0	GO:0004702	Receptor Signaling Protein Serine/Threonine Kinase Activity
0	GO:0004716	Receptor Signaling Protein Tyrosine Kinase Activity
0	GO:0030971	Receptor Tyrosine Kinase Binding
0	GO:0006898	Receptor-Mediated Endocytosis
0	GO:0035825	Reciprocal Dna Recombination
0	GO:0007131	Reciprocal Meiotic Recombination
0	GO:0000725	Recombinational Repair
0	GO:0055037	Recycling Endosome
0	GO:0055038	Recycling Endosome Membrane
0	GO:0060004	Reflex
0	GO:0031099	Regeneration
0	GO:0003002	Regionalization
0	GO:0045055	Regulated Secretory Pathway
0	GO:0010510	Regulation Of Acetyl-Coa Biosynthetic Process From Pyruvate
0	GO:0032956	Regulation Of Actin Cytoskeleton Organization
0	GO:0032231	Regulation Of Actin Filament Bundle Assembly
0	GO:0030834	Regulation Of Actin Filament Depolymerization
0	GO:0030832	Regulation Of Actin Filament Length
0	GO:0030833	Regulation Of Actin Filament Polymerization
0	GO:0032970	Regulation Of Actin Filament-Based Process

0	GO:0008064	Regulation Of Actin Polymerization Or Depolymerization
1	GO:0001508	Regulation Of Action Potential
1	GO:0019228	Regulation Of Action Potential In Neuron
0	GO:0046006	Regulation Of Activated T Cell Proliferation
0	GO:0032925	Regulation Of Activin Receptor Signaling Pathway
0	GO:0002673	Regulation Of Acute Inflammatory Response
0	GO:0002819	Regulation Of Adaptive Immune Response
0	GO:0002822	Regulation Of Adaptive Immune Response Based On Somatic Recombination Of Immune Receptors Built From Immunoglobulin Superfamily Domains
0	GO:0045761	Regulation Of Adenylate Cyclase Activity
0	GO:0010578	Regulation Of Adenylate Cyclase Activity Involved In G-Protein Coupled Receptor Signaling Pathway
1	GO:2000311	Regulation Of Alpha-Amino-3-Hydroxy-5-Methyl-4-Isoxazole Propionate Selective Glutamate Receptor Activity
0	GO:0046634	Regulation Of Alpha-Beta T Cell Activation
0	GO:0046637	Regulation Of Alpha-Beta T Cell Differentiation
0	GO:0046640	Regulation Of Alpha-Beta T Cell Proliferation
0	GO:0000381	Regulation Of Alternative Nuclear Mrna Splicing, Via Spliceosome
0	GO:0051952	Regulation Of Amine Transport
0	GO:0051955	Regulation Of Amino Acid Transport
0	GO:0022603	Regulation Of Anatomical Structure Morphogenesis
0	GO:0090066	Regulation Of Anatomical Structure Size
0	GO:0060765	Regulation Of Androgen Receptor Signaling Pathway
0	GO:0045765	Regulation Of Angiogenesis
0	GO:0044070	Regulation Of Anion Transport
0	GO:0045767	Regulation Of Anti-Apoptosis
0	GO:0002577	Regulation Of Antigen Processing And Presentation
0	GO:0050854	Regulation Of Antigen Receptor-Mediated Signaling Pathway
0	GO:0032098	Regulation Of Appetite
0	GO:0032312	Regulation Of Arf Gtpase Activity
0	GO:0032012	Regulation Of Arf Protein Signal Transduction
0	GO:0048710	Regulation Of Astrocyte Differentiation
0	GO:0043462	Regulation Of Atpase Activity
0	GO:0010506	Regulation Of Autophagy
1	GO:0030516	Regulation Of Axon Extension
1	GO:0048841	Regulation Of Axon Extension Involved In Axon Guidance
1	GO:0048679	Regulation Of Axon Regeneration
1	GO:0050770	Regulation Of Axonogenesis
0	GO:0050864	Regulation Of B Cell Activation
0	GO:0002902	Regulation Of B Cell Apoptotic Process
0	GO:0045577	Regulation Of B Cell Differentiation
0	GO:0002712	Regulation Of B Cell Mediated Immunity
0	GO:0030888	Regulation Of B Cell Proliferation
1	GO:0050795	Regulation Of Behavior
0	GO:0051098	Regulation Of Binding
0	GO:0070167	Regulation Of Biomineral Tissue Development
0	GO:0030193	Regulation Of Blood Coagulation
0	GO:0008217	Regulation Of Blood Pressure
0	GO:0043535	Regulation Of Blood Vessel Endothelial Cell Migration
0	GO:0050880	Regulation Of Blood Vessel Size
0	GO:0002016	Regulation Of Blood Volume By Renin-Angiotensin
0	GO:0030510	Regulation Of Bmp Signaling Pathway
0	GO:0030500	Regulation Of Bone Mineralization
0	GO:0046850	Regulation Of Bone Remodeling
0	GO:0045124	Regulation Of Bone Resorption
0	GO:0090189	Regulation Of Branching Involved In Ureteric Bud Morphogenesis
0	GO:0051924	Regulation Of Calcium Ion Transport
0	GO:0010522	Regulation Of Calcium Ion Transport Into Cytosol
1	GO:0051925	Regulation Of Calcium Ion Transport Via Voltage-Gated Calcium Channel Activity

1	GO:0017158	Regulation Of Calcium Ion-Dependent Exocytosis
1	GO:0050848	Regulation Of Calcium-Mediated Signaling
0	GO:0030817	Regulation Of Camp Biosynthetic Process
0	GO:0030814	Regulation Of Camp Metabolic Process
0	GO:0060828	Regulation Of Canonical Wnt Receptor Signaling Pathway
0	GO:0043255	Regulation Of Carbohydrate Biosynthetic Process
0	GO:0043470	Regulation Of Carbohydrate Catabolic Process
0	GO:0006109	Regulation Of Carbohydrate Metabolic Process
0	GO:0060043	Regulation Of Cardiac Muscle Cell Proliferation
0	GO:0055117	Regulation Of Cardiac Muscle Contraction
0	GO:0010611	Regulation Of Cardiac Muscle Hypertrophy
0	GO:0055024	Regulation Of Cardiac Muscle Tissue Development
0	GO:0055021	Regulation Of Cardiac Muscle Tissue Growth
0	GO:0051890	Regulation Of Cardioblast Differentiation
0	GO:0061035	Regulation Of Cartilage Development
0	GO:0009894	Regulation Of Catabolic Process
0	GO:0042069	Regulation Of Catecholamine Metabolic Process
0	GO:0050433	Regulation Of Catecholamine Secretion
0	GO:0035412	Regulation Of Catenin Import Into Nucleus
0	GO:2000514	Regulation Of Cd4-Positive, Alpha-Beta T Cell Activation
0	GO:0043370	Regulation Of Cd4-Positive, Alpha-Beta T Cell Differentiation
0	GO:0043088	Regulation Of Cdc42 Gtpase Activity
0	GO:0032489	Regulation Of Cdc42 Protein Signal Transduction
0	GO:0050865	Regulation Of Cell Activation
0	GO:0030155	Regulation Of Cell Adhesion
0	GO:0033628	Regulation Of Cell Adhesion Mediated By Integrin
0	GO:0090342	Regulation Of Cell Aging
0	GO:0071156	Regulation Of Cell Cycle Arrest
0	GO:0010564	Regulation Of Cell Cycle Process
0	GO:0060284	Regulation Of Cell Development
0	GO:0051302	Regulation Of Cell Division
0	GO:0010453	Regulation Of Cell Fate Commitment
0	GO:0042659	Regulation Of Cell Fate Specification
0	GO:0001558	Regulation Of Cell Growth
0	GO:0031341	Regulation Of Cell Killing
0	GO:0030334	Regulation Of Cell Migration
0	GO:0022604	Regulation Of Cell Morphogenesis
0	GO:0010769	Regulation Of Cell Morphogenesis Involved In Differentiation
0	GO:2000145	Regulation Of Cell Motility
0	GO:0060491	Regulation Of Cell Projection Assembly
0	GO:0031344	Regulation Of Cell Projection Organization
0	GO:0008360	Regulation Of Cell Shape
0	GO:0008361	Regulation Of Cell Size
0	GO:0022407	Regulation Of Cell-Cell Adhesion
0	GO:0001952	Regulation Of Cell-Matrix Adhesion
0	GO:0010810	Regulation Of Cell-Substrate Adhesion
0	GO:0090109	Regulation Of Cell-Substrate Junction Assembly
0	GO:0033238	Regulation Of Cellular Amine Metabolic Process
0	GO:0006521	Regulation Of Cellular Amino Acid Metabolic Process
0	GO:0043471	Regulation Of Cellular Carbohydrate Catabolic Process
0	GO:0010675	Regulation Of Cellular Carbohydrate Metabolic Process
0	GO:0031329	Regulation Of Cellular Catabolic Process
0	GO:0044087	Regulation Of Cellular Component Biogenesis
0	GO:0051270	Regulation Of Cellular Component Movement
0	GO:0032535	Regulation Of Cellular Component Size
0	GO:0010565	Regulation Of Cellular Ketone Metabolic Process

0	GO:0060341	Regulation Of Cellular Localization
0	GO:0030641	Regulation Of Cellular Ph
0	GO:0090287	Regulation Of Cellular Response To Growth Factor Stimulus
0	GO:0080135	Regulation Of Cellular Response To Stress
0	GO:0046605	Regulation Of Centrosome Cycle
0	GO:0010824	Regulation Of Centrosome Duplication
0	GO:0030826	Regulation Of Cgmp Biosynthetic Process
0	GO:0030823	Regulation Of Cgmp Metabolic Process
0	GO:0045073	Regulation Of Chemokine Biosynthetic Process
0	GO:0032642	Regulation Of Chemokine Production
0	GO:0050920	Regulation Of Chemotaxis
0	GO:0045540	Regulation Of Cholesterol Biosynthetic Process
0	GO:0010874	Regulation Of Cholesterol Efflux
0	GO:0090181	Regulation Of Cholesterol Metabolic Process
0	GO:0010885	Regulation Of Cholesterol Storage
0	GO:0032374	Regulation Of Cholesterol Transport
0	GO:0032330	Regulation Of Chondrocyte Differentiation
0	GO:0033044	Regulation Of Chromosome Organization
0	GO:0051983	Regulation Of Chromosome Segregation
1	GO:0042752	Regulation Of Circadian Rhythm
1	GO:0042749	Regulation Of Circadian Sleep/Wake Cycle
1	GO:0045187	Regulation Of Circadian Sleep/Wake Cycle, Sleep
0	GO:0050818	Regulation Of Coagulation
0	GO:0051196	Regulation Of Coenzyme Metabolic Process
0	GO:0051193	Regulation Of Cofactor Metabolic Process
0	GO:0032965	Regulation Of Collagen Biosynthetic Process
0	GO:0010712	Regulation Of Collagen Metabolic Process
0	GO:0031279	Regulation Of Cyclase Activity
0	GO:0030802	Regulation Of Cyclic Nucleotide Biosynthetic Process
0	GO:0030799	Regulation Of Cyclic Nucleotide Metabolic Process
0	GO:0000079	Regulation Of Cyclin-Dependent Protein Kinase Activity
0	GO:2000116	Regulation Of Cysteine-Type Endopeptidase Activity
0	GO:0043281	Regulation Of Cysteine-Type Endopeptidase Activity Involved In Apoptotic Process
0	GO:0042035	Regulation Of Cytokine Biosynthetic Process
0	GO:0001817	Regulation Of Cytokine Production
0	GO:0002718	Regulation Of Cytokine Production Involved In Immune Response
0	GO:0050707	Regulation Of Cytokine Secretion
0	GO:0001959	Regulation Of Cytokine-Mediated Signaling Pathway
0	GO:0032465	Regulation Of Cytokinesis
0	GO:0051493	Regulation Of Cytoskeleton Organization
0	GO:0031347	Regulation Of Defense Response
0	GO:0050688	Regulation Of Defense Response To Virus
0	GO:0050691	Regulation Of Defense Response To Virus By Host
0	GO:0050690	Regulation Of Defense Response To Virus By Virus
1	GO:0050773	Regulation Of Dendrite Development
1	GO:0048814	Regulation Of Dendrite Morphogenesis
1	GO:0060998	Regulation Of Dendritic Spine Development
1	GO:0061001	Regulation Of Dendritic Spine Morphogenesis
0	GO:0035303	Regulation Of Dephosphorylation
0	GO:0048638	Regulation Of Developmental Growth
0	GO:0048070	Regulation Of Developmental Pigmentation
0	GO:0044058	Regulation Of Digestive System Process
0	GO:0051101	Regulation Of Dna Binding
0	GO:0043516	Regulation Of Dna Damage Response, Signal Transduction By P53 Class Mediator
0	GO:0051052	Regulation Of Dna Metabolic Process
0	GO:0000018	Regulation Of Dna Recombination

0	GO:0006282	Regulation Of Dna Repair
0	GO:0006275	Regulation Of Dna Replication
0	GO:0090329	Regulation Of Dna-Dependent Dna Replication
1	GO:0042053	Regulation Of Dopamine Metabolic Process
1	GO:0014059	Regulation Of Dopamine Secretion
0	GO:0045995	Regulation Of Embryonic Development
0	GO:0044060	Regulation Of Endocrine Process
0	GO:0030100	Regulation Of Endocytosis
0	GO:0052548	Regulation Of Endopeptidase Activity
0	GO:0045601	Regulation Of Endothelial Cell Differentiation
0	GO:0010594	Regulation Of Endothelial Cell Migration
0	GO:0001936	Regulation Of Endothelial Cell Proliferation
0	GO:0045604	Regulation Of Epidermal Cell Differentiation
0	GO:0042058	Regulation Of Epidermal Growth Factor Receptor Signaling Pathway
0	GO:0007176	Regulation Of Epidermal Growth Factor-Activated Receptor Activity
0	GO:0045682	Regulation Of Epidermis Development
0	GO:0030856	Regulation Of Epithelial Cell Differentiation
0	GO:2000696	Regulation Of Epithelial Cell Differentiation Involved In Kidney Development
0	GO:0010632	Regulation Of Epithelial Cell Migration
0	GO:0050678	Regulation Of Epithelial Cell Proliferation
0	GO:0060768	Regulation Of Epithelial Cell Proliferation Involved In Prostate Gland Development
0	GO:0010717	Regulation Of Epithelial To Mesenchymal Transition
0	GO:0070372	Regulation Of Erk1 And Erk2 Cascade
0	GO:0045646	Regulation Of Erythrocyte Differentiation
0	GO:0090175	Regulation Of Establishment Of Planar Polarity
0	GO:0090178	Regulation Of Establishment Of Planar Polarity Involved In Neural Tube Closure
0	GO:0070201	Regulation Of Establishment Of Protein Localization
0	GO:0090003	Regulation Of Establishment Of Protein Localization In Plasma Membrane
1	GO:0060079	Regulation Of Excitatory Postsynaptic Membrane Potential
0	GO:0044062	Regulation Of Excretion
0	GO:0007096	Regulation Of Exit From Mitosis
0	GO:0017157	Regulation Of Exocytosis
0	GO:0061387	Regulation Of Extent Of Cell Growth
0	GO:0045598	Regulation Of Fat Cell Differentiation
0	GO:0031998	Regulation Of Fatty Acid Beta-Oxidation
0	GO:0042304	Regulation Of Fatty Acid Biosynthetic Process
0	GO:0019217	Regulation Of Fatty Acid Metabolic Process
0	GO:0046320	Regulation Of Fatty Acid Oxidation
0	GO:2000191	Regulation Of Fatty Acid Transport
0	GO:0051917	Regulation Of Fibrinolysis
0	GO:0040036	Regulation Of Fibroblast Growth Factor Receptor Signaling Pathway
0	GO:0048145	Regulation Of Fibroblast Proliferation
0	GO:0051489	Regulation Of Filopodium Assembly
0	GO:0051893	Regulation Of Focal Adhesion Assembly
1	GO:0008277	Regulation Of G-Protein Coupled Receptor Protein Signaling Pathway
0	GO:2000045	Regulation Of G1/S Transition Of Mitotic Cell Cycle
0	GO:0010389	Regulation Of G2/M Transition Of Mitotic Cell Cycle
0	GO:0010470	Regulation Of Gastrulation
0	GO:0006349	Regulation Of Gene Expression By Genetic Imprinting
0	GO:0040029	Regulation Of Gene Expression, Epigenetic
0	GO:0060968	Regulation Of Gene Silencing
0	GO:0043467	Regulation Of Generation Of Precursor Metabolites And Energy
1	GO:0045685	Regulation Of Glial Cell Differentiation
1	GO:0060251	Regulation Of Glial Cell Proliferation
1	GO:0014013	Regulation Of Gliogenesis
0	GO:0090192	Regulation Of Glomerulus Development

0	GO:0010962	Regulation Of Glucan Biosynthetic Process
0	GO:0006111	Regulation Of Gluconeogenesis
0	GO:0046324	Regulation Of Glucose Import
0	GO:0010906	Regulation Of Glucose Metabolic Process
0	GO:0010827	Regulation Of Glucose Transport
1	GO:0014048	Regulation Of Glutamate Secretion
0	GO:0005979	Regulation Of Glycogen Biosynthetic Process
0	GO:0070873	Regulation Of Glycogen Metabolic Process
0	GO:0006110	Regulation Of Glycolysis
0	GO:0010559	Regulation Of Glycoprotein Biosynthetic Process
0	GO:0071622	Regulation Of Granulocyte Chemotaxis
0	GO:0030852	Regulation Of Granulocyte Differentiation
0	GO:0040008	Regulation Of Growth
0	GO:0060123	Regulation Of Growth Hormone Secretion
0	GO:0044126	Regulation Of Growth Of Symbiont In Host
0	GO:0033124	Regulation Of Gtp Catabolic Process
0	GO:0043087	Regulation Of Gtpase Activity
0	GO:0042634	Regulation Of Hair Cycle
0	GO:0051797	Regulation Of Hair Follicle Development
0	GO:0008016	Regulation Of Heart Contraction
0	GO:0060420	Regulation Of Heart Growth
0	GO:2000826	Regulation Of Heart Morphogenesis
0	GO:0002027	Regulation Of Heart Rate
0	GO:0031650	Regulation Of Heat Generation
0	GO:0035065	Regulation Of Histone Acetylation
0	GO:0031063	Regulation Of Histone Deacetylation
0	GO:0051569	Regulation Of Histone H3-K4 Methylation
0	GO:0031060	Regulation Of Histone Methylation
0	GO:0031056	Regulation Of Histone Modification
0	GO:0032844	Regulation Of Homeostatic Process
0	GO:0046885	Regulation Of Hormone Biosynthetic Process
0	GO:0010817	Regulation Of Hormone Levels
0	GO:0032350	Regulation Of Hormone Metabolic Process
0	GO:0046883	Regulation Of Hormone Secretion
0	GO:0002920	Regulation Of Humoral Immune Response
0	GO:0043122	Regulation Of I-Kappab Kinase/Nf-Kappab Cascade
0	GO:0002697	Regulation Of Immune Effector Process
0	GO:0050776	Regulation Of Immune Response
0	GO:0002889	Regulation Of Immunoglobulin Mediated Immune Response
0	GO:0002637	Regulation Of Immunoglobulin Production
0	GO:0051023	Regulation Of Immunoglobulin Secretion
0	GO:0050727	Regulation Of Inflammatory Response
0	GO:0002861	Regulation Of Inflammatory Response To Antigenic Stimulus
0	GO:0045088	Regulation Of Innate Immune Response
0	GO:0046626	Regulation Of Insulin Receptor Signaling Pathway
0	GO:0050796	Regulation Of Insulin Secretion
0	GO:0061178	Regulation Of Insulin Secretion Involved In Cellular Response To Glucose Stimulus
0	GO:0043567	Regulation Of Insulin-Like Growth Factor Receptor Signaling Pathway
0	GO:0032647	Regulation Of Interferon-Alpha Production
0	GO:0032648	Regulation Of Interferon-Beta Production
0	GO:0045072	Regulation Of Interferon-Gamma Biosynthetic Process
0	GO:0032649	Regulation Of Interferon-Gamma Production
0	GO:0060334	Regulation Of Interferon-Gamma-Mediated Signaling Pathway
0	GO:0032651	Regulation Of Interleukin-1 Beta Production
0	GO:0050706	Regulation Of Interleukin-1 Beta Secretion
0	GO:0032652	Regulation Of Interleukin-1 Production

0	GO:0050704	Regulation Of Interleukin-1 Secretion
0	GO:0032653	Regulation Of Interleukin-10 Production
0	GO:0032655	Regulation Of Interleukin-12 Production
0	GO:0032660	Regulation Of Interleukin-17 Production
0	GO:0045076	Regulation Of Interleukin-2 Biosynthetic Process
0	GO:0032663	Regulation Of Interleukin-2 Production
0	GO:0032673	Regulation Of Interleukin-4 Production
0	GO:0045408	Regulation Of Interleukin-6 Biosynthetic Process
0	GO:0032675	Regulation Of Interleukin-6 Production
0	GO:0032677	Regulation Of Interleukin-8 Production
0	GO:2000602	Regulation Of Interphase Of Mitotic Cell Cycle
0	GO:0033146	Regulation Of Intracellular Estrogen Receptor Signaling Pathway
0	GO:0051453	Regulation Of Intracellular Ph
0	GO:0010627	Regulation Of Intracellular Protein Kinase Cascade
0	GO:0033157	Regulation Of Intracellular Protein Transport
0	GO:0033143	Regulation Of Intracellular Steroid Hormone Receptor Signaling Pathway
0	GO:0032386	Regulation Of Intracellular Transport
0	GO:2000021	Regulation Of Ion Homeostasis
0	GO:0034765	Regulation Of Ion Transmembrane Transport
0	GO:0032412	Regulation Of Ion Transmembrane Transporter Activity
0	GO:0043269	Regulation Of Ion Transport
0	GO:0045191	Regulation Of Isotype Switching
0	GO:0048302	Regulation Of Isotype Switching To Igg Isotypes
0	GO:0046425	Regulation Of Jak-Stat Cascade
0	GO:0046328	Regulation Of Jnk Cascade
0	GO:0043506	Regulation Of Jun Kinase Activity
0	GO:0045616	Regulation Of Keratinocyte Differentiation
0	GO:0090183	Regulation Of Kidney Development
0	GO:0010591	Regulation Of Lamellipodium Assembly
0	GO:0002694	Regulation Of Leukocyte Activation
0	GO:2000106	Regulation Of Leukocyte Apoptotic Process
0	GO:0002688	Regulation Of Leukocyte Chemotaxis
0	GO:0043300	Regulation Of Leukocyte Degranulation
0	GO:0001910	Regulation Of Leukocyte Mediated Cytotoxicity
0	GO:0002703	Regulation Of Leukocyte Mediated Immunity
0	GO:0002685	Regulation Of Leukocyte Migration
0	GO:0070663	Regulation Of Leukocyte Proliferation
0	GO:0051340	Regulation Of Ligase Activity
0	GO:0060191	Regulation Of Lipase Activity
0	GO:0046890	Regulation Of Lipid Biosynthetic Process
0	GO:0050994	Regulation Of Lipid Catabolic Process
0	GO:0043550	Regulation Of Lipid Kinase Activity
0	GO:0019216	Regulation Of Lipid Metabolic Process
0	GO:0010883	Regulation Of Lipid Storage
0	GO:0032368	Regulation Of Lipid Transport
0	GO:0051004	Regulation Of Lipoprotein Lipase Activity
0	GO:0040012	Regulation Of Locomotion
1	GO:0048169	Regulation Of Long-Term Neuronal Synaptic Plasticity
0	GO:0051339	Regulation Of Lyase Activity
0	GO:0051249	Regulation Of Lymphocyte Activation
0	GO:0070228	Regulation Of Lymphocyte Apoptotic Process
0	GO:0045619	Regulation Of Lymphocyte Differentiation
0	GO:0002706	Regulation Of Lymphocyte Mediated Immunity
0	GO:0050670	Regulation Of Lymphocyte Proliferation
0	GO:0043030	Regulation Of Macrophage Activation
0	GO:0010743	Regulation Of Macrophage Derived Foam Cell Differentiation

0	GO:0045649	Regulation Of Macrophage Differentiation
0	GO:0033599	Regulation Of Mammary Gland Epithelial Cell Proliferation
0	GO:0043405	Regulation Of Map Kinase Activity
0	GO:0043408	Regulation Of Mapk Cascade
0	GO:0033003	Regulation Of Mast Cell Activation
0	GO:0033006	Regulation Of Mast Cell Activation Involved In Immune Response
0	GO:0043304	Regulation Of Mast Cell Degranulation
0	GO:0045652	Regulation Of Megakaryocyte Differentiation
0	GO:0040020	Regulation Of Meiosis
0	GO:0051445	Regulation Of Meiotic Cell Cycle
0	GO:0003254	Regulation Of Membrane Depolarization
0	GO:0042391	Regulation Of Membrane Potential
0	GO:0051043	Regulation Of Membrane Protein Ectodomain Proteolysis
0	GO:0010464	Regulation Of Mesenchymal Cell Proliferation
0	GO:0010959	Regulation Of Metal Ion Transport
0	GO:0072215	Regulation Of Metanephros Development
0	GO:0045346	Regulation Of Mhc Class Ii Biosynthetic Process
0	GO:0070507	Regulation Of Microtubule Cytoskeleton Organization
0	GO:0031114	Regulation Of Microtubule Depolymerization
0	GO:0031113	Regulation Of Microtubule Polymerization
0	GO:0031110	Regulation Of Microtubule Polymerization Or Depolymerization
0	GO:0032886	Regulation Of Microtubule-Based Process
0	GO:0051900	Regulation Of Mitochondrial Depolarization
0	GO:0046902	Regulation Of Mitochondrial Membrane Permeability
0	GO:0051881	Regulation Of Mitochondrial Membrane Potential
0	GO:0010821	Regulation Of Mitochondrion Organization
0	GO:0007088	Regulation Of Mitosis
0	GO:0007346	Regulation Of Mitotic Cell Cycle
0	GO:0030071	Regulation Of Mitotic Metaphase/Anaphase Transition
0	GO:0032944	Regulation Of Mononuclear Cell Proliferation
0	GO:0032768	Regulation Of Monooxygenase Activity
0	GO:0060688	Regulation Of Morphogenesis Of A Branching Structure
0	GO:0050684	Regulation Of Mrna Processing
0	GO:0043488	Regulation Of Mrna Stability
0	GO:0043900	Regulation Of Multi-Organism Process
0	GO:0040014	Regulation Of Multicellular Organism Growth
0	GO:0044246	Regulation Of Multicellular Organismal Metabolic Process
0	GO:0043502	Regulation Of Muscle Adaptation
0	GO:0010660	Regulation Of Muscle Cell Apoptotic Process
0	GO:0051147	Regulation Of Muscle Cell Differentiation
0	GO:0006937	Regulation Of Muscle Contraction
0	GO:0014743	Regulation Of Muscle Hypertrophy
0	GO:0048634	Regulation Of Muscle Organ Development
0	GO:0090257	Regulation Of Muscle System Process
1	GO:0031641	Regulation Of Myelination
0	GO:0033032	Regulation Of Myeloid Cell Apoptotic Process
0	GO:0045637	Regulation Of Myeloid Cell Differentiation
0	GO:0002761	Regulation Of Myeloid Leukocyte Differentiation
0	GO:0002886	Regulation Of Myeloid Leukocyte Mediated Immunity
0	GO:0045661	Regulation Of Myoblast Differentiation
0	GO:0010830	Regulation Of Myotube Differentiation
0	GO:0032814	Regulation Of Natural Killer Cell Activation
0	GO:0042269	Regulation Of Natural Killer Cell Mediated Cytotoxicity
0	GO:0002715	Regulation Of Natural Killer Cell Mediated Immunity
0	GO:0051960	Regulation Of Nervous System Development
1	GO:2000177	Regulation Of Neural Precursor Cell Proliferation

1	GO:0050767	Regulation Of Neurogenesis
1	GO:0031644	Regulation Of Neurological System Process
1	GO:0043523	Regulation Of Neuron Apoptotic Process
1	GO:0045664	Regulation Of Neuron Differentiation
1	GO:0010975	Regulation Of Neuron Projection Development
1	GO:0070570	Regulation Of Neuron Projection Regeneration
1	GO:0048168	Regulation Of Neuronal Synaptic Plasticity
1	GO:0001505	Regulation Of Neurotransmitter Levels
1	GO:0046928	Regulation Of Neurotransmitter Secretion
1	GO:0051588	Regulation Of Neurotransmitter Transport
0	GO:0090022	Regulation Of Neutrophil Chemotaxis
0	GO:0042345	Regulation Of Nf-Kappab Import Into Nucleus
0	GO:0045428	Regulation Of Nitric Oxide Biosynthetic Process
0	GO:0050999	Regulation Of Nitric-Oxide Synthase Activity
1	GO:0014061	Regulation Of Norepinephrine Secretion
0	GO:0008593	Regulation Of Notch Signaling Pathway
0	GO:0051783	Regulation Of Nuclear Division
0	GO:0048024	Regulation Of Nuclear Mrna Splicing, Via Spliceosome
0	GO:0032069	Regulation Of Nuclease Activity
0	GO:0046822	Regulation Of Nucleocytoplasmic Transport
0	GO:0030808	Regulation Of Nucleotide Biosynthetic Process
0	GO:0030811	Regulation Of Nucleotide Catabolic Process
0	GO:0006140	Regulation Of Nucleotide Metabolic Process
0	GO:0042481	Regulation Of Odontogenesis
1	GO:0048713	Regulation Of Oligodendrocyte Differentiation
0	GO:0003156	Regulation Of Organ Formation
0	GO:0046620	Regulation Of Organ Growth
0	GO:2000027	Regulation Of Organ Morphogenesis
0	GO:0033043	Regulation Of Organelle Organization
0	GO:0032890	Regulation Of Organic Acid Transport
0	GO:0030278	Regulation Of Ossification
0	GO:0045667	Regulation Of Osteoblast Differentiation
0	GO:0033688	Regulation Of Osteoblast Proliferation
0	GO:0045670	Regulation Of Osteoclast Differentiation
0	GO:0051341	Regulation Of Oxidoreductase Activity
0	GO:0060393	Regulation Of Pathway-Restricted Smad Protein Phosphorylation
0	GO:0052547	Regulation Of Peptidase Activity
0	GO:0090276	Regulation Of Peptide Hormone Secretion
0	GO:0002791	Regulation Of Peptide Secretion
0	GO:0090087	Regulation Of Peptide Transport
0	GO:2000756	Regulation Of Peptidyl-Lysine Acetylation
0	GO:0033135	Regulation Of Peptidyl-Serine Phosphorylation
0	GO:0010799	Regulation Of Peptidyl-Threonine Phosphorylation
0	GO:0050730	Regulation Of Peptidyl-Tyrosine Phosphorylation
0	GO:0006885	Regulation Of Ph
0	GO:0050764	Regulation Of Phagocytosis
0	GO:0010921	Regulation Of Phosphatase Activity
0	GO:0043551	Regulation Of Phosphatidylinositol 3-Kinase Activity
0	GO:0014066	Regulation Of Phosphatidylinositol 3-Kinase Cascade
0	GO:0010517	Regulation Of Phospholipase Activity
0	GO:0043666	Regulation Of Phosphoprotein Phosphatase Activity
0	GO:0097006	Regulation Of Plasma Lipoprotein Particle Levels
0	GO:0010543	Regulation Of Platelet Activation
0	GO:0032885	Regulation Of Polysaccharide Biosynthetic Process
0	GO:0032881	Regulation Of Polysaccharide Metabolic Process
0	GO:0050926	Regulation Of Positive Chemotaxis

1	GO:0060078	Regulation Of Postsynaptic Membrane Potential
1	GO:0043266	Regulation Of Potassium Ion Transport
0	GO:0002700	Regulation Of Production Of Molecular Mediator Of Immune Response
0	GO:0061136	Regulation Of Proteasomal Protein Catabolic Process
0	GO:0032434	Regulation Of Proteasomal Ubiquitin-Dependent Protein Catabolic Process
0	GO:0031952	Regulation Of Protein Autophosphorylation
0	GO:0043393	Regulation Of Protein Binding
0	GO:0042176	Regulation Of Protein Catabolic Process
0	GO:0043254	Regulation Of Protein Complex Assembly
0	GO:0043244	Regulation Of Protein Complex Disassembly
0	GO:0090311	Regulation Of Protein Deacetylation
0	GO:0035304	Regulation Of Protein Dephosphorylation
0	GO:0046825	Regulation Of Protein Export From Nucleus
0	GO:0043496	Regulation Of Protein Homodimerization Activity
0	GO:0032462	Regulation Of Protein Homooligomerization
0	GO:0042306	Regulation Of Protein Import Into Nucleus
0	GO:0033158	Regulation Of Protein Import Into Nucleus, Translocation
0	GO:0051896	Regulation Of Protein Kinase B Signaling Cascade
0	GO:0032880	Regulation Of Protein Localization
0	GO:0032459	Regulation Of Protein Oligomerization
0	GO:0032271	Regulation Of Protein Polymerization
0	GO:0070613	Regulation Of Protein Processing
0	GO:0050708	Regulation Of Protein Secretion
0	GO:0071900	Regulation Of Protein Serine/Threonine Kinase Activity
0	GO:0031647	Regulation Of Protein Stability
0	GO:0051223	Regulation Of Protein Transport
0	GO:0061097	Regulation Of Protein Tyrosine Kinase Activity
0	GO:0031396	Regulation Of Protein Ubiquitination
0	GO:2000058	Regulation Of Protein Ubiquitination Involved In Ubiquitin-Dependent Protein Catabolic Process
0	GO:0030162	Regulation Of Proteolysis
0	GO:0031272	Regulation Of Pseudopodium Assembly
0	GO:0033121	Regulation Of Purine Nucleotide Catabolic Process
0	GO:0032313	Regulation Of Rab Gtpase Activity
0	GO:0032483	Regulation Of Rab Protein Signal Transduction
0	GO:0032314	Regulation Of Rac Gtpase Activity
0	GO:0035020	Regulation Of Rac Protein Signal Transduction
0	GO:0032318	Regulation Of Ras Gtpase Activity
0	GO:0046578	Regulation Of Ras Protein Signal Transduction
0	GO:2000377	Regulation Of Reactive Oxygen Species Metabolic Process
0	GO:0010469	Regulation Of Receptor Activity
0	GO:0010869	Regulation Of Receptor Biosynthetic Process
0	GO:0002090	Regulation Of Receptor Internalization
0	GO:0001919	Regulation Of Receptor Recycling
0	GO:0048259	Regulation Of Receptor-Mediated Endocytosis
0	GO:0090199	Regulation Of Release Of Cytochrome C From Mitochondria
0	GO:0051279	Regulation Of Release Of Sequestered Calcium Ion Into Cytosol
0	GO:0035813	Regulation Of Renal Sodium Excretion
0	GO:2000241	Regulation Of Reproductive Process
0	GO:0043576	Regulation Of Respiratory Gaseous Exchange
1	GO:0002087	Regulation Of Respiratory Gaseous Exchange By Neurological System Process
0	GO:0044065	Regulation Of Respiratory System Process
0	GO:0002831	Regulation Of Response To Biotic Stimulus
0	GO:0060759	Regulation Of Response To Cytokine Stimulus
0	GO:2001020	Regulation Of Response To Dna Damage Stimulus
0	GO:0032101	Regulation Of Response To External Stimulus
0	GO:0032104	Regulation Of Response To Extracellular Stimulus

0	GO:0032095	Regulation Of Response To Food
0	GO:0060330	Regulation Of Response To Interferon-Gamma
0	GO:0032107	Regulation Of Response To Nutrient Levels
0	GO:0032319	Regulation Of Rho Gtpase Activity
0	GO:0035023	Regulation Of Rho Protein Signal Transduction
0	GO:0043484	Regulation Of Rna Splicing
0	GO:0043487	Regulation Of Rna Stability
0	GO:0033261	Regulation Of S Phase
0	GO:0007090	Regulation Of S Phase Of Mitotic Cell Cycle
0	GO:0051046	Regulation Of Secretion
0	GO:0051931	Regulation Of Sensory Perception
0	GO:0051930	Regulation Of Sensory Perception Of Pain
0	GO:0051090	Regulation Of Sequence-Specific Dna Binding Transcription Factor Activity
0	GO:0051282	Regulation Of Sequestering Of Calcium Ion
0	GO:2001014	Regulation Of Skeletal Muscle Cell Differentiation
0	GO:0048742	Regulation Of Skeletal Muscle Fiber Development
0	GO:0048641	Regulation Of Skeletal Muscle Tissue Development
0	GO:0051056	Regulation Of Small Gtpase Mediated Signal Transduction
0	GO:0051150	Regulation Of Smooth Muscle Cell Differentiation
0	GO:0014910	Regulation Of Smooth Muscle Cell Migration
0	GO:0048660	Regulation Of Smooth Muscle Cell Proliferation
0	GO:0006940	Regulation Of Smooth Muscle Contraction
0	GO:0008589	Regulation Of Smoothened Signaling Pathway
0	GO:0002028	Regulation Of Sodium Ion Transport
0	GO:2000736	Regulation Of Stem Cell Differentiation
0	GO:0050810	Regulation Of Steroid Biosynthetic Process
0	GO:0090030	Regulation Of Steroid Hormone Biosynthetic Process
0	GO:0019218	Regulation Of Steroid Metabolic Process
0	GO:0032371	Regulation Of Sterol Transport
0	GO:0051492	Regulation Of Stress Fiber Assembly
0	GO:0032872	Regulation Of Stress-Activated Mapk Cascade
0	GO:0070302	Regulation Of Stress-Activated Protein Kinase Signaling Cascade
0	GO:0010662	Regulation Of Striated Muscle Cell Apoptotic Process
0	GO:0051153	Regulation Of Striated Muscle Cell Differentiation
0	GO:0006942	Regulation Of Striated Muscle Contraction
0	GO:0016202	Regulation Of Striated Muscle Tissue Development
0	GO:0045884	Regulation Of Survival Gene Product Expression
0	GO:0043903	Regulation Of Symbiosis, Encompassing Mutualism Through Parasitism
1	GO:0051963	Regulation Of Synapse Assembly
1	GO:0050807	Regulation Of Synapse Organization
1	GO:0050803	Regulation Of Synapse Structure And Activity
1	GO:0048167	Regulation Of Synaptic Plasticity
1	GO:0050804	Regulation Of Synaptic Transmission
1	GO:0032225	Regulation Of Synaptic Transmission, Dopaminergic
1	GO:0032228	Regulation Of Synaptic Transmission, Gabaergic
1	GO:0051966	Regulation Of Synaptic Transmission, Glutamatergic
0	GO:0044057	Regulation Of System Process
0	GO:0003073	Regulation Of Systemic Arterial Blood Pressure
0	GO:0001990	Regulation Of Systemic Arterial Blood Pressure By Hormone
0	GO:0003081	Regulation Of Systemic Arterial Blood Pressure By Renin-Angiotensin
0	GO:0003044	Regulation Of Systemic Arterial Blood Pressure Mediated By A Chemical Signal
0	GO:0050863	Regulation Of T Cell Activation
0	GO:0070232	Regulation Of T Cell Apoptotic Process
0	GO:0045580	Regulation Of T Cell Differentiation
0	GO:0033081	Regulation Of T Cell Differentiation In Thymus
0	GO:0001914	Regulation Of T Cell Mediated Cytotoxicity

0	GO:0002709	Regulation Of T Cell Mediated Immunity
0	GO:0042129	Regulation Of T Cell Proliferation
0	GO:0050856	Regulation Of T Cell Receptor Signaling Pathway
0	GO:0002825	Regulation Of T-Helper 1 Type Immune Response
0	GO:0045622	Regulation Of T-Helper Cell Differentiation
0	GO:0051972	Regulation Of Telomerase Activity
0	GO:0032204	Regulation Of Telomere Maintenance
0	GO:0002026	Regulation Of The Force Of Heart Contraction
0	GO:0070243	Regulation Of Thymocyte Apoptotic Process
0	GO:0034103	Regulation Of Tissue Remodeling
0	GO:0034121	Regulation Of Toll-Like Receptor Signaling Pathway
0	GO:0032006	Regulation Of Tor Signaling Cascade
0	GO:0032784	Regulation Of Transcription Elongation, Dna-Dependent
0	GO:0042990	Regulation Of Transcription Factor Import Into Nucleus
0	GO:0034339	Regulation Of Transcription From Rna Polymerase Ii Promoter By Nuclear Hormone Receptor
0	GO:0006359	Regulation Of Transcription From Rna Polymerase Iii Promoter
0	GO:0060260	Regulation Of Transcription Initiation From Rna Polymerase Ii Promoter
0	GO:2000142	Regulation Of Transcription Initiation, Dna-Dependent
0	GO:0000083	Regulation Of Transcription Involved In G1/S Phase Of Mitotic Cell Cycle
0	GO:2000677	Regulation Of Transcription Regulatory Region Dna Binding
0	GO:0071634	Regulation Of Transforming Growth Factor Beta Production
0	GO:0017015	Regulation Of Transforming Growth Factor Beta Receptor Signaling Pathway
0	GO:0006417	Regulation Of Translation
0	GO:0043555	Regulation Of Translation In Response To Stress
0	GO:0006446	Regulation Of Translational Initiation
0	GO:0090092	Regulation Of Transmembrane Receptor Protein Serine/Threonine Kinase Signaling Pathway
0	GO:0034762	Regulation Of Transmembrane Transport
0	GO:0022898	Regulation Of Transmembrane Transporter Activity
1	GO:0051969	Regulation Of Transmission Of Nerve Impulse
0	GO:0032409	Regulation Of Transporter Activity
0	GO:0090207	Regulation Of Triglyceride Metabolic Process
0	GO:0035150	Regulation Of Tube Size
0	GO:0042534	Regulation Of Tumor Necrosis Factor Biosynthetic Process
0	GO:0032680	Regulation Of Tumor Necrosis Factor Production
0	GO:0002828	Regulation Of Type 2 Immune Response
0	GO:0032479	Regulation Of Type I Interferon Production
0	GO:0060338	Regulation Of Type I Interferon-Mediated Signaling Pathway
0	GO:0042509	Regulation Of Tyrosine Phosphorylation Of Stat Protein
0	GO:0042510	Regulation Of Tyrosine Phosphorylation Of Stat1 Protein
0	GO:0042516	Regulation Of Tyrosine Phosphorylation Of Stat3 Protein
0	GO:0042522	Regulation Of Tyrosine Phosphorylation Of Stat5 Protein
0	GO:0051438	Regulation Of Ubiquitin-Protein Ligase Activity
0	GO:0051439	Regulation Of Ubiquitin-Protein Ligase Activity Involved In Mitotic Cell Cycle
0	GO:0035809	Regulation Of Urine Volume
0	GO:0010574	Regulation Of Vascular Endothelial Growth Factor Production
0	GO:0030947	Regulation Of Vascular Endothelial Growth Factor Receptor Signaling Pathway
0	GO:0043114	Regulation Of Vascular Permeability
0	GO:0019229	Regulation Of Vasoconstriction
0	GO:0042312	Regulation Of Vasodilation
0	GO:0060627	Regulation Of Vesicle-Mediated Transport
0	GO:0045069	Regulation Of Viral Genome Replication
0	GO:0050792	Regulation Of Viral Reproduction
0	GO:0046782	Regulation Of Viral Transcription
0	GO:0030111	Regulation Of Wnt Receptor Signaling Pathway
0	GO:0061041	Regulation Of Wound Healing
0	GO:0000975	Regulatory Region Dna Binding

0	GO:0001067	Regulatory Region Nucleic Acid Binding
0	GO:0001836	Release Of Cytochrome C From Mitochondria
0	GO:0051209	Release Of Sequestered Calcium Ion Into Cytosol
0	GO:0019430	Removal Of Superoxide Radicals
0	GO:0035812	Renal Sodium Excretion
0	GO:0072001	Renal System Development
0	GO:0003014	Renal System Process
0	GO:0003071	Renal System Process Involved In Regulation Of Systemic Arterial Blood Pressure
0	GO:0061326	Renal Tubule Development
0	GO:0061333	Renal Tubule Morphogenesis
0	GO:0072087	Renal Vesicle Development
0	GO:0072077	Renal Vesicle Morphogenesis
0	GO:0005657	Replication Fork
0	GO:0030894	Replisome
0	GO:0070491	Repressing Transcription Factor Binding
0	GO:0019098	Reproductive Behavior
0	GO:0048608	Reproductive Structure Development
0	GO:0045730	Respiratory Burst
0	GO:0070469	Respiratory Chain
0	GO:0045271	Respiratory Chain Complex I
0	GO:0022904	Respiratory Electron Transport Chain
0	GO:0007585	Respiratory Gaseous Exchange
0	GO:0060541	Respiratory System Development
0	GO:0003016	Respiratory System Process
0	GO:0030323	Respiratory Tube Development
0	GO:0001101	Response To Acid
0	GO:0014823	Response To Activity
0	GO:0043279	Response To Alkaloid
0	GO:0014075	Response To Amine Stimulus
0	GO:0043200	Response To Amino Acid Stimulus
0	GO:0001975	Response To Amphetamine
0	GO:0046677	Response To Antibiotic
0	GO:0046685	Response To Arsenic-Containing Substance
0	GO:0033198	Response To Atp
1	GO:0048678	Response To Axon Injury
0	GO:0009617	Response To Bacterium
0	GO:0009607	Response To Biotic Stimulus
0	GO:0046686	Response To Cadmium Ion
0	GO:0031000	Response To Caffeine
0	GO:0051592	Response To Calcium Ion
0	GO:0051591	Response To Camp
0	GO:0009743	Response To Carbohydrate Stimulus
0	GO:0070723	Response To Cholesterol
0	GO:0042220	Response To Cocaine
0	GO:0009409	Response To Cold
0	GO:0046688	Response To Copper Ion
0	GO:0031960	Response To Corticosteroid Stimulus
0	GO:0051412	Response To Corticosterone Stimulus
0	GO:0051414	Response To Cortisol Stimulus
0	GO:0034097	Response To Cytokine Stimulus
0	GO:0071548	Response To Dexamethasone Stimulus
0	GO:0002021	Response To Dietary Excess
0	GO:0034285	Response To Disaccharide Stimulus
0	GO:0042493	Response To Drug
0	GO:0043331	Response To Dsrna
0	GO:0051602	Response To Electrical Stimulus

0	GO:0034976	Response To Endoplasmic Reticulum Stress
0	GO:0032355	Response To Estradiol Stimulus
0	GO:0043627	Response To Estrogen Stimulus
0	GO:0045471	Response To Ethanol
0	GO:0043330	Response To Exogenous Dsrna
0	GO:0009991	Response To Extracellular Stimulus
0	GO:0070542	Response To Fatty Acid
0	GO:0071774	Response To Fibroblast Growth Factor Stimulus
0	GO:0034405	Response To Fluid Shear Stress
0	GO:0051593	Response To Folic Acid
0	GO:0032354	Response To Follicle-Stimulating Hormone Stimulus
0	GO:0032094	Response To Food
0	GO:0060992	Response To Fungicide
0	GO:0009620	Response To Fungus
0	GO:0010332	Response To Gamma Radiation
0	GO:0033762	Response To Glucagon Stimulus
0	GO:0051384	Response To Glucocorticoid Stimulus
0	GO:0009749	Response To Glucose Stimulus
0	GO:0034698	Response To Gonadotropin Stimulus
0	GO:0009629	Response To Gravity
0	GO:0070848	Response To Growth Factor Stimulus
0	GO:0060416	Response To Growth Hormone Stimulus
0	GO:0009408	Response To Heat
0	GO:0009635	Response To Herbicide
0	GO:0009746	Response To Hexose Stimulus
0	GO:0042542	Response To Hydrogen Peroxide
0	GO:0055093	Response To Hyperoxia
0	GO:0001666	Response To Hypoxia
0	GO:0010035	Response To Inorganic Substance
0	GO:0017085	Response To Insecticide
0	GO:0032868	Response To Insulin Stimulus
0	GO:0034341	Response To Interferon-Gamma
0	GO:0070555	Response To Interleukin-1
0	GO:0070670	Response To Interleukin-4
0	GO:0070741	Response To Interleukin-6
0	GO:0010212	Response To Ionizing Radiation
0	GO:0010039	Response To Iron Ion
0	GO:0014072	Response To Isoquinoline Alkaloid
0	GO:0010288	Response To Lead Ion
0	GO:0009416	Response To Light Stimulus
0	GO:0033993	Response To Lipid
0	GO:0032496	Response To Lipopolysaccharide
0	GO:0010226	Response To Lithium Ion
0	GO:0032026	Response To Magnesium Ion
0	GO:0010042	Response To Manganese Ion
0	GO:0009612	Response To Mechanical Stimulus
0	GO:0046689	Response To Mercury Ion
0	GO:0010038	Response To Metal Ion
0	GO:0051597	Response To Methylmercury
0	GO:0051385	Response To Mineralocorticoid Stimulus
0	GO:0002237	Response To Molecule Of Bacterial Origin
0	GO:0034284	Response To Monosaccharide Stimulus
0	GO:0043278	Response To Morphine
0	GO:0035094	Response To Nicotine
0	GO:0007584	Response To Nutrient
0	GO:0031667	Response To Nutrient Levels

0	GO:0014070	Response To Organic Cyclic Compound
0	GO:0010243	Response To Organic Nitrogen
0	GO:0006970	Response To Osmotic Stress
0	GO:0051707	Response To Other Organism
0	GO:0006979	Response To Oxidative Stress
0	GO:0070482	Response To Oxygen Levels
0	GO:0000305	Response To Oxygen Radical
0	GO:0048265	Response To Pain
0	GO:0043434	Response To Peptide Hormone Stimulus
0	GO:0032494	Response To Peptidoglycan
0	GO:0009268	Response To Ph
0	GO:0032570	Response To Progesterone Stimulus
0	GO:0034695	Response To Prostaglandin E Stimulus
0	GO:0034694	Response To Prostaglandin Stimulus
0	GO:0001562	Response To Protozoan
0	GO:0014074	Response To Purine-Containing Compound
0	GO:0009314	Response To Radiation
0	GO:0000302	Response To Reactive Oxygen Species
0	GO:0032526	Response To Retinoic Acid
0	GO:0009651	Response To Salt Stress
0	GO:0010269	Response To Selenium Ion
0	GO:0042594	Response To Starvation
0	GO:0048545	Response To Steroid Hormone Stimulus
0	GO:0009744	Response To Sucrose Stimulus
0	GO:0000303	Response To Superoxide
0	GO:0009266	Response To Temperature Stimulus
0	GO:0033574	Response To Testosterone Stimulus
0	GO:0035966	Response To Topologically Incorrect Protein
0	GO:0009636	Response To Toxin
0	GO:0071559	Response To Transforming Growth Factor Beta Stimulus
0	GO:0014073	Response To Tropane
0	GO:0002347	Response To Tumor Cell
0	GO:0034612	Response To Tumor Necrosis Factor
0	GO:0034340	Response To Type I Interferon
0	GO:0006986	Response To Unfolded Protein
0	GO:0009411	Response To Uv
0	GO:0009615	Response To Virus
0	GO:0033273	Response To Vitamin
0	GO:0033189	Response To Vitamin A
0	GO:0033280	Response To Vitamin D
0	GO:0033197	Response To Vitamin E
0	GO:0010165	Response To X-Ray
0	GO:0009410	Response To Xenobiotic Stimulus
0	GO:0010043	Response To Zinc Ion
0	GO:0060041	Retina Development In Camera-Type Eye
0	GO:0060042	Retina Morphogenesis In Camera-Type Eye
0	GO:0016918	Retinal Binding
0	GO:0031290	Retinal Ganglion Cell Axon Guidance
0	GO:0042573	Retinoic Acid Metabolic Process
0	GO:0042974	Retinoic Acid Receptor Binding
0	GO:0048384	Retinoic Acid Receptor Signaling Pathway
0	GO:0005501	Retinoid Binding
0	GO:0001523	Retinoid Metabolic Process
0	GO:0046965	Retinoid X Receptor Binding
0	GO:0019841	Retinol Binding
0	GO:0004745	Retinol Dehydrogenase Activity

0	GO:0042572	Retinol Metabolic Process
0	GO:0042147	Retrograde Transport, Endosome To Golgi
0	GO:0000301	Retrograde Transport, Vesicle Recycling Within Golgi
0	GO:0006890	Retrograde Vesicle-Mediated Transport, Golgi To Er
0	GO:0043691	Reverse Cholesterol Transport
0	GO:0005100	Rho Gtpase Activator Activity
0	GO:0017048	Rho Gtpase Binding
0	GO:0005089	Rho Guanyl-Nucleotide Exchange Factor Activity
0	GO:0007266	Rho Protein Signal Transduction
1	GO:0007622	Rhythmic Behavior
0	GO:0048511	Rhythmic Process
0	GO:0004540	Ribonuclease Activity
0	GO:0030529	Ribonucleoprotein Complex
0	GO:0022618	Ribonucleoprotein Complex Assembly
0	GO:0043021	Ribonucleoprotein Complex Binding
0	GO:0022613	Ribonucleoprotein Complex Biogenesis
0	GO:0071826	Ribonucleoprotein Complex Subunit Organization
0	GO:0035770	Ribonucleoprotein Granule
0	GO:0042455	Ribonucleoside Biosynthetic Process
0	GO:0033875	Ribonucleoside Bisphosphate Metabolic Process
0	GO:0042454	Ribonucleoside Catabolic Process
0	GO:0009185	Ribonucleoside Diphosphate Metabolic Process
0	GO:0009119	Ribonucleoside Metabolic Process
0	GO:0009156	Ribonucleoside Monophosphate Biosynthetic Process
0	GO:0009161	Ribonucleoside Monophosphate Metabolic Process
0	GO:0009201	Ribonucleoside Triphosphate Biosynthetic Process
0	GO:0009260	Ribonucleotide Biosynthetic Process
0	GO:0042274	Ribosomal Small Subunit Biogenesis
0	GO:0005840	Ribosome
0	GO:0043022	Ribosome Binding
0	GO:0042254	Ribosome Biogenesis
0	GO:0031123	Rna 3'-End Processing
0	GO:0009452	Rna Capping
0	GO:0006401	Rna Catabolic Process
0	GO:0006405	Rna Export From Nucleus
0	GO:0003724	Rna Helicase Activity
0	GO:0006403	Rna Localization
0	GO:0001510	Rna Methylation
0	GO:0008173	Rna Methyltransferase Activity
0	GO:0009451	Rna Modification
0	GO:0043631	Rna Polyadenylation
0	GO:0034062	Rna Polymerase Activity
0	GO:0030880	Rna Polymerase Complex
0	GO:0008353	Rna Polymerase Ii Carboxy-Terminal Domain Kinase Activity
0	GO:0000978	Rna Polymerase Ii Core Promoter Proximal Region Sequence-Specific Dna Binding
0	GO:0000982	Rna Polymerase Ii Core Promoter Proximal Region Sequence-Specific Dna Binding Transcription Factor Activity
0	GO:0001078	Rna Polymerase Ii Core Promoter Proximal Region Sequence-Specific Dna Binding Transcription Factor Activity Involved In Negative Regulation Of Transcription
0	GO:0001077	Rna Polymerase Ii Core Promoter Proximal Region Sequence-Specific Dna Binding Transcription Factor Activity Involved In Positive Regulation Of Transcription
0	GO:0000979	Rna Polymerase Ii Core Promoter Sequence-Specific Dna Binding
0	GO:0003705	Rna Polymerase Ii Distal Enhancer Sequence-Specific Dna Binding Transcription Factor Activity
0	GO:0001012	Rna Polymerase Ii Regulatory Region Dna Binding
0	GO:0000977	Rna Polymerase Ii Regulatory Region Sequence-Specific Dna Binding
0	GO:0001105	Rna Polymerase Ii Transcription Coactivator Activity
0	GO:0001104	Rna Polymerase Ii Transcription Cofactor Activity
0	GO:0001106	Rna Polymerase Ii Transcription Corepressor Activity
0	GO:0001085	Rna Polymerase Ii Transcription Factor Binding

0	GO:0001076	Rna Polymerase Ii Transcription Factor Binding Transcription Factor Activity
0	GO:0001191	Rna Polymerase Ii Transcription Factor Binding Transcription Factor Activity Involved In Negative Regulation Of Transcription
0	GO:0001190	Rna Polymerase Ii Transcription Factor Binding Transcription Factor Activity Involved In Positive Regulation Of Transcription
0	GO:0008380	Rna Splicing
0	GO:0000375	Rna Splicing, Via Transesterification Reactions
0	GO:0000377	Rna Splicing, Via Transesterification Reactions With Bulged Adenosine As Nucleophile
0	GO:0043489	Rna Stabilization
0	GO:0050658	Rna Transport
0	GO:0008186	Rna-Dependent Atpase Activity
0	GO:0006278	Rna-Dependent Dna Replication
1	GO:0021903	Rostrocaudal Neural Tube Patterning
0	GO:0005791	Rough Endoplasmic Reticulum
0	GO:0030867	Rough Endoplasmic Reticulum Membrane
0	GO:0019843	Rrna Binding
0	GO:0016072	Rrna Metabolic Process
0	GO:0006364	Rrna Processing
0	GO:0009303	Rrna Transcription
0	GO:0001726	Ruffle
0	GO:0032587	Ruffle Membrane
0	GO:0031529	Ruffle Organization
0	GO:0051320	S Phase
0	GO:0000084	S Phase Of Mitotic Cell Cycle
0	GO:0008757	S-Adenosylmethionine-Dependent Methyltransferase Activity
0	GO:0070461	Saga-Type Complex
0	GO:0007431	Salivary Gland Development
0	GO:0007435	Salivary Gland Morphogenesis
0	GO:0042383	Sarcolemma
0	GO:0030017	Sarcomere
0	GO:0045214	Sarcomere Organization
0	GO:0016528	Sarcoplasm
0	GO:0016529	Sarcoplasmic Reticulum
0	GO:0033017	Sarcoplasmic Reticulum Membrane
0	GO:0005044	Scavenger Receptor Activity
0	GO:0019005	Scf Ubiquitin Ligase Complex
0	GO:0031146	Scf-Dependent Proteasomal Ubiquitin-Dependent Protein Catabolic Process
1	GO:0014044	Schwann Cell Development
1	GO:0014037	Schwann Cell Differentiation
0	GO:0019932	Second-Messenger-Mediated Signaling
0	GO:0015291	Secondary Active Transmembrane Transporter Activity
0	GO:0019748	Secondary Metabolic Process
0	GO:0030141	Secretory Granule
0	GO:0034774	Secretory Granule Lumen
0	GO:0030667	Secretory Granule Membrane
0	GO:0007379	Segment Specification
0	GO:0035282	Segmentation
0	GO:0008430	Selenium Binding
0	GO:0007423	Sensory Organ Development
0	GO:0007600	Sensory Perception
0	GO:0007606	Sensory Perception Of Chemical Stimulus
0	GO:0050953	Sensory Perception Of Light Stimulus
0	GO:0050954	Sensory Perception Of Mechanical Stimulus
0	GO:0019233	Sensory Perception Of Pain
0	GO:0007608	Sensory Perception Of Smell
0	GO:0007605	Sensory Perception Of Sound
0	GO:0050909	Sensory Perception Of Taste
0	GO:0031105	Septin Complex

0	GO:0032156	Septin Cytoskeleton
0	GO:0000981	Sequence-Specific Dna Binding Rna Polymerase Ii Transcription Factor Activity
0	GO:0051208	Sequestering Of Calcium Ion
0	GO:0051238	Sequestering Of Metal Ion
0	GO:0030730	Sequestering Of Triglyceride
0	GO:0009070	Serine Family Amino Acid Biosynthetic Process
0	GO:0009071	Serine Family Amino Acid Catabolic Process
0	GO:0009069	Serine Family Amino Acid Metabolic Process
0	GO:0017171	Serine Hydrolase Activity
0	GO:0004252	Serine-Type Endopeptidase Activity
0	GO:0004867	Serine-Type Endopeptidase Inhibitor Activity
0	GO:0070008	Serine-Type Exopeptidase Activity
0	GO:0008236	Serine-Type Peptidase Activity
0	GO:0051378	Serotonin Binding
0	GO:0004993	Serotonin Receptor Activity
0	GO:0007210	Serotonin Receptor Signaling Pathway
0	GO:0060008	Sertoli Cell Differentiation
0	GO:0000803	Sex Chromosome
0	GO:0007530	Sex Determination
0	GO:0007548	Sex Differentiation
0	GO:0019953	Sexual Reproduction
0	GO:0042169	Sh2 Domain Binding
0	GO:0017124	Sh3 Domain Binding
0	GO:0005070	Sh3/Sh2 Adaptor Activity
0	GO:0046459	Short-Chain Fatty Acid Metabolic Process
0	GO:0008373	Sialyltransferase Activity
0	GO:0023061	Signal Release
0	GO:0005048	Signal Sequence Binding
0	GO:0072331	Signal Transduction By P53 Class Mediator
0	GO:0072332	Signal Transduction By P53 Class Mediator Resulting In Induction Of Apoptosis
0	GO:0042770	Signal Transduction In Response To Dna Damage
0	GO:0072395	Signal Transduction Involved In Cell Cycle Checkpoint
0	GO:0072422	Signal Transduction Involved In Dna Damage Checkpoint
0	GO:0072401	Signal Transduction Involved In Dna Integrity Checkpoint
0	GO:0072404	Signal Transduction Involved In G1/S Transition Checkpoint
0	GO:0072413	Signal Transduction Involved In Mitotic Cell Cycle Checkpoint
0	GO:0072474	Signal Transduction Involved In Mitotic Cell Cycle G1/S Checkpoint
0	GO:0072431	Signal Transduction Involved In Mitotic Cell Cycle G1/S Transition Dna Damage Checkpoint
0	GO:0023019	Signal Transduction Involved In Regulation Of Gene Expression
0	GO:0035591	Signaling Adaptor Activity
0	GO:0008180	Signalosome
0	GO:0007338	Single Fertilization
0	GO:0003697	Single-Stranded Dna Binding
0	GO:0003727	Single-Stranded Rna Binding
0	GO:0007062	Sister Chromatid Cohesion
0	GO:0000819	Sister Chromatid Segregation
0	GO:0030427	Site Of Polarized Growth
0	GO:0035914	Skeletal Muscle Cell Differentiation
0	GO:0003009	Skeletal Muscle Contraction
0	GO:0048741	Skeletal Muscle Fiber Development
0	GO:0060538	Skeletal Muscle Organ Development
0	GO:0007519	Skeletal Muscle Tissue Development
0	GO:0043403	Skeletal Muscle Tissue Regeneration
0	GO:0001501	Skeletal System Development
0	GO:0048705	Skeletal System Morphogenesis
0	GO:0043588	Skin Development

0	GO:0030431	Sleep
0	GO:0046332	Smad Binding
0	GO:0007183	Smad Protein Complex Assembly
0	GO:0007184	Smad Protein Import Into Nucleus
0	GO:0060395	Smad Protein Signal Transduction
0	GO:0032182	Small Conjugating Protein Binding
0	GO:0019787	Small Conjugating Protein Ligase Activity
0	GO:0019783	Small Conjugating Protein-Specific Protease Activity
0	GO:0031267	Small Gtpase Binding
0	GO:0007264	Small Gtpase Mediated Signal Transduction
0	GO:0005083	Small Gtpase Regulator Activity
0	GO:0044283	Small Molecule Biosynthetic Process
0	GO:0044282	Small Molecule Catabolic Process
0	GO:0030532	Small Nuclear Ribonucleoprotein Complex
0	GO:0005732	Small Nucleolar Ribonucleoprotein Complex
0	GO:0008641	Small Protein Activating Enzyme Activity
0	GO:0015935	Small Ribosomal Subunit
0	GO:0005790	Smooth Endoplasmic Reticulum
0	GO:0051145	Smooth Muscle Cell Differentiation
0	GO:0014909	Smooth Muscle Cell Migration
0	GO:0048659	Smooth Muscle Cell Proliferation
0	GO:0006939	Smooth Muscle Contraction
0	GO:0048745	Smooth Muscle Tissue Development
0	GO:0007224	Smoothened Signaling Pathway
0	GO:0005484	Snap Receptor Activity
0	GO:0000149	Snare Binding
0	GO:0031201	Snare Complex
0	GO:0017069	Snrna Binding
0	GO:0016073	Snrna Metabolic Process
0	GO:0016180	Snrna Processing
1	GO:0035176	Social Behavior
0	GO:0005272	Sodium Channel Activity
0	GO:0034706	Sodium Channel Complex
0	GO:0071436	Sodium Ion Export
0	GO:0055078	Sodium Ion Homeostasis
0	GO:0035725	Sodium Ion Transmembrane Transport
0	GO:0015081	Sodium Ion Transmembrane Transporter Activity
0	GO:0006814	Sodium Ion Transport
0	GO:0043252	Sodium-Independent Organic Anion Transport
0	GO:0005283	Sodium:Amino Acid Symporter Activity
0	GO:0017153	Sodium:Dicarboxylate Symporter Activity
0	GO:0005625	Soluble Fraction
0	GO:0015298	Solute:Cation Antiporter Activity
0	GO:0015294	Solute:Cation Symporter Activity
0	GO:0015299	Solute:Hydrogen Antiporter Activity
0	GO:0015295	Solute:Hydrogen Symporter Activity
0	GO:0015370	Solute:Sodium Symporter Activity
0	GO:0015300	Solute:Solute Antiporter Activity
0	GO:0016444	Somatic Cell Dna Recombination
0	GO:0002200	Somatic Diversification Of Immune Receptors
0	GO:0002562	Somatic Diversification Of Immune Receptors Via Germline Recombination Within A Single Locus
0	GO:0016445	Somatic Diversification Of Immunoglobulins
0	GO:0002208	Somatic Diversification Of Immunoglobulins Involved In Immune Response
0	GO:0016447	Somatic Recombination Of Immunoglobulin Gene Segments
0	GO:0002204	Somatic Recombination Of Immunoglobulin Genes Involved In Immune Response
0	GO:0048103	Somatic Stem Cell Division

0	GO:0035019	Somatic Stem Cell Maintenance
0	GO:0061053	Somite Development
0	GO:0001756	Somitogenesis
0	GO:0010092	Specification Of Organ Identity
0	GO:0009799	Specification Of Symmetry
0	GO:0030317	Sperm Motility
0	GO:0035036	Sperm-Egg Recognition
0	GO:0007286	Spermatid Development
0	GO:0048515	Spermatid Differentiation
0	GO:0007289	Spermatid Nucleus Differentiation
0	GO:0007283	Spermatogenesis
0	GO:0046520	Sphingoid Biosynthetic Process
0	GO:0046519	Sphingoid Metabolic Process
0	GO:0046625	Sphingolipid Binding
0	GO:0030148	Sphingolipid Biosynthetic Process
0	GO:0030149	Sphingolipid Catabolic Process
0	GO:0006665	Sphingolipid Metabolic Process
0	GO:0006684	Sphingomyelin Metabolic Process
0	GO:0021527	Spinal Cord Association Neuron Differentiation
0	GO:0021510	Spinal Cord Development
0	GO:0021513	Spinal Cord Dorsal/Ventral Patterning
0	GO:0021522	Spinal Cord Motor Neuron Differentiation
0	GO:0021511	Spinal Cord Patterning
0	GO:0005819	Spindle
0	GO:0051225	Spindle Assembly
0	GO:0071173	Spindle Assembly Checkpoint
0	GO:0090307	Spindle Assembly Involved In Mitosis
0	GO:0031577	Spindle Checkpoint
0	GO:0051653	Spindle Localization
0	GO:0005876	Spindle Microtubule
0	GO:0051233	Spindle Midzone
0	GO:0007051	Spindle Organization
0	GO:0000922	Spindle Pole
0	GO:0048536	Spleen Development
0	GO:0005681	Spliceosomal Complex
0	GO:0000245	Spliceosomal Complex Assembly
0	GO:0000387	Spliceosomal Snrnp Assembly
0	GO:0002040	Sprouting Angiogenesis
0	GO:0032933	Srebp-Mediated Signaling Pathway
0	GO:0030914	Staga Complex
0	GO:0001964	Startle Response
0	GO:0048864	Stem Cell Development
0	GO:0048863	Stem Cell Differentiation
0	GO:0017145	Stem Cell Division
0	GO:0019827	Stem Cell Maintenance
0	GO:0072089	Stem Cell Proliferation
0	GO:0032420	Stereocilium
0	GO:0032421	Stereocilium Bundle
0	GO:0005496	Steroid Binding
0	GO:0006694	Steroid Biosynthetic Process
0	GO:0006706	Steroid Catabolic Process
0	GO:0016229	Steroid Dehydrogenase Activity
0	GO:0033764	Steroid Dehydrogenase Activity, Acting On The Ch-Oh Group Of Donors, Nad Or Nadp As Acceptor
0	GO:0034433	Steroid Esterification
0	GO:0043401	Steroid Hormone Mediated Signaling Pathway
0	GO:0003707	Steroid Hormone Receptor Activity

0	GO:0035258	Steroid Hormone Receptor Binding
0	GO:0008395	Steroid Hydroxylase Activity
0	GO:0008202	Steroid Metabolic Process
0	GO:0032934	Sterol Binding
0	GO:0016126	Sterol Biosynthetic Process
0	GO:0016127	Sterol Catabolic Process
0	GO:0034434	Sterol Esterification
0	GO:0055092	Sterol Homeostasis
0	GO:0016125	Sterol Metabolic Process
0	GO:0015918	Sterol Transport
0	GO:0015248	Sterol Transporter Activity
0	GO:0001725	Stress Fiber
0	GO:0043149	Stress Fiber Assembly
0	GO:0051403	Stress-Activated Mapk Cascade
0	GO:0031098	Stress-Activated Protein Kinase Signaling Cascade
0	GO:0014888	Striated Muscle Adaptation
0	GO:0010658	Striated Muscle Cell Apoptotic Process
0	GO:0055002	Striated Muscle Cell Development
0	GO:0051146	Striated Muscle Cell Differentiation
0	GO:0014855	Striated Muscle Cell Proliferation
0	GO:0006941	Striated Muscle Contraction
0	GO:0014897	Striated Muscle Hypertrophy
0	GO:0005865	Striated Muscle Thin Filament
0	GO:0014706	Striated Muscle Tissue Development
0	GO:0021756	Striatum Development
0	GO:0005200	Structural Constituent Of Cytoskeleton
0	GO:0005212	Structural Constituent Of Eye Lens
0	GO:0008307	Structural Constituent Of Muscle
0	GO:0003735	Structural Constituent Of Ribosome
0	GO:0043566	Structure-Specific Dna Binding
1	GO:0021544	Subpallium Development
0	GO:0034446	Substrate Adhesion-Dependent Cell Spreading
0	GO:0006929	Substrate-Dependent Cell Migration
0	GO:0022838	Substrate-Specific Channel Activity
0	GO:0001967	Suckling Behavior
0	GO:0051119	Sugar Transmembrane Transporter Activity
0	GO:0050308	Sugar-Phosphatase Activity
0	GO:0015116	Sulfate Transmembrane Transporter Activity
0	GO:0008272	Sulfate Transport
0	GO:0051923	Sulfation
0	GO:0008146	Sulfotransferase Activity
0	GO:0000097	Sulfur Amino Acid Biosynthetic Process
0	GO:0000096	Sulfur Amino Acid Metabolic Process
0	GO:0044272	Sulfur Compound Biosynthetic Process
0	GO:0006790	Sulfur Compound Metabolic Process
0	GO:0008484	Sulfuric Ester Hydrolase Activity
0	GO:0042554	Superoxide Anion Generation
0	GO:0006801	Superoxide Metabolic Process
1	GO:0016514	Swi/Snf Complex
1	GO:0070603	Swi/Snf-Type Complex
0	GO:0044403	Symbiosis, Encompassing Mutualism Through Parasitism
1	GO:0048485	Sympathetic Nervous System Development
0	GO:0015293	Symporter Activity
1	GO:0045202	Synapse
1	GO:0007416	Synapse Assembly
1	GO:0050808	Synapse Organization

1	GO:0044456	Synapse Part
1	GO:0007129	Synapsis
1	GO:0097060	Synaptic Membrane
1	GO:0007271	Synaptic Transmission, Cholinergic
1	GO:0001963	Synaptic Transmission, Dopaminergic
1	GO:0051932	Synaptic Transmission, Gabaergic
1	GO:0035249	Synaptic Transmission, Glutamatergic
1	GO:0008021	Synaptic Vesicle
1	GO:0048488	Synaptic Vesicle Endocytosis
1	GO:0016079	Synaptic Vesicle Exocytosis
1	GO:0030672	Synaptic Vesicle Membrane
1	GO:0048489	Synaptic Vesicle Transport
1	GO:0000795	Synaptonemal Complex
1	GO:0007130	Synaptonemal Complex Assembly
1	GO:0070193	Synaptonemal Complex Organization
1	GO:0019717	Synaptosome
0	GO:0006949	Syncytium Formation
0	GO:0000768	Syncytium Formation By Plasma Membrane Fusion
0	GO:0019905	Syntaxin Binding
0	GO:0017075	Syntaxin-1 Binding
0	GO:0042110	T Cell Activation
0	GO:0002286	T Cell Activation Involved In Immune Response
0	GO:0070231	T Cell Apoptotic Process
0	GO:0031295	T Cell Costimulation
0	GO:0002369	T Cell Cytokine Production
0	GO:0030217	T Cell Differentiation
0	GO:0033077	T Cell Differentiation In Thymus
0	GO:0002292	T Cell Differentiation Involved In Immune Response
0	GO:0043029	T Cell Homeostasis
0	GO:0002360	T Cell Lineage Commitment
0	GO:0001913	T Cell Mediated Cytotoxicity
0	GO:0002456	T Cell Mediated Immunity
0	GO:0042098	T Cell Proliferation
0	GO:0042101	T Cell Receptor Complex
0	GO:0050852	T Cell Receptor Signaling Pathway
0	GO:0045058	T Cell Selection
0	GO:0045063	T-Helper 1 Cell Differentiation
0	GO:0042088	T-Helper 1 Type Immune Response
0	GO:0042093	T-Helper Cell Differentiation
0	GO:0030315	T-Tubule
0	GO:0035121	Tail Morphogenesis
0	GO:0008527	Taste Receptor Activity
0	GO:0050321	Tau-Protein Kinase Activity
0	GO:0017025	Tbp-Class Protein Binding
1	GO:0022029	Telencephalon Cell Migration
1	GO:0021537	Telencephalon Development
0	GO:0000782	Telomere Cap Complex
0	GO:0000723	Telomere Maintenance
0	GO:0000722	Telomere Maintenance Via Recombination
0	GO:0032201	Telomere Maintenance Via Semi-Conservative Replication
0	GO:0007004	Telomere Maintenance Via Telomerase
0	GO:0010833	Telomere Maintenance Via Telomere Lengthening
0	GO:0032200	Telomere Organization
0	GO:0042162	Telomeric Dna Binding
0	GO:0001659	Temperature Homeostasis
0	GO:0043195	Terminal Button

0	GO:0038032	Termination Of G-Protein Coupled Receptor Signaling Pathway
0	GO:0006363	Termination Of Rna Polymerase I Transcription
0	GO:0006369	Termination Of Rna Polymerase Ii Transcription
0	GO:0006386	Termination Of Rna Polymerase Iii Transcription
0	GO:0023021	Termination Of Signal Transduction
0	GO:0006721	Terpenoid Metabolic Process
0	GO:0046906	Tetrapyrrole Binding
0	GO:0033014	Tetrapyrrole Biosynthetic Process
0	GO:0033013	Tetrapyrrole Metabolic Process
1	GO:0021794	Thalamus Development
0	GO:0035384	Thioester Biosynthetic Process
0	GO:0035383	Thioester Metabolic Process
0	GO:0016790	Thiolester Hydrolase Activity
0	GO:0004298	Threonine-Type Endopeptidase Activity
0	GO:0070003	Threonine-Type Peptidase Activity
0	GO:0045061	Thymic T Cell Selection
0	GO:0070242	Thymocyte Apoptotic Process
0	GO:0048538	Thymus Development
0	GO:0030878	Thyroid Gland Development
0	GO:0042403	Thyroid Hormone Metabolic Process
0	GO:0046966	Thyroid Hormone Receptor Binding
0	GO:0005923	Tight Junction
0	GO:0070830	Tight Junction Assembly
0	GO:0001894	Tissue Homeostasis
0	GO:0090130	Tissue Migration
0	GO:0048729	Tissue Morphogenesis
0	GO:0042246	Tissue Regeneration
0	GO:0048771	Tissue Remodeling
0	GO:0031432	Titin Binding
0	GO:0002507	Tolerance Induction
0	GO:0008063	Toll Signaling Pathway
0	GO:0034130	Toll-Like Receptor 1 Signaling Pathway
0	GO:0034134	Toll-Like Receptor 2 Signaling Pathway
0	GO:0034138	Toll-Like Receptor 3 Signaling Pathway
0	GO:0034142	Toll-Like Receptor 4 Signaling Pathway
0	GO:0002224	Toll-Like Receptor Signaling Pathway
0	GO:0043586	Tongue Development
0	GO:0043587	Tongue Morphogenesis
0	GO:0034505	Tooth Mineralization
0	GO:0031929	Tor Signaling Cascade
0	GO:0015643	Toxin Binding
0	GO:0060343	Trabecula Formation
0	GO:0061383	Trabecula Morphogenesis
0	GO:0060438	Trachea Development
0	GO:0005802	Trans-Golgi Network
0	GO:0030140	Trans-Golgi Network Transport Vesicle
0	GO:0012510	Trans-Golgi Network Transport Vesicle Membrane
0	GO:0008483	Transaminase Activity
0	GO:0003713	Transcription Coactivator Activity
0	GO:0003712	Transcription Cofactor Activity
0	GO:0003714	Transcription Corepressor Activity
0	GO:0008023	Transcription Elongation Factor Complex
0	GO:0006362	Transcription Elongation From Rna Polymerase I Promoter
0	GO:0006368	Transcription Elongation From Rna Polymerase Ii Promoter
0	GO:0006385	Transcription Elongation From Rna Polymerase Iii Promoter
0	GO:0006354	Transcription Elongation, Dna-Dependent

0	GO:0008134	Transcription Factor Binding
0	GO:0000989	Transcription Factor Binding Transcription Factor Activity
0	GO:0005667	Transcription Factor Complex
0	GO:0042991	Transcription Factor Import Into Nucleus
0	GO:0005669	Transcription Factor Tfiid Complex
0	GO:0033276	Transcription Factor Tftc Complex
0	GO:0006360	Transcription From Rna Polymerase I Promoter
0	GO:0006383	Transcription From Rna Polymerase Iii Promoter
0	GO:0006361	Transcription Initiation From Rna Polymerase I Promoter
0	GO:0006367	Transcription Initiation From Rna Polymerase Ii Promoter
0	GO:0006352	Transcription Initiation, Dna-Dependent
0	GO:0044212	Transcription Regulatory Region Dna Binding
0	GO:0000976	Transcription Regulatory Region Sequence-Specific Dna Binding
0	GO:0006353	Transcription Termination, Dna-Dependent
0	GO:0006283	Transcription-Coupled Nucleotide-Excision Repair
0	GO:0017053	Transcriptional Repressor Complex
0	GO:0070633	Transepithelial Transport
0	GO:0016746	Transferase Activity, Transferring Acyl Groups
0	GO:0016747	Transferase Activity, Transferring Acyl Groups Other Than Amino-Acyl Groups
0	GO:0016765	Transferase Activity, Transferring Alkyl Or Aryl (Other Than Methyl) Groups
0	GO:0016755	Transferase Activity, Transferring Amino-Acyl Groups
0	GO:0016757	Transferase Activity, Transferring Glycosyl Groups
0	GO:0016758	Transferase Activity, Transferring Hexosyl Groups
0	GO:0016769	Transferase Activity, Transferring Nitrogenous Groups
0	GO:0016741	Transferase Activity, Transferring One-Carbon Groups
0	GO:0016763	Transferase Activity, Transferring Pentosyl Groups
0	GO:0016782	Transferase Activity, Transferring Sulfur-Containing Groups
0	GO:0033572	Transferrin Transport
0	GO:0050431	Transforming Growth Factor Beta Binding
0	GO:0071604	Transforming Growth Factor Beta Production
0	GO:0005160	Transforming Growth Factor Beta Receptor Binding
0	GO:0007179	Transforming Growth Factor Beta Receptor Signaling Pathway
0	GO:0005072	Transforming Growth Factor Beta Receptor, Cytoplasmic Mediator Activity
0	GO:0005024	Transforming Growth Factor Beta-Activated Receptor Activity
0	GO:0046915	Transition Metal Ion Transmembrane Transporter Activity
0	GO:0000041	Transition Metal Ion Transport
0	GO:0006412	Translation
0	GO:0003746	Translation Elongation Factor Activity
0	GO:0008135	Translation Factor Activity, Nucleic Acid Binding
0	GO:0003743	Translation Initiation Factor Activity
0	GO:0031369	Translation Initiation Factor Binding
0	GO:0045182	Translation Regulator Activity
0	GO:0090079	Translation Regulator Activity, Nucleic Acid Binding
0	GO:0006414	Translational Elongation
0	GO:0006413	Translational Initiation
0	GO:0006415	Translational Termination
0	GO:0019199	Transmembrane Receptor Protein Kinase Activity
0	GO:0019198	Transmembrane Receptor Protein Phosphatase Activity
0	GO:0004675	Transmembrane Receptor Protein Serine/Threonine Kinase Activity
0	GO:0007178	Transmembrane Receptor Protein Serine/Threonine Kinase Signaling Pathway
0	GO:0004714	Transmembrane Receptor Protein Tyrosine Kinase Activity
0	GO:0005001	Transmembrane Receptor Protein Tyrosine Phosphatase Activity
0	GO:0030133	Transport Vesicle
0	GO:0030658	Transport Vesicle Membrane
0	GO:0006099	Tricarboxylic Acid Cycle
0	GO:0019432	Triglyceride Biosynthetic Process

0	GO:0019433	Triglyceride Catabolic Process
0	GO:0070328	Triglyceride Homeostasis
0	GO:0004806	Triglyceride Lipase Activity
0	GO:0006641	Triglyceride Metabolic Process
0	GO:0034385	Triglyceride-Rich Lipoprotein Particle
0	GO:0007351	Tripartite Regional Subdivision
0	GO:0072506	Trivalent Inorganic Anion Homeostasis
0	GO:0043039	Trna Aminoacylation
0	GO:0006418	Trna Aminoacylation For Protein Translation
0	GO:0000049	Trna Binding
0	GO:0006399	Trna Metabolic Process
0	GO:0008175	Trna Methyltransferase Activity
0	GO:0006400	Trna Modification
0	GO:0008033	Trna Processing
0	GO:0004549	Trna-Specific Ribonuclease Activity
0	GO:0001829	Trophectodermal Cell Differentiation
0	GO:0005523	Tropomyosin Binding
0	GO:0006569	Tryptophan Catabolic Process
0	GO:0006568	Tryptophan Metabolic Process
0	GO:0060606	Tube Closure
0	GO:0035295	Tube Development
0	GO:0035148	Tube Formation
0	GO:0035239	Tube Morphogenesis
0	GO:0015631	Tubulin Binding
0	GO:0004835	Tubulin-Tyrosine Ligase Activity
0	GO:0042533	Tumor Necrosis Factor Biosynthetic Process
0	GO:0032640	Tumor Necrosis Factor Production
0	GO:0005164	Tumor Necrosis Factor Receptor Binding
0	GO:0032813	Tumor Necrosis Factor Receptor Superfamily Binding
0	GO:0071706	Tumor Necrosis Factor Superfamily Cytokine Production
0	GO:0005031	Tumor Necrosis Factor-Activated Receptor Activity
0	GO:0033209	Tumor Necrosis Factor-Mediated Signaling Pathway
0	GO:0000155	Two-Component Sensor Activity
0	GO:0042092	Type 2 Immune Response
0	GO:0003309	Type B Pancreatic Cell Differentiation
0	GO:0045351	Type I Interferon Biosynthetic Process
0	GO:0032606	Type I Interferon Production
0	GO:0060337	Type I Interferon-Mediated Signaling Pathway
0	GO:0007260	Tyrosine Phosphorylation Of Stat Protein
0	GO:0042508	Tyrosine Phosphorylation Of Stat1 Protein
0	GO:0042503	Tyrosine Phosphorylation Of Stat3 Protein
0	GO:0042506	Tyrosine Phosphorylation Of Stat5 Protein
0	GO:0005689	U12-Type Spliceosomal Complex
0	GO:0043130	Ubiquitin Binding
0	GO:0000151	Ubiquitin Ligase Complex
0	GO:0031625	Ubiquitin Protein Ligase Binding
0	GO:0004221	Ubiquitin Thiolesterase Activity
0	GO:0006511	Ubiquitin-Dependent Protein Catabolic Process
0	GO:0004842	Ubiquitin-Protein Ligase Activity
0	GO:0004843	Ubiquitin-Specific Protease Activity
0	GO:0035250	Udp-Galactosyltransferase Activity
0	GO:0008194	Udp-Glycosyltransferase Activity
0	GO:0051082	Unfolded Protein Binding
0	GO:0006636	Unsaturated Fatty Acid Biosynthetic Process
0	GO:0033559	Unsaturated Fatty Acid Metabolic Process
0	GO:0046415	Urate Metabolic Process

0	GO:0001657	Ureteric Bud Development
0	GO:0060675	Ureteric Bud Morphogenesis
0	GO:0001655	Urogenital System Development
0	GO:0060065	Uterus Development
0	GO:0033151	V(D)J Recombination
0	GO:0005775	Vacuolar Lumen
0	GO:0005774	Vacuolar Membrane
0	GO:0044437	Vacuolar Part
0	GO:0016471	Vacuolar Proton-Transporting V-Type Atpase Complex
0	GO:0007034	Vacuolar Transport
0	GO:0005773	Vacuole
0	GO:0007033	Vacuole Organization
0	GO:0060068	Vagina Development
0	GO:0010573	Vascular Endothelial Growth Factor Production
0	GO:0048010	Vascular Endothelial Growth Factor Receptor Signaling Pathway
0	GO:0003018	Vascular Process In Circulatory System
0	GO:0014829	Vascular Smooth Muscle Contraction
0	GO:0001944	Vasculature Development
0	GO:0001570	Vasculogenesis
0	GO:0042310	Vasoconstriction
0	GO:0042311	Vasodilation
0	GO:0060841	Venous Blood Vessel Development
1	GO:0021517	Ventral Spinal Cord Development
1	GO:0021514	Ventral Spinal Cord Interneuron Differentiation
0	GO:0055015	Ventricular Cardiac Muscle Cell Development
0	GO:0055012	Ventricular Cardiac Muscle Cell Differentiation
0	GO:0003229	Ventricular Cardiac Muscle Tissue Development
0	GO:0055010	Ventricular Cardiac Muscle Tissue Morphogenesis
0	GO:0003281	Ventricular Septum Development
0	GO:0060412	Ventricular Septum Morphogenesis
0	GO:0021591	Ventricular System Development
0	GO:0000038	Very Long-Chain Fatty Acid Metabolic Process
0	GO:0034361	Very-Low-Density Lipoprotein Particle
0	GO:0030120	Vesicle Coat
0	GO:0006901	Vesicle Coating
0	GO:0048278	Vesicle Docking
0	GO:0006904	Vesicle Docking Involved In Exocytosis
0	GO:0006906	Vesicle Fusion
0	GO:0051648	Vesicle Localization
0	GO:0031983	Vesicle Lumen
0	GO:0012506	Vesicle Membrane
0	GO:0016050	Vesicle Organization
0	GO:0006903	Vesicle Targeting
0	GO:0048199	Vesicle Targeting, To, From Or Within Golgi
0	GO:0047496	Vesicle Transport Along Microtubule
0	GO:0042598	Vesicular Fraction
0	GO:0046718	Viral Entry Into Host Cell
0	GO:0019080	Viral Genome Expression
0	GO:0019079	Viral Genome Replication
0	GO:0019058	Viral Infectious Cycle
0	GO:0016032	Viral Reproduction
0	GO:0022415	Viral Reproductive Process
0	GO:0019083	Viral Transcription
0	GO:0019048	Virus-Host Interaction
1	GO:0007632	Visual Behavior
1	GO:0008542	Visual Learning

0	GO:0007601	Visual Perception
0	GO:0006776	Vitamin A Metabolic Process
0	GO:0070279	Vitamin B6 Binding
0	GO:0019842	Vitamin Binding
0	GO:0009110	Vitamin Biosynthetic Process
0	GO:0042359	Vitamin D Metabolic Process
0	GO:0042809	Vitamin D Receptor Binding
0	GO:0006766	Vitamin Metabolic Process
0	GO:0051180	Vitamin Transport
0	GO:0051183	Vitamin Transporter Activity
1	GO:0008308	Voltage-Gated Anion Channel Activity
1	GO:0005245	Voltage-Gated Calcium Channel Activity
1	GO:0005891	Voltage-Gated Calcium Channel Complex
1	GO:0022843	Voltage-Gated Cation Channel Activity
1	GO:0022832	Voltage-Gated Channel Activity
1	GO:0005247	Voltage-Gated Chloride Channel Activity
1	GO:0005244	Voltage-Gated Ion Channel Activity
1	GO:0005249	Voltage-Gated Potassium Channel Activity
1	GO:0008076	Voltage-Gated Potassium Channel Complex
1	GO:0005248	Voltage-Gated Sodium Channel Activity
1	GO:0001518	Voltage-Gated Sodium Channel Complex
0	GO:0030104	Water Homeostasis
0	GO:0005372	Water Transmembrane Transporter Activity
0	GO:0006833	Water Transport
0	GO:0006767	Water-Soluble Vitamin Metabolic Process
0	GO:0050872	White Fat Cell Differentiation
0	GO:0022829	Wide Pore Channel Activity
0	GO:0016055	Wnt Receptor Signaling Pathway
0	GO:0007223	Wnt Receptor Signaling Pathway, Calcium Modulating Pathway
0	GO:0060071	Wnt Receptor Signaling Pathway, Planar Cell Polarity Pathway
0	GO:0042813	Wnt-Activated Receptor Activity
0	GO:0017147	Wnt-Protein Binding
0	GO:0044319	Wound Healing, Spreading Of Cells
0	GO:0035313	Wound Healing, Spreading Of Epidermal Cells
0	GO:0050699	Ww Domain Binding
0	GO:0006805	Xenobiotic Metabolic Process
0	GO:0001741	Xy Body
0	GO:0030018	Z Disc
0	GO:0055069	Zinc Ion Homeostasis
0	GO:0071577	Zinc Ion Transmembrane Transport
0	GO:0005385	Zinc Ion Transmembrane Transporter Activity
0	GO:0006829	Zinc Ion Transport
0	GO:0031638	Zymogen Activation
0	GO:0042588	Zymogen Granule

Related to neuronal function	Gene Set ID	Gene Set Name
0	REACTOME_3_-UTR-MEDIATED_TRANSLATIONAL_REGULATION	3 -Utr-Mediated Translational Regulation
0	REACTOME_A_THIRD_PROTEOLYTIC_CLEAVAGE_RELEASES_NICD	A Third Proteolytic Cleavage Releases Nicd
0	REACTOME_ABC-FAMILY_PROTEINS_MEDIATED_TRANSPORT	Abc-Family Proteins Mediated Transport
0	REACTOME_ABCA_TRANSPORTERS_IN_LIPID_HOMEOSTASIS	Abca Transporters In Lipid Homeostasis
0	REACTOME_ABORTIVE_ELONGATION_OF_HIV-1_TRANSCRIPT_IN_THE_ABSENCE_OF_TAT	Abortive Elongation Of Hiv-1 Transcript In The Absence Of Tat
1	REACTOME_ACETYLCHOLINE_BINDING_AND_DOWNSTREAM_EVENTS	Acetylcholine Binding And Downstream Events
1	REACTOME_ACETYLCHOLINE_NEUROTRANSMITTER_RELEASE_CYCLE	Acetylcholine Neurotransmitter Release Cycle
0	REACTOME_ACTIVATED_AMPK_STIMULATES_FATTY-ACID_OXIDATION_IN_MUSCLE	Activated Ampk Stimulates Fatty-Acid Oxidation In Muscle
0	REACTOME_ACTIVATED_TAK1_MEDIATES_P38_MAPK_ACTIVATION	Activated Tak1 Mediates P38 Mapk Activation
0	REACTOME_ACTIVATED_TLR4_SIGNALLING	Activated Tlr4 Signalling
0	REACTOME_ACTIVATION_OF_APCC_AND_APCCCDC20_MEDIATED_DEGRADATION_OF_MITOTIC_PROTEINS	Activation Of Apcc And Apcccdc20 Mediated Degradation Of Mitotic Proteins
0	REACTOME_ACTIVATION_OF_ATR_IN_RESPONSE_TO_REPLICATION_STRESS	Activation Of Atr In Response To Replication Stress
0	REACTOME_ACTIVATION_OF_BH3-ONLY_PROTEINS	Activation Of Bh3-Only Proteins
1	REACTOME_ACTIVATION_OF_CA-PERMEABLE_KAINATE_RECEPTOR	Activation Of Ca-Permeable Kainate Receptor
0	REACTOME_ACTIVATION_OF_CHAPERONE_GENES_BY_XBP1S	Activation Of Chaperone Genes By Xbp1S
0	REACTOME_ACTIVATION_OF_CHAPERONES_BY_ATF6-ALPHA	Activation Of Chaperones By Atf6-Alpha
0	REACTOME_ACTIVATION_OF_CHAPERONES_BY_IRE1ALPHA	Activation Of Chaperones By Ire1Alpha
0	REACTOME_ACTIVATION_OF_DNA_FRAGMENTATION_FACTOR	Activation Of Dna Fragmentation Factor
1	REACTOME_ACTIVATION_OF_G_PROTEIN_GATED_POTASSIUM_CHANNELS	Activation Of G Protein Gated Potassium Channels
1	REACTOME_ACTIVATION_OF_GABAB_RECEPTORS	Activation Of Gabab Receptors
0	REACTOME_ACTIVATION_OF_GENES_BY_ATF4	Activation Of Genes By Atf4
1	REACTOME_ACTIVATION_OF_KAINATE_RECEPTORS_UPON_GLUTAMATE_BINDING	Activation Of Kainate Receptors Upon Glutamate Binding
1	REACTOME_ACTIVATION_OF_NICOTINIC_ACETYLCHOLINE_RECEPTORS	Activation Of Nicotinic Acetylcholine Receptors
1	REACTOME_ACTIVATION_OF_NMDA_RECEPTOR_UPON_GLUTAMATE_BINDING_AND_POSTSYNAPTIC_EVENTS	Activation Of Nmda Receptor Upon Glutamate Binding And Postsynaptic Events
0	REACTOME_ACTIVATION_OF_RAC	Activation Of Rac
0	REACTOME_ACTIVATION_OF_THE_AP-1_FAMILY_OF_TRANSCRIPTION_FACTORS	Activation Of The Ap-1 Family Of Transcription Factors
0	REACTOME_ACTIVATION_OF_THE_MRNA_UPON_BINDING_OF_THE_CAP-BINDING_COMPLEX_AND_EIFS_AND_	Activation Of The Mrna Upon Binding Of The Cap-Binding Complex And Eifs And Subsequent Binding To 43S
0	REACTOME_ACTIVATION_OF_THE_PRE-REPLICATIVE_COMPLEX	Activation Of The Pre-Replicative Complex
0	REACTOME_ADAPTIVE_IMMUNE_SYSTEM	Adaptive Immune System
0	REACTOME_ADENYLATE_CYCLASE_ACTIVATING_PATHWAY	Adenylate Cyclase Activating Pathway
0	REACTOME_ADENYLATE_CYCLASE_INHIBITORY_PATHWAY	Adenylate Cyclase Inhibitory Pathway
0	REACTOME_ADHERENS_JUNCTIONS_INTERACTIONS	Adherens Junctions Interactions
0	REACTOME_ADP_SIGNALLING_THROUGH_P2Y_PURINOCEPTOR_1	Adp Signalling Through P2Y Purinoceptor 1
0	REACTOME_ADP_SIGNALLING_THROUGH_P2Y_PURINOCEPTOR_12	Adp Signalling Through P2Y Purinoceptor 12
0	REACTOME_ADVANCED_GLYCOSYLATION_ENDPRODUCT_RECEPTOR_SIGNALING	Advanced Glycosylation Endproduct Receptor Signaling
0	REACTOME_AKT_PHOSPHORYLATES_TARGETS_IN_THE_CYTOSOL	Akt Phosphorylates Targets In The Cytosol
0	REACTOME_AMINE_COMPOUND_SLC_TRANSPORTERS	Amine Compound Slc Transporters
0	REACTOME_AMINE_LIGAND-BINDING_RECEPTORS	Amine Ligand-Binding Receptors
0	REACTOME_AMINE-DERIVED_HORMONES	Amine-Derived Hormones
0	REACTOME_AMINO_ACID_AND_OLIGOPEPTIDE_SLC_TRANSPORTERS	Amino Acid And Oligopeptide Slc Transporters
0	REACTOME_AMINO_ACID_SYNTHESIS_AND_INTERCONVERSION_TRANSAMINATION	Amino Acid Synthesis And Interconversion Transamination
0	REACTOME_AMINO_ACID_TRANSPORT_ACROSS_THE_PLASMA_MEMBRANE	Amino Acid Transport Across The Plasma Membrane
0	REACTOME_AMYLOIDS	Amyloids
0	REACTOME_ANDROGEN_BIOSYNTHESIS	Androgen Biosynthesis
0	REACTOME_ANTIGEN_PRESENTATION_FOLDING_ASSEMBLY_AND_PEPTIDE_LOADING_OF_CLASS_I_MHC	Antigen Presentation Folding Assembly And Peptide Loading Of Class I Mhc
0	REACTOME_ANTIGEN_PROCESSING_UBIQUITINATION__PROTEASOME_DEGRADATION	Antigen Processing Ubiquitination Proteasome Degradation
0	REACTOME_ANTIGEN_PROCESSING-CROSS_PRESENTATION	Antigen Processing-Cross Presentation
0	REACTOME_ANTIVIRAL_MECHANISM_BY_IFN-STIMULATED_GENES	Antiviral Mechanism By Ifn-Stimulated Genes
0	REACTOME_APC-CDC20_MEDIATED_DEGRADATION_OF_NEK2A	Apc-Cdc20 Mediated Degradation Of Nek2A
0	REACTOME_APCC-MEDIATED_DEGRADATION_OF_CELL_CYCLE_PROTEINS	Apcc-Mediated Degradation Of Cell Cycle Proteins
0	REACTOME_APCCCDC20_MEDIATED_DEGRADATION_OF_CYCLIN_B	Apcccdc20 Mediated Degradation Of Cyclin B
0	REACTOME_APCCCDC20_MEDIATED_DEGRADATION_OF_MITOTIC_PROTEINS	Apcccdc20 Mediated Degradation Of Mitotic Proteins
0	REACTOME_APCCCDC20_MEDIATED_DEGRADATION_OF_SECURIN	Apcccdc20 Mediated Degradation Of Securin
0	REACTOME_APCCCDH1_MEDIATED_DEGRADATION_OF_CDC20_AND_OTHER_APCCCDH1_TARGETED_PROTEIN	Apcccdh1 Mediated Degradation Of Cdc20 And Other Apcccdh1 Targeted Proteins In Late Mitosisearly G1
0	REACTOME_APOPTOSIS	Apoptosis
0	REACTOME_APOPTOSIS_INDUCED_DNA_FRAGMENTATION	Apoptosis Induced Dna Fragmentation
0	REACTOME_APOPTOTIC_CLEAVAGE_OF_CELL_ADHESION__PROTEINS	Apoptotic Cleavage Of Cell Adhesion Proteins

0	REACTOME_APOPTOTIC_CLEAVAGE_OF_CELLULAR_PROTEINS	Apoptotic Cleavage Of Cellular Proteins
0	REACTOME_APOPTOTIC_EXECUTION__PHASE	Apoptotic Execution Phase
0	REACTOME_AQUAPORIN-MEDIATED_TRANSPORT	Aquaporin-Mediated Transport
0	REACTOME_ARMS-MEDIATED_ACTIVATION	Arms-Mediated Activation
0	REACTOME_ASPARAGINE_N-LINKED_GLYCOSYLATION	Asparagine N-Linked Glycosylation
0	REACTOME_ASSEMBLY_OF_HIV_VIRION	Assembly Of Hiv Virion
0	REACTOME_ASSEMBLY_OF_THE_PRE-REPLICATIVE_COMPLEX	Assembly Of The Pre-Replicative Complex
0	REACTOME_ASSOCIATION_OF_LICENSING_FACTORS_WITH_THE_PRE-REPLICATIVE_COMPLEX	Association Of Licensing Factors With The Pre-Replicative Complex
0	REACTOME_ASSOCIATION_OF_TRICCCT_WITH_TARGET_PROTEINS_DURING_BIOSYNTHESIS	Association Of Triccct With Target Proteins During Biosynthesis
0	REACTOME_AUTODEGRADATION_OF_CDH1_BY_CDH1APCC	Autodegradation Of Cdh1 By Cdh1Apcc
0	REACTOME_AUTODEGRADATION_OF_THE_E3_UBIQUITIN_LIGASE_COP1	Autodegradation Of The E3 Ubiquitin Ligase Cop1
1	REACTOME_AXON_GUIDANCE	Axon Guidance
0	REACTOME_BASE_EXCISION_REPAIR	Base Excision Repair
0	REACTOME_BASE-FREE_SUGAR-PHOSPHATE_REMOVAL_VIA_THE_SINGLE-NUCLEOTIDE_REPLACEMENT_PATHW	Base-Free Sugar-Phosphate Removal Via The Single-Nucleotide Replacement Pathway
0	REACTOME_BASIGIN_INTERACTIONS	Basigin Interactions
0	REACTOME_BETA_DEFENSINS	Beta Defensins
0	REACTOME_BETA-CATENIN_PHOSPHORYLATION_CASCADE	Beta-Catenin Phosphorylation Cascade
0	REACTOME_BILE_ACID_AND_BILE_SALT_METABOLISM	Bile Acid And Bile Salt Metabolism
0	REACTOME_BILE_SALT_AND_ORGANIC_ANION_SLC_TRANSPORTERS	Bile Salt And Organic Anion Slc Transporters
0	REACTOME_BIOLOGICAL_OXIDATIONS	Biological Oxidations
0	REACTOME_BIOSYNTHESIS_OF_THE_N-GLYCAN_PRECURSOR_DOLICHOL_LIPID-LINKED_OLIGOSACCHARIDE_LLC	Biosynthesis Of The N-Glycan Precursor Dolichol Lipid-Linked Oligosaccharide Llo And Transfer To A Nascent Protein
0	REACTOME_BMAL1CLOCKNPAS2_ACTIVATES_GENE_EXPRESSION	Bmal1Clocknpas2 Activates Gene Expression
0	REACTOME_BOTULINUM_NEUROTOXICITY	Botulinum Neurotoxicity
0	REACTOME_BRANCHED-CHAIN_AMINO_ACID_CATABOLISM	Branched-Chain Amino Acid Catabolism
1	REACTOME_CA-DEPENDENT_EVENTS	Ca-Dependent Events
0	REACTOME_CALCITONIN-LIKE_LIGAND_RECEPTORS	Calcitonin-Like Ligand Receptors
0	REACTOME_CALMODULIN_INDUCED_EVENTS	Calmodulin Induced Events
0	REACTOME_CALNEXINCALRETICULIN_CYCLE	Calnexincalreticulin Cycle
0	REACTOME_CAM_PATHWAY	Cam Pathway
0	REACTOME_CAP-DEPENDENT_TRANSLATION_INITIATION	Cap-Dependent Translation Initiation
0	REACTOME_CASPASE-MEDIATED_CLEAVAGE_OF_CYTOSKELETAL_PROTEINS	Caspase-Mediated Cleavage Of Cytoskeletal Proteins
0	REACTOME_CD28_CO-STIMULATION	Cd28 Co-Stimulation
0	REACTOME_CD28_DEPENDENT_PI3KAKT_SIGNALING	Cd28 Dependent Pi3Kakt Signaling
0	REACTOME_CD28_DEPENDENT_VAV1_PATHWAY	Cd28 Dependent Vav1 Pathway
0	REACTOME_CDC20PHOSPHO-APCC_MEDIATED_DEGRADATION_OF_CYCLIN_A	Cdc20Phospho-Apcc Mediated Degradation Of Cyclin A
0	REACTOME_CDC6_ASSOCIATION_WITH_THE_ORCORIGIN_COMPLEX	Cdc6 Association With The Orcorigin Complex
0	REACTOME_CDK-MEDIATED_PHOSPHORYLATION_AND_REMOVAL_OF_CDC6	Cdk-Mediated Phosphorylation And Removal Of Cdc6
0	REACTOME_CDO_IN_MYOGENESIS	Cdo In Myogenesis
0	REACTOME_CDT1_ASSOCIATION_WITH_THE_CDC6ORCORIGIN_COMPLEX	Cdt1 Association With The Cdc6Orcorigin Complex
0	REACTOME_CELL_CYCLE	Cell Cycle
0	REACTOME_CELL_CYCLE_CHECKPOINTS	Cell Cycle Checkpoints
0	REACTOME_CELL_CYCLE_MITOTIC	Cell Cycle Mitotic
0	REACTOME_CELL_DEATH_SIGNALLING_VIA_NRAGE_NRIF_AND_NADE	Cell Death Signalling Via Nrage Nrif And Nade
0	REACTOME_CELL_JUNCTION_ORGANIZATION	Cell Junction Organization
0	REACTOME_CELL_SURFACE_INTERACTIONS_AT_THE_VASCULAR_WALL	Cell Surface Interactions At The Vascular Wall
0	REACTOME_CELL-CELL_COMMUNICATION	Cell-Cell Communication
0	REACTOME_CELL-CELL_JUNCTION_ORGANIZATION	Cell-Cell Junction Organization
0	REACTOME_CELL-EXTRACELLULAR_MATRIX_INTERACTIONS	Cell-Extracellular Matrix Interactions
0	REACTOME_CENTROSOME_MATURATION	Centrosome Maturation
0	REACTOME_CGMP_EFFECTS	Cgmp Effects
0	REACTOME_CHAPERONIN-MEDIATED_PROTEIN_FOLDING	Chaperonin-Mediated Protein Folding
0	REACTOME_CHEMOKINE_RECEPTORS_BIND_CHEMOKINES	Chemokine Receptors Bind Chemokines
0	REACTOME_CHOLESTEROL_BIOSYNTHESIS	Cholesterol Biosynthesis
0	REACTOME_CHROMOSOME_MAINTENANCE	Chromosome Maintenance
0	REACTOME_CHYLOMICRON-MEDIATED_LIPID_TRANSPORT	Chylomicron-Mediated Lipid Transport
1	REACTOME_CIRCADIAN_CLOCK	Circadian Clock
0	REACTOME_CITRIC_ACID_CYCLE_TCA_CYCLE	Citric Acid Cycle Tca Cycle
0	REACTOME_CLASS_A1_RHODOPSIN-LIKE_RECEPTORS	Class A1 Rhodopsin-Like Receptors
0	REACTOME_CLASS_B2_SECRETIN_FAMILY_RECEPTORS	Class B2 Secretin Family Receptors

1	REACTOME_CLASS_C3_METABOTROPIC_GLUTAMATEPHEROMONE_RECEPTORS	Class C3 Metabotropic Glutamatepheromone Receptors
0	REACTOME_CLASS_I_MHC_MEDIATED_ANTIGEN_PROCESSING__PRESENTATION	Class I Mhc Mediated Antigen Processing Presentation
0	REACTOME_CLASSICAL_ANTIBODY-MEDIATED_COMPLEMENT_ACTIVATION	Classical Antibody-Mediated Complement Activation
0	REACTOME_CLATHRIN_DERIVED_VESICLE_BUDDING	Clathrin Derived Vesicle Budding
0	REACTOME_CLEAVAGE_OF_GROWING_TRANSCRIPT_IN_THE_TERMINATION_REGION	Cleavage Of Growing Transcript In The Termination Region
0	REACTOME_COMMON_PATHWAY	Common Pathway
0	REACTOME_COMPLEMENT_CASCADE	Complement Cascade
0	REACTOME_CONVERSION_FROM_APCCCDC20_TO_APCCCDH1_IN_LATE_ANAPHASE	Conversion From Apcccdc20 To Apcccdh1 In Late Anaphase
0	REACTOME_COOPERATION_OF_PREFOLDIN_AND_TRICCCT__IN_ACTIN_AND_TUBULIN_FOLDING	Cooperation Of Prefoldin And Triccct In Actin And Tubulin Folding
0	REACTOME_COPI_MEDIATED_TRANSPORT	Copi Mediated Transport
0	REACTOME_COSTIMULATION_BY_THE_CD28_FAMILY	Costimulation By The Cd28 Family
0	REACTOME_CREATION_OF_C4_AND_C2_ACTIVATORS	Creation Of C4 And C2 Activators
1	REACTOME_CREB_PHOSPHORYLATION_THROUGH_THE_ACTIVATION_OF_CAMKII	Creb Phosphorylation Through The Activation Of Camkii
1	REACTOME_CREB_PHOSPHORYLATION_THROUGH_THE_ACTIVATION_OF_RAS	Creb Phosphorylation Through The Activation Of Ras
1	REACTOME_CRMPS_IN_SEMA3A_SIGNALING	Crmps In Sema3A Signaling
0	REACTOME_CROSS-PRESENTATION_OF_SOLUBLE_EXOGENOUS_ANTIGENS_ENDOSOMES	Cross-Presentation Of Soluble Exogenous Antigens Endosomes
0	REACTOME_CTLA4_INHIBITORY_SIGNALING	Ctla4 Inhibitory Signaling
0	REACTOME_CYCLIN_AB1_ASSOCIATED_EVENTS_DURING_G2M_TRANSITION	Cyclin Ab1 Associated Events During G2M Transition
0	REACTOME_CYCLIN_ACDK2-ASSOCIATED_EVENTS_AT_S_PHASE_ENTRY	Cyclin Acdk2-Associated Events At S Phase Entry
0	REACTOME_CYCLIN_D_ASSOCIATED_EVENTS_IN_G1	Cyclin D Associated Events In G1
0	REACTOME_CYCLIN_E_ASSOCIATED_EVENTS_DURING_G1S_TRANSITION	Cyclin E Associated Events During G1S Transition
0	REACTOME_CYTOCHROME_P450_-_ARRANGED_BY_SUBSTRATE_TYPE	Cytochrome P450 - Arranged By Substrate Type
0	REACTOME_CYTOKINE_SIGNALING_IN_IMMUNE_SYSTEM	Cytokine Signaling In Immune System
0	REACTOME_CYTOSOLIC_SULFONATION_OF_SMALL_MOLECULES	Cytosolic Sulfonation Of Small Molecules
0	REACTOME_CYTOSOLIC_TRNA_AMINOACYLATION	Cytosolic Trna Aminoacylation
1	REACTOME_DAG_AND_IP3_SIGNALING	Dag And Ip3 Signaling
1	REACTOME_DARPP-32_EVENTS	Darpp-32 Events
1	REACTOME_DCC_MEDIATED_ATTRACTIVE_SIGNALING	Dcc Mediated Attractive Signaling
0	REACTOME_DEADENYLATION_OF_MRNA	Deadenylation Of Mrna
0	REACTOME_DEADENYLATION-DEPENDENT_MRNA_DECAY	Deadenylation-Dependent Mrna Decay
0	REACTOME_DEATH_RECEPTOR__SIGNALLING	Death Receptor Signalling
0	REACTOME_DEFENSINS	Defensins
0	REACTOME_DEGRADATION_OF_BETA-CATENIN_BY_THE_DESTRUCTION_COMPLEX	Degradation Of Beta-Catenin By The Destruction Complex
1	REACTOME_DEPOLARIZATION_OF_THE_PRESYNAPTIC_TERMINAL_TRIGGERS_THE_OPENING_OF_CALCIUM_CH	Depolarization Of The Presynaptic Terminal Triggers The Opening Of Calcium Channels
0	REACTOME_DEPOSITION_OF_NEW_CENPA-CONTAINING_NUCLEOSOMES_AT_THE_CENTROMERE	Deposition Of New Cenpa-Containing Nucleosomes At The Centromere
0	REACTOME_DESTABILIZATION_OF_MRNA_BY_AUF1_HNRNP_D0	Destabilization Of Mrna By Auf1 Hnrnp D0
0	REACTOME_DESTABILIZATION_OF_MRNA_BY_BUTYRATE_RESPONSE_FACTOR_1_BRF1	Destabilization Of Mrna By Butyrate Response Factor 1 Brf1
0	REACTOME_DESTABILIZATION_OF_MRNA_BY_KSRP	Destabilization Of Mrna By Ksrp
0	REACTOME_DESTABILIZATION_OF_MRNA_BY_TRISTETRAPROLIN_TTP	Destabilization Of Mrna By Tristetraprolin Ttp
0	REACTOME_DEVELOPMENTAL_BIOLOGY	Developmental Biology
0	REACTOME_DIABETES_PATHWAYS	Diabetes Pathways
0	REACTOME_DNA_REPAIR	Dna Repair
0	REACTOME_DNA_REPLICATION	Dna Replication
0	REACTOME_DNA_REPLICATION_PRE-INITIATION	Dna Replication Pre-Initiation
0	REACTOME_DNA_STRAND_ELONGATION	Dna Strand Elongation
1	REACTOME_DOPAMINE_NEUROTRANSMITTER_RELEASE_CYCLE	Dopamine Neurotransmitter Release Cycle
0	REACTOME_DOUBLE-STRAND_BREAK_REPAIR	Double-Strand Break Repair
0	REACTOME_DOWNREGULATION_OF_ERRB2ERBB3_SIGNALING	Downregulation Of Errb2Erbb3 Signaling
0	REACTOME_DOWNSTREAM_SIGNAL_TRANSDUCTION	Downstream Signal Transduction
0	REACTOME_DOWNSTREAM_SIGNALING_OF_ACTIVATED_FGFR	Downstream Signaling Of Activated Fgfr
0	REACTOME_DOWNSTREAM_TCR_SIGNALING	Downstream Tcr Signaling
1	REACTOME_DSCAM_INTERACTIONS	Dscam Interactions
0	REACTOME_DUAL_INCISION_REACTION_IN_GG-NER	Dual Incision Reaction In Gg-Ner
0	REACTOME_DUAL_INCISION_REACTION_IN_TC-NER	Dual Incision Reaction In Tc-Ner
0	REACTOME_E2F_MEDIATED_REGULATION_OF_DNA_REPLICATION	E2F Mediated Regulation Of Dna Replication
0	REACTOME_E2F-ENABLED_INHIBITION_OF_PRE-REPLICATION_COMPLEX_FORMATION	E2F-Enabled Inhibition Of Pre-Replication Complex Formation
0	REACTOME_EARLY_PHASE_OF_HIV_LIFE_CYCLE	Early Phase Of Hiv Life Cycle
0	REACTOME_EFFECTS_OF_PIP2_HYDROLYSIS	Effects Of Pip2 Hydrolysis
0	REACTOME_EGFR_DOWNREGULATION	Egfr Downregulation

0	REACTOME_EGFR_INTERACTS_WITH_PHOSPHOLIPASE_C-GAMMA	Egfr Interacts With Phospholipase C-Gamma
0	REACTOME_EICOSANOID_LIGAND-BINDING_RECEPTORS	Eicosanoid Ligand-Binding Receptors
0	REACTOME_ELONGATION_ARREST_AND_RECOVERY	Elongation Arrest And Recovery
0	REACTOME_ENDOGENOUS_STEROLS	Endogenous Sterols
0	REACTOME_ENDOSOMAL_SORTING_COMPLEX_REQUIRED_FOR_TRANSPORT_ESCRT	Endosomal Sorting Complex Required For Transport Escrt
0	REACTOME_ENERGY_DEPENDENT_REGULATION_OF_MTOR_BY_LKB1-AMPK	Energy Dependent Regulation Of Mtor By Lkb1-Ampk
0	REACTOME_ENOS_ACTIVATION_AND_REGULATION	Enos Activation And Regulation
0	REACTOME_ER-PHAGOSOME_PATHWAY	Er-Phagosome Pathway
0	REACTOME_ERKMAPK_TARGETS	Erkmapk Targets
0	REACTOME_ERKS_ARE_INACTIVATED	Erks Are Inactivated
0	REACTOME_ETHANOL_OXIDATION	Ethanol Oxidation
0	REACTOME_EUKARYOTIC_TRANSLATION_ELONGATION	Eukaryotic Translation Elongation
0	REACTOME_EUKARYOTIC_TRANSLATION_INITIATION	Eukaryotic Translation Initiation
0	REACTOME_EUKARYOTIC_TRANSLATION_TERMINATION	Eukaryotic Translation Termination
0	REACTOME_EXPORT_OF_VIRAL_RIBONUCLEOPROTEINS_FROM_NUCLEUS	Export Of Viral Ribonucleoproteins From Nucleus
0	REACTOME_EXTENSION_OF_TELOMERES	Extension Of Telomeres
0	REACTOME_EXTRINSIC_PATHWAY_FOR_APOPTOSIS	Extrinsic Pathway For Apoptosis
0	REACTOME_FACILITATIVE_NA-INDEPENDENT_GLUCOSE_TRANSPORTERS	Facilitative Na-Independent Glucose Transporters
0	REACTOME_FACTORS_INVOLVED_IN_MEGAKARYOCYTE_DEVELOPMENT_AND_PLATELET_PRODUCTION	Factors Involved In Megakaryocyte Development And Platelet Production
0	REACTOME_FANCONI_ANEMIA_PATHWAY	Fanconi Anemia Pathway
0	REACTOME_FATTY_ACID_TRIACYLGLYCEROL_AND_KETONE_BODY_METABOLISM	Fatty Acid Triacylglycerol And Ketone Body Metabolism
0	REACTOME_FATTY_ACYL-COA_BIOSYNTHESIS	Fatty Acyl-Coa Biosynthesis
0	REACTOME_FGFR_LIGAND_BINDING_AND_ACTIVATION	Fgfr Ligand Binding And Activation
0	REACTOME_FGFR1_LIGAND_BINDING_AND_ACTIVATION	Fgfr1 Ligand Binding And Activation
0	REACTOME_FGFR1C_LIGAND_BINDING_AND_ACTIVATION	Fgfr1C Ligand Binding And Activation
0	REACTOME_FGFR2_LIGAND_BINDING_AND_ACTIVATION	Fgfr2 Ligand Binding And Activation
0	REACTOME_FGFR2C_LIGAND_BINDING_AND_ACTIVATION	Fgfr2C Ligand Binding And Activation
0	REACTOME_FGFR3_LIGAND_BINDING_AND_ACTIVATION	Fgfr3 Ligand Binding And Activation
0	REACTOME_FGFR3C_LIGAND_BINDING_AND_ACTIVATION	Fgfr3C Ligand Binding And Activation
0	REACTOME_FGFR4_LIGAND_BINDING_AND_ACTIVATION	Fgfr4 Ligand Binding And Activation
0	REACTOME_FORMATION_OF_A_POOL_OF_FREE_40S_SUBUNITS	Formation Of A Pool Of Free 40S Subunits
0	REACTOME_FORMATION_OF_ATP_BY_CHEMIOSMOTIC_COUPLING	Formation Of Atp By Chemiosmotic Coupling
0	REACTOME_FORMATION_OF_FIBRIN_CLOT_CLOTTING_CASCADE	Formation Of Fibrin Clot Clotting Cascade
0	REACTOME_FORMATION_OF_HIV-1_ELONGATION_COMPLEX_CONTAINING_HIV-1_TAT	Formation Of Hiv-1 Elongation Complex Containing Hiv-1 Tat
0	REACTOME_FORMATION_OF_HIV-1_ELONGATION_COMPLEX_IN_THE_ABSENCE_OF_HIV-1_TAT	Formation Of Hiv-1 Elongation Complex In The Absence Of Hiv-1 Tat
0	REACTOME_FORMATION_OF_INCISION_COMPLEX_IN_GG-NER	Formation Of Incision Complex In Gg-Ner
0	REACTOME_FORMATION_OF_RNA_POL_II_ELONGATION_COMPLEX	Formation Of Rna Pol Ii Elongation Complex
0	REACTOME_FORMATION_OF_THE_EARLY_ELONGATION_COMPLEX	Formation Of The Early Elongation Complex
0	REACTOME_FORMATION_OF_THE_HIV-1_EARLY_ELONGATION_COMPLEX	Formation Of The Hiv-1 Early Elongation Complex
0	REACTOME_FORMATION_OF_THE_TERNARY_COMPLEX_AND_SUBSEQUENTLY_THE_43S_COMPLEX	Formation Of The Ternary Complex And Subsequently The 43S Complex
0	REACTOME_FORMATION_OF_TRANSCRIPTION-COUPLED_NER_TC-NER_REPAIR_COMPLEX	Formation Of Transcription-Coupled Ner Tc-Ner Repair Complex
0	REACTOME_FORMATION_OF_TUBULIN_FOLDING_INTERMEDIATES_BY_CCTTRIC	Formation Of Tubulin Folding Intermediates By Ccttric
0	REACTOME_FRS2-MEDIATED_ACTIVATION	Frs2-Mediated Activation
0	REACTOME_FRS2-MEDIATED_CASCADE	Frs2-Mediated Cascade
0	REACTOME_G_ALPHA_1213_SIGNALLING_EVENTS	G Alpha 1213 Signalling Events
0	REACTOME_G_ALPHA_I_SIGNALLING_EVENTS	G Alpha I Signalling Events
0	REACTOME_G_ALPHA_Q_SIGNALLING_EVENTS	G Alpha Q Signalling Events
0	REACTOME_G_ALPHA_S_SIGNALLING_EVENTS	G Alpha S Signalling Events
0	REACTOME_G_ALPHA_Z_SIGNALLING_EVENTS	G Alpha Z Signalling Events
0	REACTOME_G_BETAGAMMA_SIGNALLING_THROUGH_PI3KGAMMA	G Betagamma Signalling Through Pi3Kgamma
0	REACTOME_G_BETAGAMMA_SIGNALLING_THROUGH_PLC_BETA	G Betagamma Signalling Through Plc Beta
1	REACTOME_G_PROTEIN_GATED_POTASSIUM_CHANNELS	G Protein Gated Potassium Channels
1	REACTOME_G-PROTEIN_ACTIVATION	G-Protein Activation
1	REACTOME_G-PROTEIN_BETAGAMMA_SIGNALLING	G-Protein Betagamma Signalling
1	REACTOME_G-PROTEIN_MEDIATED_EVENTS	G-Protein Mediated Events
0	REACTOME_G0_AND_EARLY_G1	G0 And Early G1
0	REACTOME_G1_PHASE	G1 Phase
0	REACTOME_G1S_DNA_DAMAGE_CHECKPOINTS	G1S Dna Damage Checkpoints
0	REACTOME_G1S_TRANSITION	G1S Transition

0	REACTOME_G1S-SPECIFIC_TRANSCRIPTION	G1S-Specific Transcription
0	REACTOME_G2M_CHECKPOINTS	G2M Checkpoints
0	REACTOME_G2M_TRANSITION	G2M Transition
1	REACTOME_GAB1_SIGNALOSOME	Gab1 Signalosome
1	REACTOME_GABA_A_RECEPTOR_ACTIVATION	Gaba A Receptor Activation
1	REACTOME_GABA_B_RECEPTOR_ACTIVATION	Gaba B Receptor Activation
1	REACTOME_GABA_RECEPTOR_ACTIVATION	Gaba Receptor Activation
1	REACTOME_GABA_SYNTHESIS_RELEASE_REUPTAKE_AND_DEGRADATION	Gaba Synthesis Release Reuptake And Degradation
0	REACTOME_GAMMA-CARBOXYLATION_TRANSPORT_AND_AMINO-TERMINAL_CLEAVAGE_OF_PROTEINS	Gamma-Carboxylation Transport And Amino-Terminal Cleavage Of Proteins
0	REACTOME_GAP_JUNCTION_ASSEMBLY	Gap Junction Assembly
0	REACTOME_GAP_JUNCTION_DEGRADATION	Gap Junction Degradation
0	REACTOME_GAP_JUNCTION_TRAFFICKING	Gap Junction Trafficking
0	REACTOME_GAP_JUNCTION_TRAFFICKING_AND_REGULATION	Gap Junction Trafficking And Regulation
0	REACTOME_GAP-FILLING_DNA_REPAIR_SYNTHESIS_AND_LIGATION_IN_GG-NER	Gap-Filling Dna Repair Synthesis And Ligation In Gg-Ner
0	REACTOME_GAP-FILLING_DNA_REPAIR_SYNTHESIS_AND_LIGATION_IN_TC-NER	Gap-Filling Dna Repair Synthesis And Ligation In Tc-Ner
0	REACTOME_GENERATION_OF_SECOND_MESSENGER_MOLECULES	Generation Of Second Messenger Molecules
0	REACTOME_GENERIC_TRANSCRIPTION_PATHWAY	Generic Transcription Pathway
0	REACTOME_GLOBAL_GENOMIC_NER_GG-NER	Global Genomic Ner Gg-Ner
0	REACTOME_GLUCAGON_SIGNALING_IN_METABOLIC_REGULATION	Glucagon Signaling In Metabolic Regulation
0	REACTOME_GLUCAGON-TYPE_LIGAND_RECEPTORS	Glucagon-Type Ligand Receptors
0	REACTOME_GLUCONEOGENESIS	Gluconeogenesis
0	REACTOME_GLUCOSE_METABOLISM	Glucose Metabolism
0	REACTOME_GLUCOSE_TRANSPORT	Glucose Transport
1	REACTOME_GLUTAMATE_BINDING_ACTIVATION_OF_AMPA_RECEPTORS_AND_SYNAPTIC_PLASTICITY	Glutamate Binding Activation Of Ampa Receptors And Synaptic Plasticity
1	REACTOME_GLUTAMATE_NEUROTRANSMITTER_RELEASE_CYCLE	Glutamate Neurotransmitter Release Cycle
0	REACTOME_GLUTATHIONE_CONJUGATION	Glutathione Conjugation
0	REACTOME_GLUTATHIONE_SYNTHESIS_AND_RECYCLING	Glutathione Synthesis And Recycling
0	REACTOME_GLYCOGEN_BREAKDOWN_GLYCOGENOLYSIS	Glycogen Breakdown Glycogenolysis
0	REACTOME_GLYCOLYSIS	Glycolysis
0	REACTOME_GLYCOSPHINGOLIPID_METABOLISM	Glycosphingolipid Metabolism
0	REACTOME_GOLGI_ASSOCIATED_VESICLE_BIOGENESIS	Golgi Associated Vesicle Biogenesis
0	REACTOME_GOLGI_TO_ER_RETROGRADE_TRANSPORT	Golgi To Er Retrograde Transport
1	REACTOME_GPCR_LIGAND_BINDING	Gpcr Ligand Binding
0	REACTOME_GPVI-MEDIATED_ACTIVATION_CASCADE	Gpvi-Mediated Activation Cascade
0	REACTOME_GRB2_EVENTS_IN_EGFR_SIGNALING	Grb2 Events In Egfr Signaling
0	REACTOME_GRB2_EVENTS_IN_ERBB2_SIGNALING	Grb2 Events In Erbb2 Signaling
0	REACTOME_GRB2SOS_PROVIDES_LINKAGE_TO_MAPK_SIGNALING_FOR_INTERGRINS	Grb2Sos Provides Linkage To Mapk Signaling For Intergrins
0	REACTOME_GROWTH_HORMONE_RECEPTOR_SIGNALING	Growth Hormone Receptor Signaling
0	REACTOME_GTP_HYDROLYSIS_AND_JOINING_OF_THE_60S_RIBOSOMAL_SUBUNIT	Gtp Hydrolysis And Joining Of The 60S Ribosomal Subunit
0	REACTOME_HDL-MEDIATED_LIPID_TRANSPORT	Hdl-Mediated Lipid Transport
0	REACTOME_HEMOSTASIS	Hemostasis
0	REACTOME_HEXOSE_TRANSPORT	Hexose Transport
1	REACTOME_HIGHLY_CALCIUM_PERMEABLE_POSTSYNAPTIC_NICOTINIC_ACETYLCHOLINE_RECEPTORS	Highly Calcium Permeable Postsynaptic Nicotinic Acetylcholine Receptors
0	REACTOME_HIV_INFECTION	Hiv Infection
0	REACTOME_HIV_LIFE_CYCLE	Hiv Life Cycle
0	REACTOME_HIV-1_ELONGATION_ARREST_AND_RECOVERY	Hiv-1 Elongation Arrest And Recovery
0	REACTOME_HIV-1_TRANSCRIPTION_ELONGATION	Hiv-1 Transcription Elongation
0	REACTOME_HIV-1_TRANSCRIPTION_INITIATION	Hiv-1 Transcription Initiation
0	REACTOME_HOMOLOGOUS_RECOMBINATION_REPAIR	Homologous Recombination Repair
0	REACTOME_HOMOLOGOUS_RECOMBINATION_REPAIR_OF_REPLICATION-INDEPENDENT_DOUBLE-STRAND_BRE	Homologous Recombination Repair Of Replication-Independent Double-Strand Breaks
0	REACTOME_HORMONE_LIGAND-BINDING_RECEPTORS	Hormone Ligand-Binding Receptors
0	REACTOME_HORMONE-SENSITIVE_LIPASE_HSL-MEDIATED_TRIACYLGLYCEROL_HYDROLYSIS	Hormone-Sensitive Lipase Hsl-Mediated Triacylglycerol Hydrolysis
0	REACTOME_HOST_INTERACTIONS_OF_HIV_FACTORS	Host Interactions Of Hiv Factors
0	REACTOME_IMMUNOREGULATORY_INTERACTIONS_BETWEEN_A_LYMPHOID_AND_A_NON-LYMPHOID_CELL	Immunoregulatory Interactions Between A Lymphoid And A Non-Lymphoid Cell
0	REACTOME_INACTIVATION_OF_APCC_VIA_DIRECT_INHIBITION_OF_THE_APCC_COMPLEX	Inactivation Of Apcc Via Direct Inhibition Of The Apcc Complex
0	REACTOME_INCRETIN_SYNTHESIS_SECRETION_AND_INACTIVATION	Incretin Synthesis Secretion And Inactivation
0	REACTOME_INFLAMMASOMES	Inflammasomes
0	REACTOME_INFLUENZA_INFECTION	Influenza Infection
0	REACTOME_INFLUENZA_LIFE_CYCLE	Influenza Life Cycle

0	REACTOME_INFLUENZA_VIRAL_RNA_TRANSCRIPTION_AND_REPLICATION	Influenza Viral Rna Transcription And Replication
1	REACTOME_INHIBITION__OF_VOLTAGE_GATED_CA2_CHANNELS_VIA_GBETAGAMMA_SUBUNITS	Inhibition Of Voltage Gated Ca2 Channels Via Gbetagamma Subunits
0	REACTOME_INHIBITION_OF_ADENYLATE_CYCLASE_PATHWAY	Inhibition Of Adenylate Cyclase Pathway
0	REACTOME_INHIBITION_OF_INSULIN_SECRETION_BY_ADRENALINENORADRENALINE	Inhibition Of Insulin Secretion By Adrenalinenoradrenaline
0	REACTOME_INHIBITION_OF_REPLICATION_INITIATION_OF_DAMAGED_DNA_BY_RBE2F1	Inhibition Of Replication Initiation Of Damaged Dna By Rbe2F1
0	REACTOME_INHIBITION_OF_THE_PROTEOLYTIC_ACTIVITY_OF_APCC_REQUIRED_FOR_THE_ONSET_OF_ANAPHA	Inhibition Of The Proteolytic Activity Of Apcc Required For The Onset Of Anaphase By Mitotic Spindle Checkpoint Components
0	REACTOME_INITIAL_TRIGGERING_OF_COMPLEMENT	Initial Triggering Of Complement
0	REACTOME_INNATE_IMMUNE_SYSTEM	Innate Immune System
0	REACTOME_INSULIN_RECEPTOR_RECYCLING	Insulin Receptor Recycling
0	REACTOME_INSULIN_RECEPTOR_SIGNALLING_CASCADE	Insulin Receptor Signalling Cascade
0	REACTOME_INSULIN_SYNTHESIS_AND_PROCESSING	Insulin Synthesis And Processing
0	REACTOME_INTEGRATION_OF_ENERGY_METABOLISM	Integration Of Energy Metabolism
0	REACTOME_INTEGRIN_ALPHAIIB_BETA3_SIGNALING	Integrin Alphaiib Beta3 Signaling
0	REACTOME_INTEGRIN_CELL_SURFACE_INTERACTIONS	Integrin Cell Surface Interactions
0	REACTOME_INTERACTION_BETWEEN_L1_AND_ANKYRINS	Interaction Between L1 And Ankyrins
0	REACTOME_INTERACTIONS_OF_REV_WITH_HOST_CELLULAR_PROTEINS	Interactions Of Rev With Host Cellular Proteins
0	REACTOME_INTERACTIONS_OF_VPR_WITH_HOST_CELLULAR_PROTEINS	Interactions Of Vpr With Host Cellular Proteins
0	REACTOME_INTERFERON_ALPHABETA_SIGNALING	Interferon Alphabeta Signaling
0	REACTOME_INTERFERON_GAMMA_SIGNALING	Interferon Gamma Signaling
0	REACTOME_INTERFERON_SIGNALING	Interferon Signaling
0	REACTOME_INTERLEUKIN_RECEPTOR_SHC_SIGNALING	Interleukin Receptor Shc Signaling
0	REACTOME_INTERLEUKIN-1_SIGNALING	Interleukin-1 Signaling
0	REACTOME_INTERLEUKIN-2_SIGNALING	Interleukin-2 Signaling
0	REACTOME_INTERLEUKIN-3_5_AND_GM-CSF_SIGNALING	Interleukin-3 5 And Gm-Csf Signaling
0	REACTOME_INTERLEUKIN-6_SIGNALING	Interleukin-6 Signaling
0	REACTOME_INTERLEUKIN-7_SIGNALING	Interleukin-7 Signaling
0	REACTOME_INTRINSIC_PATHWAY	Intrinsic Pathway
0	REACTOME_INTRINSIC_PATHWAY_FOR_APOPTOSIS	Intrinsic Pathway For Apoptosis
0	REACTOME_INWARDLY_RECTIFYING_K_CHANNELS	Inwardly Rectifying K Channels
0	REACTOME_ION_CHANNEL_TRANSPORT	Ion Channel Transport
0	REACTOME_ION_TRANSPORT_BY_P-TYPE_ATPASES	Ion Transport By P-Type Atpases
0	REACTOME_IONOTROPIC_ACTIVITY_OF_KAINATE_RECEPTORS	Ionotropic Activity Of Kainate Receptors
0	REACTOME_IRAK2_MEDIATED_ACTIVATION_OF_TAK1_COMPLEX	Irak2 Mediated Activation Of Tak1 Complex
0	REACTOME_IRAK2_MEDIATED_ACTIVATION_OF_TAK1_COMPLEX_UPON_TLR78_OR_9_STIMULATION	Irak2 Mediated Activation Of Tak1 Complex Upon Tlr78 Or 9 Stimulation
0	REACTOME_IRON_UPTAKE_AND_TRANSPORT	Iron Uptake And Transport
0	REACTOME_IRS-MEDIATED_SIGNALLING	Irs-Mediated Signalling
0	REACTOME_IRS-RELATED_EVENTS	Irs-Related Events
0	REACTOME_ISG15_ANTIVIRAL_MECHANISM	Isg15 Antiviral Mechanism
0	REACTOME_JNK_C-JUN_KINASES_PHOSPHORYLATION_AND__ACTIVATION_MEDIATED_BY_ACTIVATED_HUMAN	Jnk C-Jun Kinases Phosphorylation And Activation Mediated By Activated Human Tak1
0	REACTOME_KINESINS	Kinesins
0	REACTOME_L13A-MEDIATED_TRANSLATIONAL_SILENCING_OF_CERULOPLASMIN_EXPRESSION	L13A-Mediated Translational Silencing Of Ceruloplasmin Expression
0	REACTOME_L1CAM_INTERACTIONS	L1Cam Interactions
0	REACTOME_LAGGING_STRAND_SYNTHESIS	Lagging Strand Synthesis
0	REACTOME_LATE_PHASE_OF_HIV_LIFE_CYCLE	Late Phase Of Hiv Life Cycle
0	REACTOME_LEADING_STRAND_SYNTHESIS	Leading Strand Synthesis
0	REACTOME_LIGAND-GATED_ION_CHANNEL_TRANSPORT	Ligand-Gated Ion Channel Transport
0	REACTOME_LIPID_DIGESTION_MOBILIZATION_AND_TRANSPORT	Lipid Digestion Mobilization And Transport
0	REACTOME_LIPOPROTEIN_METABOLISM	Lipoprotein Metabolism
0	REACTOME_LOSS_OF_NLP_FROM_MITOTIC_CENTROSOMES	Loss Of Nlp From Mitotic Centrosomes
0	REACTOME_LOSS_OF_PROTEINS_REQUIRED_FOR_INTERPHASE_MICROTUBULE_ORGANIZATIONFROM_THE_CE	Loss Of Proteins Required For Interphase Microtubule Organizationfrom The Centrosome
0	REACTOME_LYSOSOME_VESICLE_BIOGENESIS	Lysosome Vesicle Biogenesis
0	REACTOME_M_PHASE	M Phase
0	REACTOME_MAP_KINASE_ACTIVATION_IN_TLR_CASCADE	Map Kinase Activation In Tlr Cascade
0	REACTOME_MAPK_TARGETS_NUCLEAR_EVENTS_MEDIATED_BY_MAP_KINASES	Mapk Targets Nuclear Events Mediated By Map Kinases
0	REACTOME_MEIOSIS	Meiosis
0	REACTOME_MEIOTIC_RECOMBINATION	Meiotic Recombination
0	REACTOME_MEIOTIC_SYNAPSIS	Meiotic Synapsis
0	REACTOME_MEMBRANE_BINDING_AND_TARGETTING_OF_GAG_PROTEINS	Membrane Binding And Targetting Of Gag Proteins
0	REACTOME_MEMBRANE_TRAFFICKING	Membrane Trafficking

0	REACTOME_METABOLISM_OF_AMINO_ACIDS_AND_DERIVATIVES	Metabolism Of Amino Acids And Derivatives
0	REACTOME_METABOLISM_OF_CARBOHYDRATES	Metabolism Of Carbohydrates
0	REACTOME_METABOLISM_OF_LIPIDS_AND_LIPOPROTEINS	Metabolism Of Lipids And Lipoproteins
0	REACTOME_METABOLISM_OF_MRNA	Metabolism Of Mrna
0	REACTOME_METABOLISM_OF_NITRIC_OXIDE	Metabolism Of Nitric Oxide
0	REACTOME_METABOLISM_OF_NON-CODING_RNA	Metabolism Of Non-Coding Rna
0	REACTOME_METABOLISM_OF_NUCLEOTIDES	Metabolism Of Nucleotides
0	REACTOME_METABOLISM_OF_POLYAMINES	Metabolism Of Polyamines
0	REACTOME_METABOLISM_OF_PORPHYRINS	Metabolism Of Porphyrins
0	REACTOME_METABOLISM_OF_PROTEINS	Metabolism Of Proteins
0	REACTOME_METABOLISM_OF_RNA	Metabolism Of Rna
0	REACTOME_METABOLISM_OF_STEROID_HORMONES_AND_VITAMINS_A_AND_D	Metabolism Of Steroid Hormones And Vitamins A And D
0	REACTOME_METABOLISM_OF_VITAMINS_AND_COFACTORS	Metabolism Of Vitamins And Cofactors
0	REACTOME_METABOLISM_OF_WATER-SOLUBLE_VITAMINS_AND_COFACTORS	Metabolism Of Water-Soluble Vitamins And Cofactors
0	REACTOME_METAL_ION_SLC_TRANSPORTERS	Metal Ion Slc Transporters
0	REACTOME_MG1_TRANSITION	Mg1 Transition
0	REACTOME_MICRORNA_MIRNA_BIOGENESIS	Microrna Mirna Biogenesis
0	REACTOME_MITOCHONDRIAL_FATTY_ACID_BETA-OXIDATION	Mitochondrial Fatty Acid Beta-Oxidation
0	REACTOME_MITOCHONDRIAL_TRNA_AMINOACYLATION	Mitochondrial Trna Aminoacylation
0	REACTOME_MITOTIC_G1-G1S_PHASES	Mitotic G1-G1S Phases
0	REACTOME_MITOTIC_G2-G2M_PHASES	Mitotic G2-G2M Phases
0	REACTOME_MITOTIC_M-MG1_PHASES	Mitotic M-Mg1 Phases
0	REACTOME_MITOTIC_PROMETAPHASE	Mitotic Prometaphase
0	REACTOME_MITOTIC_SPINDLE_CHECKPOINT	Mitotic Spindle Checkpoint
0	REACTOME_MRNA_3-END_PROCESSING	Mrna 3-End Processing
0	REACTOME_MRNA_CAPPING	Mrna Capping
0	REACTOME_MRNA_DECAY_BY_3_TO_5_EXORIBONUCLEASE	Mrna Decay By 3 To 5 Exoribonuclease
0	REACTOME_MRNA_DECAY_BY_5_TO_3_EXORIBONUCLEASE	Mrna Decay By 5 To 3 Exoribonuclease
0	REACTOME_MRNA_PROCESSING	Mrna Processing
0	REACTOME_MRNA_SPLICING	Mrna Splicing
0	REACTOME_MRNA_SPLICING_-_MAJOR_PATHWAY	Mrna Splicing - Major Pathway
0	REACTOME_MRNA_SPLICING_-_MINOR_PATHWAY	Mrna Splicing - Minor Pathway
0	REACTOME_MTOR_SIGNALLING	Mtor Signalling
0	REACTOME_MTORC1-MEDIATED_SIGNALLING	Mtorc1-Mediated Signalling
0	REACTOME_MUSCLE_CONTRACTION	Muscle Contraction
0	REACTOME_MYD88_CASCADE_INITIATED_ON_PLASMA_MEMBRANE	Myd88 Cascade Initiated On Plasma Membrane
0	REACTOME_MYD88_DEPENDENT_CASCADE_INITIATED_ON_ENDOSOME	Myd88 Dependent Cascade Initiated On Endosome
0	REACTOME_MYD88-INDEPENDENT_CASCADE_INITIATED_ON_PLASMA_MEMBRANE	Myd88-Independent Cascade Initiated On Plasma Membrane
0	REACTOME_MYD88MAL_CASCADE_INITIATED_ON_PLASMA_MEMBRANE	Myd88Mal Cascade Initiated On Plasma Membrane
0	REACTOME_MYOGENESIS	Myogenesis
0	REACTOME_N-GLYCAN_ANTENNAE_ELONGATION	N-Glycan Antennae Elongation
0	REACTOME_N-GLYCAN_ANTENNAE_ELONGATION_IN_THE_MEDIALTRANS-GOLGI	N-Glycan Antennae Elongation In The Medialtrans-Golgi
0	REACTOME_N-GLYCAN_TRIMMING_IN_THE_ER_AND_CALNEXINCALRETICULIN_CYCLE	N-Glycan Trimming In The Er And Calnexincalreticulin Cycle
1	REACTOME_NACL-_DEPENDENT_NEUROTRANSMITTER_TRANSPORTERS	Nacl- Dependent Neurotransmitter Transporters
1	REACTOME_NCAM_SIGNALING_FOR_NEURITE_OUT-GROWTH	Ncam Signaling For Neurite Out-Growth
1	REACTOME_NCAM1_INTERACTIONS	Ncam1 Interactions
0	REACTOME_NEF_MEDIATED_DOWNREGULATION_OF_MHC_CLASS_I_COMPLEX_CELL_SURFACE_EXPRESSION	Nef Mediated Downregulation Of Mhc Class I Complex Cell Surface Expression
0	REACTOME_NEF-MEDIATES_DOWN_MODULATION_OF_CELL_SURFACE_RECEPTORS_BY_RECRUITING_THEM_T	Nef-Mediates Down Modulation Of Cell Surface Receptors By Recruiting Them To Clathrin Adapters
0	REACTOME_NEGATIVE_REGULATION_OF_FGFR_SIGNALING	Negative Regulation Of Fgfr Signaling
0	REACTOME_NEGATIVE_REGULATORS_OF_RIG-IMDA5_SIGNALING	Negative Regulators Of Rig-Imda5 Signaling
0	REACTOME_NEPHRIN_INTERACTIONS	Nephrin Interactions
0	REACTOME_NEPNS2_INTERACTS_WITH_THE_CELLULAR_EXPORT_MACHINERY	Nepns2 Interacts With The Cellular Export Machinery
1	REACTOME_NETRIN-1_SIGNALING	Netrin-1 Signaling
1	REACTOME_NEURONAL_SYSTEM	Neuronal System
1	REACTOME_NEUROTRANSMITTER_RECEPTOR_BINDING_AND_DOWNSTREAM_TRANSMISSION_IN_THE__POSTS	Neurotransmitter Receptor Binding And Downstream Transmission In The Postsynaptic Cell
1	REACTOME_NEUROTRANSMITTER_RELEASE_CYCLE	Neurotransmitter Release Cycle
0	REACTOME_NF-KB_ACTIVATION_THROUGH_FADDRIP-1_PATHWAY_MEDIATED_BY_CASPASE-8_AND_-10	Nf-Kb Activation Through Faddrip-1 Pathway Mediated By Caspase-8 And -10
0	REACTOME_NF-KB_IS_ACTIVATED_AND_SIGNALS_SURVIVAL	Nf-Kb Is Activated And Signals Survival
0	REACTOME_NFKB_AND_MAP_KINASES_ACTIVATION_MEDIATED_BY_TLR4_SIGNALING_REPERTOIRE	Nfkb And Map Kinases Activation Mediated By Tlr4 Signaling Repertoire

0	REACTOME_NGF_SIGNALLING_VIA_TRKA_FROM_THE_PLASMA_MEMBRANE	Ngf Signalling Via Trka From The Plasma Membrane
0	REACTOME_NICD_TRAFFICS_TO_NUCLEUS	Nicd Traffics To Nucleus
0	REACTOME_NITRIC_OXIDE_STIMULATES_GUANYLATE_CYCLASE	Nitric Oxide Stimulates Guanylate Cyclase
0	REACTOME_NOD12_SIGNALING_PATHWAY	Nod12 Signaling Pathway
0	REACTOME_NONSENSE_MEDIATED_DECAY_ENHANCED_BY_THE_EXON_JUNCTION_COMPLEX	Nonsense Mediated Decay Enhanced By The Exon Junction Complex
0	REACTOME_NONSENSE_MEDIATED_DECAY_INDEPENDENT_OF_THE_EXON_JUNCTION_COMPLEX	Nonsense Mediated Decay Independent Of The Exon Junction Complex
0	REACTOME_NONSENSE-MEDIATED_DECAY	Nonsense-Mediated Decay
1	REACTOME_NOREPINEPHRINE_NEUROTRANSMITTER_RELEASE_CYCLE	Norepinephrine Neurotransmitter Release Cycle
0	REACTOME_NOTCH-HLH_TRANSCRIPTION_PATHWAY	Notch-Hlh Transcription Pathway
0	REACTOME_NRAGE_SIGNALS_DEATH_THROUGH_JNK	Nrage Signals Death Through Jnk
0	REACTOME_NRIF_SIGNALS_CELL_DEATH_FROM_THE_NUCLEUS	Nrif Signals Cell Death From The Nucleus
0	REACTOME_NUCLEAR_EVENTS_KINASE_AND_TRANSCRIPTION_FACTOR_ACTIVATION	Nuclear Events Kinase And Transcription Factor Activation
0	REACTOME_NUCLEAR_IMPORT_OF_REV_PROTEIN	Nuclear Import Of Rev Protein
0	REACTOME_NUCLEAR_RECEPTOR_TRANSCRIPTION_PATHWAY	Nuclear Receptor Transcription Pathway
0	REACTOME_NUCLEAR_SIGNALING_BY_ERBB4	Nuclear Signaling By Erbb4
0	REACTOME_NUCLEOSOME_ASSEMBLY	Nucleosome Assembly
0	REACTOME_NUCLEOTIDE_EXCISION_REPAIR	Nucleotide Excision Repair
0	REACTOME_NUCLEOTIDE-BINDING_DOMAIN_LEUCINE_RICH_REPEAT_CONTAINING_RECEPTOR_NLR_SIGNALIN	Nucleotide-Binding Domain Leucine Rich Repeat Containing Receptor Nlr Signaling Pathways
0	REACTOME_NUCLEOTIDE-LIKE_PURINERGIC_RECEPTORS	Nucleotide-Like Purinergic Receptors
0	REACTOME_O-LINKED_GLYCOSYLATION_OF_MUCINS	O-Linked Glycosylation Of Mucins
0	REACTOME_OLFACTORY_SIGNALING_PATHWAY	Olfactory Signaling Pathway
1	REACTOME_OPIOID_SIGNALLING	Opioid Signalling
0	REACTOME_ORC1_REMOVAL_FROM_CHROMATIN	Orc1 Removal From Chromatin
0	REACTOME_ORGANIC_CATIONANIONZWITTERION_TRANSPORT	Organic Cationanionzwitterion Transport
0	REACTOME_OTHER_SEMAPHORIN_INTERACTIONS	Other Semaphorin Interactions
0	REACTOME_P130CAS_LINKAGE_TO_MAPK_SIGNALING_FOR_INTEGRINS	P130Cas Linkage To Mapk Signaling For Integrins
0	REACTOME_P2Y_RECEPTORS	P2Y Receptors
0	REACTOME_P38MAPK_EVENTS	P38Mapk Events
0	REACTOME_P53-DEPENDENT_G1_DNA_DAMAGE_RESPONSE	P53-Dependent G1 Dna Damage Response
0	REACTOME_P53-DEPENDENT_G1S_DNA_DAMAGE_CHECKPOINT	P53-Dependent G1S Dna Damage Checkpoint
0	REACTOME_P53-INDEPENDENT_DNA_DAMAGE_RESPONSE	P53-Independent Dna Damage Response
0	REACTOME_P53-INDEPENDENT_G1S_DNA_DAMAGE_CHECKPOINT	P53-Independent G1S Dna Damage Checkpoint
1	REACTOME_P75_NTR_RECEPTOR-MEDIATED_SIGNALLING	P75 Ntr Receptor-Mediated Signalling
1	REACTOME_P75NTR_RECRUITS_SIGNALLING_COMPLEXES	P75Ntr Recruits Signalling Complexes
0	REACTOME_P75NTR_SIGNALS_VIA_NF-KB	P75Ntr Signals Via Nf-Kb
0	REACTOME_PACKAGING_OF_TELOMERE_ENDS	Packaging Of Telomere Ends
0	REACTOME_PASSIVE_TRANSPORT_BY_AQUAPORINS	Passive Transport By Aquaporins
0	REACTOME_PAUSING_AND_RECOVERY_OF_ELONGATION	Pausing And Recovery Of Elongation
0	REACTOME_PAUSING_AND_RECOVERY_OF_HIV-1_ELONGATION	Pausing And Recovery Of Hiv-1 Elongation
0	REACTOME_PAUSING_AND_RECOVERY_OF_TAT-MEDIATED_HIV-1_ELONGATION	Pausing And Recovery Of Tat-Mediated Hiv-1 Elongation
0	REACTOME_PD-1_SIGNALING	Pd-1 Signaling
0	REACTOME_PECAM1_INTERACTIONS	Pecam1 Interactions
0	REACTOME_PEPTIDE_CHAIN_ELONGATION	Peptide Chain Elongation
0	REACTOME_PEPTIDE_HORMONE_BIOSYNTHESIS	Peptide Hormone Biosynthesis
0	REACTOME_PEPTIDE_LIGAND-BINDING_RECEPTORS	Peptide Ligand-Binding Receptors
0	REACTOME_PERK_REGULATED_GENE_EXPRESSION	Perk Regulated Gene Expression
0	REACTOME_PEROXISOMAL_LIPID_METABOLISM	Peroxisomal Lipid Metabolism
0	REACTOME_PHASE_1_-_FUNCTIONALIZATION_OF_COMPOUNDS	Phase 1 - Functionalization Of Compounds
0	REACTOME_PHASE_II_CONJUGATION	Phase Ii Conjugation
0	REACTOME_PHOSPHOLIPASE_C-MEDIATED_CASCADE	Phospholipase C-Mediated Cascade
0	REACTOME_PHOSPHORYLATION_OF_CD3_AND_TCR_ZETA_CHAINS	Phosphorylation Of Cd3 And Tcr Zeta Chains
0	REACTOME_PHOSPHORYLATION_OF_THE_APCC	Phosphorylation Of The Apcc
0	REACTOME_PI-3K_CASCADE	Pi-3K Cascade
0	REACTOME_PI3K_CASCADE	Pi3K Cascade
0	REACTOME_PI3K_EVENTS_IN_ERBB2_SIGNALING	Pi3K Events In Erbb2 Signaling
0	REACTOME_PI3K_EVENTS_IN_ERBB4_SIGNALING	Pi3K Events In Erbb4 Signaling
0	REACTOME_PI3KAKT_ACTIVATION	Pi3Kakt Activation
0	REACTOME_PIP3_ACTIVATES_AKT_SIGNALING	Pip3 Activates Akt Signaling
0	REACTOME_PKA_ACTIVATION	Pka Activation

0	REACTOME_PKA_ACTIVATION_IN_GLUCAGON_SIGNALLING	Pka Activation In Glucagon Signalling
0	REACTOME_PKA-MEDIATED_PHOSPHORYLATION_OF_CREB	Pka-Mediated Phosphorylation Of Creb
0	REACTOME_PKB-MEDIATED_EVENTS	Pkb-Mediated Events
0	REACTOME_PLATELET_ACTIVATION_SIGNALING_AND_AGGREGATION	Platelet Activation Signaling And Aggregation
0	REACTOME_PLATELET_ADHESION_TO_EXPOSED_COLLAGEN	Platelet Adhesion To Exposed Collagen
0	REACTOME_PLATELET_AGGREGATION_PLUG_FORMATION	Platelet Aggregation Plug Formation
0	REACTOME_PLATELET_CALCIUM_HOMEOSTASIS	Platelet Calcium Homeostasis
0	REACTOME_PLATELET_DEGRANULATION	Platelet Degranulation
0	REACTOME_PLATELET_HOMEOSTASIS	Platelet Homeostasis
0	REACTOME_PLATELET_SENSITIZATION_BY_LDL	Platelet Sensitization By Ldl
0	REACTOME_PLC_BETA_MEDIATED_EVENTS	Plc Beta Mediated Events
0	REACTOME_PLC-GAMMA1_SIGNALLING	Plc-Gamma1 Signalling
0	REACTOME_PLCG1_EVENTS_IN_ERBB2_SIGNALING	Plcg1 Events In Erbb2 Signaling
0	REACTOME_POLYMERASE_SWITCHING	Polymerase Switching
0	REACTOME_POLYMERASE_SWITCHING_ON_THE_C-STRAND_OF_THE_TELOMERE	Polymerase Switching On The C-Strand Of The Telomere
1	REACTOME_POST_NMDA_RECEPTOR_ACTIVATION_EVENTS	Post Nmda Receptor Activation Events
0	REACTOME_POST-CHAPERONIN_TUBULIN_FOLDING_PATHWAY	Post-Chaperonin Tubulin Folding Pathway
0	REACTOME_POST-ELONGATION_PROCESSING_OF_INTRON-CONTAINING_PRE-MRNA	Post-Elongation Processing Of Intron-Containing Pre-Mrna
0	REACTOME_POST-ELONGATION_PROCESSING_OF_INTRONLESS_PRE-MRNA	Post-Elongation Processing Of Intronless Pre-Mrna
0	REACTOME_POST-ELONGATION_PROCESSING_OF_THE_TRANSCRIPT	Post-Elongation Processing Of The Transcript
0	REACTOME_POST-TRANSLATIONAL_MODIFICATION_SYNTHESIS_OF_GPI-ANCHORED_PROTEINS	Post-Translational Modification Synthesis Of Gpi-Anchored Proteins
0	REACTOME_POST-TRANSLATIONAL_PROTEIN_MODIFICATION	Post-Translational Protein Modification
1	REACTOME_POSTSYNAPTIC_NICOTINIC_ACETYLCHOLINE_RECEPTORS	Postsynaptic Nicotinic Acetylcholine Receptors
1	REACTOME_POTASSIUM_CHANNELS	Potassium Channels
0	REACTOME_PPARA_ACTIVATES_GENE_EXPRESSION	Ppara Activates Gene Expression
0	REACTOME_PREFOLDIN_MEDIATED_TRANSFER_OF_SUBSTRATE__TO_CCTTRIC	Prefoldin Mediated Transfer Of Substrate To Ccttric
1	REACTOME_PRESYNAPTIC_FUNCTION_OF_KAINATE_RECEPTORS	Presynaptic Function Of Kainate Receptors
1	REACTOME_PRESYNAPTIC_NICOTINIC_ACETYLCHOLINE_RECEPTORS	Presynaptic Nicotinic Acetylcholine Receptors
0	REACTOME_PROCESSING_OF_CAPPED_INTRON-CONTAINING_PRE-MRNA	Processing Of Capped Intron-Containing Pre-Mrna
0	REACTOME_PROCESSING_OF_CAPPED_INTRONLESS_PRE-MRNA	Processing Of Capped Intronless Pre-Mrna
0	REACTOME_PROCESSING_OF_INTRONLESS_PRE-MRNAS	Processing Of Intronless Pre-Mrnas
0	REACTOME_PROCESSIVE_SYNTHESIS_ON_THE_C-STRAND_OF_THE_TELOMERE	Processive Synthesis On The C-Strand Of The Telomere
0	REACTOME_PROCESSIVE_SYNTHESIS_ON_THE_LAGGING_STRAND	Processive Synthesis On The Lagging Strand
1	REACTOME_PROLACTIN_RECEPTOR_SIGNALING	Prolactin Receptor Signaling
0	REACTOME_PROLONGED_ERK_ACTIVATION_EVENTS	Prolonged Erk Activation Events
0	REACTOME_PROSTACYCLIN_SIGNALLING_THROUGH_PROSTACYCLIN_RECEPTOR	Prostacyclin Signalling Through Prostacyclin Receptor
0	REACTOME_PROSTANOID_METABOLISM	Prostanoid Metabolism
0	REACTOME_PROTEIN_FOLDING	Protein Folding
0	REACTOME_PROTEOLYTIC_CLEAVAGE_OF_SNARE_COMPLEX_PROTEINS	Proteolytic Cleavage Of Snare Complex Proteins
0	REACTOME_PTM_GAMMA_CARBOXYLATION_HYPUSINE_FORMATION_AND_ARYLSULFATASE_ACTIVATION	Ptm Gamma Carboxylation Hypusine Formation And Arylsulfatase Activation
0	REACTOME_PURINE_METABOLISM	Purine Metabolism
0	REACTOME_PURINE_RIBONUCLEOSIDE_MONOPHOSPHATE_BIOSYNTHESIS	Purine Ribonucleoside Monophosphate Biosynthesis
0	REACTOME_PURINE_SALVAGE	Purine Salvage
0	REACTOME_PYRIMIDINE_CATABOLISM	Pyrimidine Catabolism
0	REACTOME_PYRIMIDINE_METABOLISM	Pyrimidine Metabolism
0	REACTOME_PYRUVATE_METABOLISM	Pyruvate Metabolism
0	REACTOME_PYRUVATE_METABOLISM_AND_CITRIC_ACID_TCA_CYCLE	Pyruvate Metabolism And Citric Acid Tca Cycle
0	REACTOME_RAFMAP_KINASE_CASCADE	Rafmap Kinase Cascade
0	REACTOME_RAP1_SIGNALLING	Rap1 Signalling
1	REACTOME_RAS_ACTIVATION_UOPN_CA2_INFUX_THROUGH_NMDA_RECEPTOR	Ras Activation Uopn Ca2 Infux Through Nmda Receptor
0	REACTOME_RECRUITMENT_OF_MITOTIC_CENTROSOME_PROTEINS_AND_COMPLEXES	Recruitment Of Mitotic Centrosome Proteins And Complexes
0	REACTOME_RECRUITMENT_OF_NUMA_TO_MITOTIC_CENTROSOMES	Recruitment Of Numa To Mitotic Centrosomes
0	REACTOME_RECYCLING_OF_BILE_ACIDS_AND_SALTS	Recycling Of Bile Acids And Salts
0	REACTOME_RECYCLING_PATHWAY_OF_L1	Recycling Pathway Of L1
0	REACTOME_REDUCTION_OF_CYTOSOLIC_CA_LEVELS	Reduction Of Cytosolic Ca Levels
0	REACTOME_REGULATED_PROTEOLYSIS_OF_P75NTR	Regulated Proteolysis Of P75Ntr
0	REACTOME_REGULATION_OF_ACTIVATED_PAK-2P34_BY_PROTEASOME_MEDIATED_DEGRADATION	Regulation Of Activated Pak-2P34 By Proteasome Mediated Degradation
0	REACTOME_REGULATION_OF_AMPK_ACTIVITY_VIA_LKB1	Regulation Of Ampk Activity Via Lkb1
0	REACTOME_REGULATION_OF_APCC_ACTIVATORS_BETWEEN_G1S_AND_EARLY_ANAPHASE	Regulation Of Apcc Activators Between G1S And Early Anaphase

0	REACTOME_REGULATION_OF_APOPTOSIS	Regulation Of Apoptosis
0	REACTOME_REGULATION_OF_BETA-CELL_DEVELOPMENT	Regulation Of Beta-Cell Development
0	REACTOME_REGULATION_OF_DNA_REPLICATION	Regulation Of Dna Replication
0	REACTOME_REGULATION_OF_GENE_EXPRESSION_IN_BETA_CELLS	Regulation Of Gene Expression In Beta Cells
0	REACTOME_REGULATION_OF_GLUCOKINASE_BY_GLUCOKINASE_REGULATORY_PROTEIN	Regulation Of Glucokinase By Glucokinase Regulatory Protein
0	REACTOME_REGULATION_OF_IFNA_SIGNALING	Regulation Of Ifna Signaling
0	REACTOME_REGULATION_OF_IFNG_SIGNALING	Regulation Of Ifng Signaling
0	REACTOME_REGULATION_OF_INSULIN_SECRETION	Regulation Of Insulin Secretion
0	REACTOME_REGULATION_OF_INSULIN_SECRETION_BY_ACETYLCHOLINE	Regulation Of Insulin Secretion By Acetylcholine
0	REACTOME_REGULATION_OF_INSULIN_SECRETION_BY_GLUCAGON-LIKE_PEPTIDE-1	Regulation Of Insulin Secretion By Glucagon-Like Peptide-1
0	REACTOME_REGULATION_OF_INSULIN-LIKE_GROWTH_FACTOR_IGF_ACTIVITY_BY_INSULIN-LIKE_GROWTH_FAC	Regulation Of Insulin-Like Growth Factor Igf Activity By Insulin-Like Growth Factor Binding Proteins Igfbps
0	REACTOME_REGULATION_OF_KIT_SIGNALING	Regulation Of Kit Signaling
0	REACTOME_REGULATION_OF_LIPID_METABOLISM_BY_PEROXISOME_PROLIFERATOR-ACTIVATED_RECEPTOR_A	Regulation Of Lipid Metabolism By Peroxisome Proliferator-Activated Receptor Alpha Pparalpha
0	REACTOME_REGULATION_OF_MITOTIC_CELL_CYCLE	Regulation Of Mitotic Cell Cycle
0	REACTOME_REGULATION_OF_MRNA_STABILITY_BY_PROTEINS_THAT_BIND_AU-RICH_ELEMENTS	Regulation Of Mrna Stability By Proteins That Bind Au-Rich Elements
0	REACTOME_REGULATION_OF_ORNITHINE_DECARBOXYLASE_ODC	Regulation Of Ornithine Decarboxylase Odc
0	REACTOME_REGULATION_OF_PYRUVATE_DEHYDROGENASE_PDH_COMPLEX	Regulation Of Pyruvate Dehydrogenase Pdh Complex
0	REACTOME_REGULATION_OF_SIGNALING_BY_CBL	Regulation Of Signaling By Cbl
0	REACTOME_REGULATION_OF_WATER_BALANCE_BY_RENAL_AQUAPORINS	Regulation Of Water Balance By Renal Aquaporins
0	REACTOME_REGULATORY_RNA_PATHWAYS	Regulatory Rna Pathways
0	REACTOME_REMOVAL_OF_DNA_PATCH_CONTAINING_ABASIC_RESIDUE	Removal Of Dna Patch Containing Abasic Residue
0	REACTOME_REMOVAL_OF_LICENSING_FACTORS_FROM_ORIGINS	Removal Of Licensing Factors From Origins
0	REACTOME_REMOVAL_OF_THE_FLAP_INTERMEDIATE	Removal Of The Flap Intermediate
0	REACTOME_REPAIR_SYNTHESIS_FOR_GAP-FILLING_BY_DNA_POLYMERASE_IN_TC-NER	Repair Synthesis For Gap-Filling By Dna Polymerase In Tc-Ner
0	REACTOME_REPAIR_SYNTHESIS_OF_PATCH_27-30_BASES_LONG__BY_DNA_POLYMERASE	Repair Synthesis Of Patch 27-30 Bases Long By Dna Polymerase
0	REACTOME_RESOLUTION_OF_ABASIC_SITES_AP_SITES	Resolution Of Abasic Sites Ap Sites
0	REACTOME_RESOLUTION_OF_AP_SITES_VIA_THE_MULTIPLE-NUCLEOTIDE_PATCH_REPLACEMENT_PATHWAY	Resolution Of Ap Sites Via The Multiple-Nucleotide Patch Replacement Pathway
0	REACTOME_RESOLUTION_OF_AP_SITES_VIA_THE_SINGLE-NUCLEOTIDE_REPLACEMENT_PATHWAY	Resolution Of Ap Sites Via The Single-Nucleotide Replacement Pathway
0	REACTOME_RESPIRATORY_ELECTRON_TRANSPORT	Respiratory Electron Transport
0	REACTOME_RESPIRATORY_ELECTRON_TRANSPORT_ATP_SYNTHESIS_BY_CHEMIOSMOTIC_COUPLING_AND_HEA	Respiratory Electron Transport Atp Synthesis By Chemiosmotic Coupling And Heat Production By Uncoupling Proteins
0	REACTOME_RESPONSE_TO_ELEVATED_PLATELET_CYTOSOLIC_CA2	Response To Elevated Platelet Cytosolic Ca2
1	REACTOME_RETROGRADE_NEUROTROPHIN_SIGNALLING	Retrograde Neurotrophin Signalling
0	REACTOME_REV-MEDIATED_NUCLEAR_EXPORT_OF_HIV-1_RNA	Rev-Mediated Nuclear Export Of Hiv-1 Rna
0	REACTOME_RHO_GTPASE_CYCLE	Rho Gtpase Cycle
0	REACTOME_RIBOSOMAL_SCANNING_AND_START_CODON_RECOGNITION	Ribosomal Scanning And Start Codon Recognition
0	REACTOME_RIG-IMDA5_MEDIATED_INDUCTION_OF_IFN-ALPHABETA_PATHWAYS	Rig-Imda5 Mediated Induction Of Ifn-Alphabeta Pathways
0	REACTOME_RNA_POL_II_CTD_PHOSPHORYLATION_AND_INTERACTION_WITH_CE	Rna Pol Ii Ctd Phosphorylation And Interaction With Ce
0	REACTOME_RNA_POLYMERASE_I_CHAIN_ELONGATION	Rna Polymerase I Chain Elongation
0	REACTOME_RNA_POLYMERASE_I_PROMOTER_CLEARANCE	Rna Polymerase I Promoter Clearance
0	REACTOME_RNA_POLYMERASE_I_PROMOTER_ESCAPE	Rna Polymerase I Promoter Escape
0	REACTOME_RNA_POLYMERASE_I_PROMOTER_OPENING	Rna Polymerase I Promoter Opening
0	REACTOME_RNA_POLYMERASE_I_RNA_POLYMERASE_III_AND_MITOCHONDRIAL_TRANSCRIPTION	Rna Polymerase I Rna Polymerase Iii And Mitochondrial Transcription
0	REACTOME_RNA_POLYMERASE_I_TRANSCRIPTION	Rna Polymerase I Transcription
0	REACTOME_RNA_POLYMERASE_I_TRANSCRIPTION_INITIATION	Rna Polymerase I Transcription Initiation
0	REACTOME_RNA_POLYMERASE_I_TRANSCRIPTION_TERMINATION	Rna Polymerase I Transcription Termination
0	REACTOME_RNA_POLYMERASE_II_HIV-1_PROMOTER_ESCAPE	Rna Polymerase Ii Hiv-1 Promoter Escape
0	REACTOME_RNA_POLYMERASE_II_PRE-TRANSCRIPTION_EVENTS	Rna Polymerase Ii Pre-Transcription Events
0	REACTOME_RNA_POLYMERASE_II_PROMOTER_ESCAPE	Rna Polymerase Ii Promoter Escape
0	REACTOME_RNA_POLYMERASE_II_TRANSCRIPTION	Rna Polymerase Ii Transcription
0	REACTOME_RNA_POLYMERASE_II_TRANSCRIPTION_ELONGATION	Rna Polymerase Ii Transcription Elongation
0	REACTOME_RNA_POLYMERASE_II_TRANSCRIPTION_INITIATION	Rna Polymerase Ii Transcription Initiation
0	REACTOME_RNA_POLYMERASE_II_TRANSCRIPTION_INITIATION_AND_PROMOTER_CLEARANCE	Rna Polymerase Ii Transcription Initiation And Promoter Clearance
0	REACTOME_RNA_POLYMERASE_II_TRANSCRIPTION_PRE-INITIATION_AND_PROMOTER_OPENING	Rna Polymerase Ii Transcription Pre-Initiation And Promoter Opening
0	REACTOME_RNA_POLYMERASE_II_TRANSCRIPTION_TERMINATION	Rna Polymerase Ii Transcription Termination
0	REACTOME_RNA_POLYMERASE_III_ABORTIVE_AND_RETRACTIVE_INITIATION	Rna Polymerase Iii Abortive And Retractive Initiation
0	REACTOME_RNA_POLYMERASE_III_CHAIN_ELONGATION	Rna Polymerase Iii Chain Elongation
0	REACTOME_RNA_POLYMERASE_III_TRANSCRIPTION	Rna Polymerase Iii Transcription
0	REACTOME_RNA_POLYMERASE_III_TRANSCRIPTION_INITIATION	Rna Polymerase Iii Transcription Initiation
0	REACTOME_RNA_POLYMERASE_III_TRANSCRIPTION_INITIATION_FROM_TYPE_1_PROMOTER	Rna Polymerase Iii Transcription Initiation From Type 1 Promoter

0	REACTOME_RNA_POLYMERASE_III_TRANSCRIPTION_INITIATION_FROM_TYPE_2_PROMOTER	Rna Polymerase Iii Transcription Initiation From Type 2 Promoter
0	REACTOME_RNA_POLYMERASE_III_TRANSCRIPTION_INITIATION_FROM_TYPE_3_PROMOTER	Rna Polymerase Iii Transcription Initiation From Type 3 Promoter
0	REACTOME_RNA_POLYMERASE_III_TRANSCRIPTION_TERMINATION	Rna Polymerase Iii Transcription Termination
0	REACTOME_ROLE_OF_DCC_IN_REGULATING_APOPTOSIS	Role Of Dcc In Regulating Apoptosis
0	REACTOME_ROLE_OF_SECOND_MESSENGERS_IN_NETRIN-1_SIGNALING	Role Of Second Messengers In Netrin-1 Signaling
0	REACTOME_S_PHASE	S Phase
0	REACTOME_SCF-BETA-TRCP_MEDIATED_DEGRADATION_OF_EMI1	Scf-Beta-Trcp Mediated Degradation Of Emi1
0	REACTOME_SCFSKP2-MEDIATED_DEGRADATION_OF_P27P21	Scfskp2-Mediated Degradation Of P27P21
1	REACTOME_SEMA3A_PAK_DEPENDENT_AXON_REPULSION	Sema3A Pak Dependent Axon Repulsion
1	REACTOME_SEMA3A-PLEXIN_REPULSION_SIGNALING_BY_INHIBITING_INTEGRIN_ADHESION	Sema3A-Plexin Repulsion Signaling By Inhibiting Integrin Adhesion
1	REACTOME_SEMA4D_IN_SEMAPHORIN_SIGNALING	Sema4D In Semaphorin Signaling
1	REACTOME_SEMA4D_INDUCED_CELL_MIGRATION_AND_GROWTH-CONE_COLLAPSE	Sema4D Induced Cell Migration And Growth-Cone Collapse
1	REACTOME_SEMAPHORIN_INTERACTIONS	Semaphorin Interactions
1	REACTOME_SEROTONIN_NEUROTRANSMITTER_RELEASE_CYCLE	Serotonin Neurotransmitter Release Cycle
1	REACTOME_SEROTONIN_RECEPTORS	Serotonin Receptors
0	REACTOME_SHC-MEDIATED_CASCADE	Shc-Mediated Cascade
0	REACTOME_SHC-MEDIATED_SIGNALLING	Shc-Mediated Signalling
0	REACTOME_SHC-RELATED_EVENTS	Shc-Related Events
0	REACTOME_SHC1_EVENTS_IN_EGFR_SIGNALING	Shc1 Events In Egfr Signaling
0	REACTOME_SHC1_EVENTS_IN_ERBB2_SIGNALING	Shc1 Events In Erbb2 Signaling
0	REACTOME_SHC1_EVENTS_IN_ERBB4_SIGNALING	Shc1 Events In Erbb4 Signaling
0	REACTOME_SIGNAL_AMPLIFICATION	Signal Amplification
0	REACTOME_SIGNAL_ATTENUATION	Signal Attenuation
0	REACTOME_SIGNAL_REGULATORY_PROTEIN_SIRP_FAMILY_INTERACTIONS	Signal Regulatory Protein Sirp Family Interactions
0	REACTOME_SIGNAL_TRANSDUCTION_BY_L1	Signal Transduction By L1
0	REACTOME_SIGNALING_BY_BMP	Signaling By Bmp
0	REACTOME_SIGNALING_BY_CONSTITUTIVELY_ACTIVE_EGFR	Signaling By Constitutively Active Egfr
0	REACTOME_SIGNALING_BY_EGFR	Signaling By Egfr
0	REACTOME_SIGNALING_BY_EGFR_IN_CANCER	Signaling By Egfr In Cancer
0	REACTOME_SIGNALING_BY_ERBB2	Signaling By Erbb2
0	REACTOME_SIGNALING_BY_ERBB4	Signaling By Erbb4
0	REACTOME_SIGNALING_BY_FGFR	Signaling By Fgfr
0	REACTOME_SIGNALING_BY_INSULIN_RECEPTOR	Signaling By Insulin Receptor
0	REACTOME_SIGNALING_BY_INTERLEUKINS	Signaling By Interleukins
0	REACTOME_SIGNALING_BY_NODAL	Signaling By Nodal
0	REACTOME_SIGNALING_BY_NOTCH	Signaling By Notch
0	REACTOME_SIGNALING_BY_PDGF	Signaling By Pdgf
0	REACTOME_SIGNALING_BY_RHO_GTPASES	Signaling By Rho Gtpases
0	REACTOME_SIGNALING_BY_ROBO_RECEPTOR	Signaling By Robo Receptor
0	REACTOME_SIGNALING_BY_SCF-KIT	Signaling By Scf-Kit
0	REACTOME_SIGNALING_BY_TGF_BETA	Signaling By Tgf Beta
0	REACTOME_SIGNALING_BY_VEGF	Signaling By Vegf
0	REACTOME_SIGNALING_BY_WNT	Signaling By Wnt
1	REACTOME_SIGNALLING_BY_NGF	Signalling By Ngf
0	REACTOME_SIGNALLING_TO_ERKS	Signalling To Erks
0	REACTOME_SIGNALLING_TO_P38_VIA_RIT_AND_RIN	Signalling To P38 Via Rit And Rin
0	REACTOME_SIGNALLING_TO_RAS	Signalling To Ras
0	REACTOME_SLC-MEDIATED_TRANSMEMBRANE_TRANSPORT	Slc-Mediated Transmembrane Transport
0	REACTOME_SMOOTH_MUSCLE_CONTRACTION	Smooth Muscle Contraction
0	REACTOME_SNRNP_ASSEMBLY	Snrnp Assembly
0	REACTOME_SOS-MEDIATED_SIGNALLING	Sos-Mediated Signalling
0	REACTOME_SPHINGOLIPID_DE_NOVO_BIOSYNTHESIS	Sphingolipid De Novo Biosynthesis
0	REACTOME_SPHINGOLIPID_METABOLISM	Sphingolipid Metabolism
0	REACTOME_SPRY_REGULATION_OF_FGF_SIGNALING	Spry Regulation Of Fgf Signaling
0	REACTOME_SRP-DEPENDENT_COTRANSLATIONAL_PROTEIN_TARGETING_TO_MEMBRANE	Srp-Dependent Cotranslational Protein Targeting To Membrane
0	REACTOME_STABILIZATION_OF_P53	Stabilization Of P53
0	REACTOME_STEROID_HORMONES	Steroid Hormones
0	REACTOME_STRIATED_MUSCLE_CONTRACTION	Striated Muscle Contraction
0	REACTOME_SULFUR_AMINO_ACID_METABOLISM	Sulfur Amino Acid Metabolism

0	REACTOME_SWITCHING_OF_ORIGINS_TO_A_POST-REPLICATIVE_STATE	Switching Of Origins To A Post-Replicative State
0	REACTOME_SYNTHESIS_AND_INTERCONVERSION_OF_NUCLEOTIDE_DI-_AND_TRIPHOSPHATES	Synthesis And Interconversion Of Nucleotide Di- And Triphosphates
0	REACTOME_SYNTHESIS_OF_BILE_ACIDS_AND_BILE_SALTS	Synthesis Of Bile Acids And Bile Salts
0	REACTOME_SYNTHESIS_OF_BILE_ACIDS_AND_BILE_SALTS_VIA_7ALPHA-HYDROXYCHOLESTEROL	Synthesis Of Bile Acids And Bile Salts Via 7Alpha-Hydroxycholesterol
0	REACTOME_SYNTHESIS_OF_DNA	Synthesis Of Dna
0	REACTOME_SYNTHESIS_OF_GLYCOSYLPHOSPHATIDYLINOSITOL_GPI	Synthesis Of Glycosylphosphatidylinositol Gpi
0	REACTOME_SYNTHESIS_OF_SUBSTRATES_IN_N-GLYCAN_BIOSYTHESIS	Synthesis Of Substrates In N-Glycan Biosythesis
0	REACTOME_SYNTHESIS_OF_VERY_LONG-CHAIN_FATTY_ACYL-COAS	Synthesis Of Very Long-Chain Fatty Acyl-Coas
0	REACTOME_SYNTHESIS_SECRETION_AND_DEACYLATION_OF_GHRELIN	Synthesis Secretion And Deacylation Of Ghrelin
0	REACTOME_SYNTHESIS_SECRETION_AND_INACTIVATION_OF_GLUCAGON-LIKE_PEPTIDE-1_GLP-1	Synthesis Secretion And Inactivation Of Glucagon-Like Peptide-1 Glp-1
0	REACTOME_SYNTHESIS_SECRETION_AND_INACTIVATION_OF_GLUCOSE-DEPENDENT_INSULINOTROPIC_POLYPE	Synthesis Secretion And Inactivation Of Glucose-Dependent Insulinotropic Polypeptide Gip
0	REACTOME_TAK1_ACTIVATES_NFKB_BY_PHOSPHORYLATION_AND_ACTIVATION_OF_IKKS_COMPLEX	Tak1 Activates Nfkb By Phosphorylation And Activation Of Ikks Complex
1	REACTOME_TANDEM_PORE_DOMAIN_POTASSIUM_CHANNELS	Tandem Pore Domain Potassium Channels
0	REACTOME_TAT-MEDIATED_ELONGATION_OF_THE_HIV-1_TRANSCRIPT	Tat-Mediated Elongation Of The Hiv-1 Transcript
0	REACTOME_TAT-MEDIATED_HIV-1_ELONGATION_ARREST_AND_RECOVERY	Tat-Mediated Hiv-1 Elongation Arrest And Recovery
0	REACTOME_TCR_SIGNALING	Tcr Signaling
0	REACTOME_TELOMERE_C-STRAND_LAGGING_STRAND_SYNTHESIS	Telomere C-Strand Lagging Strand Synthesis
0	REACTOME_TELOMERE_MAINTENANCE	Telomere Maintenance
0	REACTOME_TERMINATION_OF_O-GLYCAN_BIOSYNTHESIS	Termination Of O-Glycan Biosynthesis
0	REACTOME_TETRAHYDROBIOPTERIN_BH4_SYNTHESIS_RECYCLING_SALVAGE_AND_REGULATION	Tetrahydrobiopterin Bh4 Synthesis Recycling Salvage And Regulation
0	REACTOME_THE_CITRIC_ACID_TCA_CYCLE_AND_RESPIRATORY_ELECTRON_TRANSPORT	The Citric Acid Tca Cycle And Respiratory Electron Transport
0	REACTOME_THE_NLRP3_INFLAMMASOME	The Nlrp3 Inflammasome
0	REACTOME_THE_ROLE_OF_NEF_IN_HIV-1_REPLICATION_AND_DISEASE_PATHOGENESIS	The Role Of Nef In Hiv-1 Replication And Disease Pathogenesis
0	REACTOME_THROMBIN_SIGNALLING_THROUGH_PROTEINASE_ACTIVATED_RECEPTORS_PARS	Thrombin Signalling Through Proteinase Activated Receptors Pars
0	REACTOME_THROMBOXANE_SIGNALLING_THROUGH_TP_RECEPTOR	Thromboxane Signalling Through Tp Receptor
0	REACTOME_TIE2_SIGNALING	Tie2 Signaling
0	REACTOME_TIGHT_JUNCTION_INTERACTIONS	Tight Junction Interactions
0	REACTOME_TOLL_LIKE_RECEPTOR_10_TLR10_CASCADE	Toll Like Receptor 10 Tlr10 Cascade
0	REACTOME_TOLL_LIKE_RECEPTOR_2_TLR2_CASCADE	Toll Like Receptor 2 Tlr2 Cascade
0	REACTOME_TOLL_LIKE_RECEPTOR_3_TLR3_CASCADE	Toll Like Receptor 3 Tlr3 Cascade
0	REACTOME_TOLL_LIKE_RECEPTOR_4_TLR4_CASCADE	Toll Like Receptor 4 Tlr4 Cascade
0	REACTOME_TOLL_LIKE_RECEPTOR_5_TLR5_CASCADE	Toll Like Receptor 5 Tlr5 Cascade
0	REACTOME_TOLL_LIKE_RECEPTOR_78_TLR78_CASCADE	Toll Like Receptor 78 Tlr78 Cascade
0	REACTOME_TOLL_LIKE_RECEPTOR_9_TLR9_CASCADE	Toll Like Receptor 9 Tlr9 Cascade
0	REACTOME_TOLL_LIKE_RECEPTOR_TLR1TLR2_CASCADE	Toll Like Receptor Tlr1Tlr2 Cascade
0	REACTOME_TOLL_LIKE_RECEPTOR_TLR6TLR2_CASCADE	Toll Like Receptor Tlr6Tlr2 Cascade
0	REACTOME_TOLL_RECEPTOR_CASCADES	Toll Receptor Cascades
0	REACTOME_TRAF3-DEPENDENT_IRF_ACTIVATION_PATHWAY	Traf3-Dependent Irf Activation Pathway
0	REACTOME_TRAF6_MEDIATED_INDUCTION_OF_NFKB_AND_MAP_KINASES_UPON_TLR78_OR_9_ACTIVATION	Traf6 Mediated Induction Of Nfkb And Map Kinases Upon Tlr78 Or 9 Activation
0	REACTOME_TRAF6_MEDIATED_INDUCTION_OF_PROINFLAMMATORY_CYTOKINES	Traf6 Mediated Induction Of Proinflammatory Cytokines
0	REACTOME_TRAF6_MEDIATED_INDUCTION_OF_TAK1_COMPLEX	Traf6 Mediated Induction Of Tak1 Complex
0	REACTOME_TRAF6_MEDIATED_IRF7_ACTIVATION	Traf6 Mediated Irf7 Activation
0	REACTOME_TRAF6_MEDIATED_NF-KB_ACTIVATION	Traf6 Mediated Nf-Kb Activation
1	REACTOME_TRAFFICKING_OF_AMPA_RECEPTORS	Trafficking Of Ampa Receptors
1	REACTOME_TRAFFICKING_OF_GLUR2-CONTAINING_AMPA_RECEPTORS	Trafficking Of Glur2-Containing Ampa Receptors
0	REACTOME_TRANS-GOLGI_NETWORK_VESICLE_BUDDING	Trans-Golgi Network Vesicle Budding
0	REACTOME_TRANSCRIPTION	Transcription
0	REACTOME_TRANSCRIPTION_OF_THE_HIV_GENOME	Transcription Of The Hiv Genome
0	REACTOME_TRANSCRIPTION-COUPLED_NER_TC-NER	Transcription-Coupled Ner Tc-Ner
0	REACTOME_TRANSCRIPTIONAL_REGULATION_OF_WHITE_ADIPOCYTE_DIFFERENTIATION	Transcriptional Regulation Of White Adipocyte Differentiation
0	REACTOME_TRANSFERRIN_ENDOCYTOSIS_AND_RECYCLING	Transferrin Endocytosis And Recycling
0	REACTOME_TRANSLATION	Translation
0	REACTOME_TRANSLATION_INITIATION_COMPLEX_FORMATION	Translation Initiation Complex Formation
0	REACTOME_TRANSLOCATION_OF_ZAP-70_TO_IMMUNOLOGICAL_SYNAPSE	Translocation Of Zap-70 To Immunological Synapse
0	REACTOME_TRANSMEMBRANE_TRANSPORT_OF_SMALL_MOLECULES	Transmembrane Transport Of Small Molecules
1	REACTOME_TRANSMISSION_ACROSS_CHEMICAL_SYNAPSES	Transmission Across Chemical Synapses
0	REACTOME_TRANSPORT_OF_GLUCOSE_AND_OTHER_SUGARS_BILE_SALTS_AND_ORGANIC_ACIDS_METAL_ION	Transport Of Glucose And Other Sugars Bile Salts And Organic Acids Metal Ions And Amine Compounds
0	REACTOME_TRANSPORT_OF_INORGANIC_CATIONSANIONS_AND_AMINO_ACIDSOLIGOPEPTIDES	Transport Of Inorganic Cationsanions And Amino Acidsoligopeptides
0	REACTOME_TRANSPORT_OF_MATURE_MRNA_DERIVED_FROM_AN_INTRON-CONTAINING_TRANSCRIPT	Transport Of Mature Mrna Derived From An Intron-Containing Transcript

0	REACTOME_TRANSPORT_OF_MATURE_MRNA_DERIVED_FROM_AN_INTRONLESS_TRANSCRIPT	Transport Of Mature Mrna Derived From An Intronless Transcript
0	REACTOME_TRANSPORT_OF_MATURE_MRNAS_DERIVED_FROM_INTRONLESS_TRANSCRIPTS	Transport Of Mature Mrnas Derived From Intronless Transcripts
0	REACTOME_TRANSPORT_OF_MATURE_TRANSCRIPT_TO_CYTOPLASM	Transport Of Mature Transcript To Cytoplasm
0	REACTOME_TRANSPORT_OF_ORGANIC_ANIONS	Transport Of Organic Anions
0	REACTOME_TRANSPORT_OF_RIBONUCLEOPROTEINS_INTO_THE_HOST_NUCLEUS	Transport Of Ribonucleoproteins Into The Host Nucleus
0	REACTOME_TRANSPORT_OF_THE_SLBP_DEPENDANT_MATURE_MRNA	Transport Of The Slbp Dependant Mature Mrna
0	REACTOME_TRANSPORT_OF_THE_SLBP_INDEPENDENT_MATURE_MRNA	Transport Of The Slbp Independent Mature Mrna
0	REACTOME_TRANSPORT_OF_VITAMINS_NUCLEOSIDES_AND_RELATED_MOLECULES	Transport Of Vitamins Nucleosides And Related Molecules
0	REACTOME_TRANSPORT_TO_THE_GOLGI_AND_SUBSEQUENT_MODIFICATION	Transport To The Golgi And Subsequent Modification
0	REACTOME_TRIF_MEDIATED_TLR3_SIGNALING	Trif Mediated Tlr3 Signaling
0	REACTOME_TRIGLYCERIDE_BIOSYNTHESIS	Triglyceride Biosynthesis
0	REACTOME_TRNA_AMINOACYLATION	Trna Aminoacylation
0	REACTOME_TRYPTOPHAN_CATABOLISM	Tryptophan Catabolism
0	REACTOME_UBIQUITIN_MEDIATED_DEGRADATION_OF_PHOSPHORYLATED_CDC25A	Ubiquitin Mediated Degradation Of Phosphorylated Cdc25A
0	REACTOME_UBIQUITIN-DEPENDENT_DEGRADATION_OF_CYCLIN_D	Ubiquitin-Dependent Degradation Of Cyclin D
0	REACTOME_UBIQUITIN-DEPENDENT_DEGRADATION_OF_CYCLIN_D1	Ubiquitin-Dependent Degradation Of Cyclin D1
1	REACTOME_UNBLOCKING_OF_NMDA_RECEPTOR_GLUTAMATE_BINDING_AND_ACTIVATION	Unblocking Of Nmda Receptor Glutamate Binding And Activation
0	REACTOME_UNFOLDED_PROTEIN_RESPONSE	Unfolded Protein Response
0	REACTOME_UNWINDING_OF_DNA	Unwinding Of Dna
0	REACTOME_VEGF_LIGAND-RECEPTOR_INTERACTIONS	Vegf Ligand-Receptor Interactions
0	REACTOME_VIF-MEDIATED_DEGRADATION_OF_APOBEC3G	Vif-Mediated Degradation Of Apobec3G
0	REACTOME_VIRAL_DSRNATLR3TRIF_COMPLEX_ACTIVATES_RIP1	Viral Dsrnatlr3Trif Complex Activates Rip1
0	REACTOME_VIRAL_MESSENGER_RNA_SYNTHESIS	Viral Messenger Rna Synthesis
0	REACTOME_VIRAL_MRNA_TRANSLATION	Viral Mrna Translation
0	REACTOME_VITAMIN_B5_PANTOTHENATE_METABOLISM	Vitamin B5 Pantothenate Metabolism
1	REACTOME_VOLTAGE_GATED_POTASSIUM_CHANNELS	Voltage Gated Potassium Channels
0	REACTOME_VPR-MEDIATED_NUCLEAR_IMPORT_OF_PICS	Vpr-Mediated Nuclear Import Of Pics
0	REACTOME_VPU_MEDIATED_DEGRADATION_OF_CD4	Vpu Mediated Degradation Of Cd4
0	REACTOME_XENOBIOTICS	Xenobiotics
0	REACTOME_ZINC_INFLUX_INTO_CELLS_BY_THE_SLC39_GENE_FAMILY	Zinc Influx Into Cells By The Slc39 Gene Family
0	REACTOME_ZINC_TRANSPORTERS	Zinc Transporters

Related to neuronal function	Gene Set ID	Gene Set Name
0	KEGG_ABC_TRANSPORTERS	Abc Transporters
0	KEGG_ACUTE_MYELOID_LEUKEMIA	Acute Myeloid Leukemia
0	KEGG_ADHERENS_JUNCTION	Adherens Junction
0	KEGG_ADIPOCYTOKINE_SIGNALING_PATHWAY	Adipocytokine Signaling Pathway
0	KEGG_ALANINE_ASPARTATE_AND_GLUTAMATE_METABOLISM	Alanine Aspartate And Glutamate Metabolism
0	KEGG_ALDOSTERONE_REGULATED_SODIUM_REABSORPTION	Aldosterone Regulated Sodium Reabsorption
0	KEGG_ALLOGRAFT_REJECTION	Allograft Rejection
0	KEGG_ALPHA_LINOLENIC_ACID_METABOLISM	Alpha Linolenic Acid Metabolism
0	KEGG_ALZHEIMERS_DISEASE	Alzheimers Disease
0	KEGG_AMINO_SUGAR_AND_NUCLEOTIDE_SUGAR_METABOLISM	Amino Sugar And Nucleotide Sugar Metabolism
0	KEGG_AMINOACYL_TRNA_BIOSYNTHESIS	Aminoacyl Trna Biosynthesis
0	KEGG_AMYOTROPHIC_LATERAL_SCLEROSIS_ALS	Amyotrophic Lateral Sclerosis Als
0	KEGG_ANTIGEN_PROCESSING_AND_PRESENTATION	Antigen Processing And Presentation
0	KEGG_APOPTOSIS	Apoptosis
0	KEGG_ARACHIDONIC_ACID_METABOLISM	Arachidonic Acid Metabolism
0	KEGG_ARGININE_AND_PROLINE_METABOLISM	Arginine And Proline Metabolism
0	KEGG_ARRHYTHMOGENIC_RIGHT_VENTRICULAR_CARDIOMYOPATHY_ARVC	Arrhythmogenic Right Ventricular Cardiomyopathy Arvc
0	KEGG_ASCORBATE_AND_ALDARATE_METABOLISM	Ascorbate And Aldarate Metabolism
0	KEGG_ASTHMA	Asthma
0	KEGG_AUTOIMMUNE_THYROID_DISEASE	Autoimmune Thyroid Disease
1	KEGG_AXON_GUIDANCE	Axon Guidance
0	KEGG_B_CELL_RECEPTOR_SIGNALING_PATHWAY	B Cell Receptor Signaling Pathway
0	KEGG_BASAL_CELL_CARCINOMA	Basal Cell Carcinoma
0	KEGG_BASAL_TRANSCRIPTION_FACTORS	Basal Transcription Factors
0	KEGG_BASE_EXCISION_REPAIR	Base Excision Repair
0	KEGG_BETA_ALANINE_METABOLISM	Beta Alanine Metabolism
0	KEGG_BIOSYNTHESIS_OF_UNSATURATED_FATTY_ACIDS	Biosynthesis Of Unsaturated Fatty Acids
0	KEGG_BLADDER_CANCER	Bladder Cancer
0	KEGG_BUTANOATE_METABOLISM	Butanoate Metabolism
1	KEGG_CALCIUM_SIGNALING_PATHWAY	Calcium Signaling Pathway
0	KEGG_CARDIAC_MUSCLE_CONTRACTION	Cardiac Muscle Contraction
0	KEGG_CELL_ADHESION_MOLECULES_CAMS	Cell Adhesion Molecules Cams
0	KEGG_CELL_CYCLE	Cell Cycle
0	KEGG_CHEMOKINE_SIGNALING_PATHWAY	Chemokine Signaling Pathway

0	KEGG_CHRONIC_MYELOID_LEUKEMIA	Chronic Myeloid Leukemia
1	KEGG_CIRCADIAN_RHYTHM_MAMMAL	Circadian Rhythm Mammal
0	KEGG_CITRATE_CYCLE_TCA_CYCLE	Citrate Cycle Tca Cycle
0	KEGG_COLORECTAL_CANCER	Colorectal Cancer
0	KEGG_COMPLEMENT_AND_COAGULATION_CASCADES	Complement And Coagulation Cascades
0	KEGG_CYSTEINE_AND_METHIONINE_METABOLISM	Cysteine And Methionine Metabolism
0	KEGG_CYTOKINE_CYTOKINE_RECEPTOR_INTERACTION	Cytokine Cytokine Receptor Interaction
0	KEGG_CYTOSOLIC_DNA_SENSING_PATHWAY	Cytosolic Dna Sensing Pathway
0	KEGG_DILATED_CARDIOMYOPATHY	Dilated Cardiomyopathy
0	KEGG_DNA_REPLICATION	Dna Replication
0	KEGG_DORSO_VENTRAL_AXIS_FORMATION	Dorso Ventral Axis Formation
0	KEGG_DRUG_METABOLISM_CYTOCHROME_P450	Drug Metabolism Cytochrome P450
0	KEGG_DRUG_METABOLISM_OTHER_ENZYMES	Drug Metabolism Other Enzymes
0	KEGG_ECM_RECEPTOR_INTERACTION	Ecm Receptor Interaction
0	KEGG_ENDOCYTOSIS	Endocytosis
0	KEGG_ENDOMETRIAL_CANCER	Endometrial Cancer
0	KEGG_EPITHELIAL_CELL_SIGNALING_IN_HELICOBACTER_PYLORI_INFECTION	Epithelial Cell Signaling In Helicobacter Pylori Infection
1	KEGG_ERBB_SIGNALING_PATHWAY	Erbb Signaling Pathway
0	KEGG_ETHER_LIPID_METABOLISM	Ether Lipid Metabolism
0	KEGG_FATTY_ACID_METABOLISM	Fatty Acid Metabolism
0	KEGG_FC_EPSILON_RI_SIGNALING_PATHWAY	Fc Epsilon Ri Signaling Pathway
0	KEGG_FC_GAMMA_R_MEDIATED_PHAGOCYTOSIS	Fc Gamma R Mediated Phagocytosis
0	KEGG_FOCAL_ADHESION	Focal Adhesion
0	KEGG_FOLATE_BIOSYNTHESIS	Folate Biosynthesis
0	KEGG_FRUCTOSE_AND_MANNOSE_METABOLISM	Fructose And Mannose Metabolism
0	KEGG_GALACTOSE_METABOLISM	Galactose Metabolism
0	KEGG_GAP_JUNCTION	Gap Junction
0	KEGG_GLIOMA	Glioma
0	KEGG_GLUTATHIONE_METABOLISM	Glutathione Metabolism
0	KEGG_GLYCEROLIPID_METABOLISM	Glycerolipid Metabolism
0	KEGG_GLYCEROPHOSPHOLIPID_METABOLISM	Glycerophospholipid Metabolism
0	KEGG_GLYCINE_SERINE_AND_THREONINE_METABOLISM	Glycine Serine And Threonine Metabolism
0	KEGG_GLYCOLYSIS_GLUCONEOGENESIS	Glycolysis Gluconeogenesis
0	KEGG_GLYCOSAMINOGLYCAN_BIOSYNTHESIS_CHONDROITIN_SULFATE	Glycosaminoglycan Biosynthesis Chondroitin Sulfate
0	KEGG_GLYCOSAMINOGLYCAN_BIOSYNTHESIS_HEPARAN_SULFATE	Glycosaminoglycan Biosynthesis Heparan Sulfate
0	KEGG_GLYCOSAMINOGLYCAN_BIOSYNTHESIS_KERATAN_SULFATE	Glycosaminoglycan Biosynthesis Keratan Sulfate

0	KEGG_GLYCOSAMINOGLYCAN_DEGRADATION	Glycosaminoglycan Degradation
0	KEGG_GLYCOSPHINGOLIPID_BIOSYNTHESIS_GANGLIO_SERIES	Glycosphingolipid Biosynthesis Ganglio Series
0	KEGG_GLYCOSPHINGOLIPID_BIOSYNTHESIS_GLOBO_SERIES	Glycosphingolipid Biosynthesis Globo Series
0	KEGG_GLYCOSPHINGOLIPID_BIOSYNTHESIS_LACTO_AND_NEOLACTO_SERIES	Glycosphingolipid Biosynthesis Lacto And Neolacto Series
0	KEGG_GLYCOSYLPHOSPHATIDYLINOSITOL_GPI_ANCHOR_BIOSYNTHESIS	Glycosylphosphatidylinositol Gpi Anchor Biosynthesis
0	KEGG_GLYOXYLATE_AND_DICARBOXYLATE_METABOLISM	Glyoxylate And Dicarboxylate Metabolism
1	KEGG_GNRH_SIGNALING_PATHWAY	Gnrh Signaling Pathway
0	KEGG_GRAFT_VERSUS_HOST_DISEASE	Graft Versus Host Disease
0	KEGG_HEDGEHOG_SIGNALING_PATHWAY	Hedgehog Signaling Pathway
0	KEGG_HEMATOPOIETIC_CELL_LINEAGE	Hematopoietic Cell Lineage
0	KEGG_HISTIDINE_METABOLISM	Histidine Metabolism
0	KEGG_HOMOLOGOUS_RECOMBINATION	Homologous Recombination
0	KEGG_HUNTINGTONS_DISEASE	Huntingtons Disease
0	KEGG_HYPERTROPHIC_CARDIOMYOPATHY_HCM	Hypertrophic Cardiomyopathy Hcm
0	KEGG_INOSITOL_PHOSPHATE_METABOLISM	Inositol Phosphate Metabolism
0	KEGG_INSULIN_SIGNALING_PATHWAY	Insulin Signaling Pathway
0	KEGG_INTESTINAL_IMMUNE_NETWORK_FOR_IGA_PRODUCTION	Intestinal Immune Network For Iga Production
0	KEGG_JAK_STAT_SIGNALING_PATHWAY	Jak Stat Signaling Pathway
0	KEGG_LEISHMANIA_INFECTION	Leishmania Infection
0	KEGG_LEUKOCYTE_TRANSENDOTHELIAL_MIGRATION	Leukocyte Transendothelial Migration
0	KEGG_LINOLEIC_ACID_METABOLISM	Linoleic Acid Metabolism
1	KEGG_LONG_TERM_DEPRESSION	Long Term Depression
1	KEGG_LONG_TERM_POTENTIATION	Long Term Potentiation
0	KEGG_LYSINE_DEGRADATION	Lysine Degradation
0	KEGG_LYSOSOME	Lysosome
0	KEGG_MAPK_SIGNALING_PATHWAY	Mapk Signaling Pathway
0	KEGG_MATURITY_ONSET_DIABETES_OF_THE_YOUNG	Maturity Onset Diabetes Of The Young
0	KEGG_MELANOGENESIS	Melanogenesis
0	KEGG_MELANOMA	Melanoma
0	KEGG_METABOLISM_OF_XENOBIOTICS_BY_CYTOCHROME_P450	Metabolism Of Xenobiotics By Cytochrome P450
0	KEGG_MISMATCH_REPAIR	Mismatch Repair
0	KEGG_MTOR_SIGNALING_PATHWAY	Mtor Signaling Pathway
0	KEGG_N_GLYCAN_BIOSYNTHESIS	N Glycan Biosynthesis
0	KEGG_NATURAL_KILLER_CELL_MEDIATED_CYTOTOXICITY	Natural Killer Cell Mediated Cytotoxicity
1	KEGG_NEUROACTIVE_LIGAND_RECEPTOR_INTERACTION	Neuroactive Ligand Receptor Interaction
1	KEGG_NEUROTROPHIN_SIGNALING_PATHWAY	Neurotrophin Signaling Pathway

0	KEGG_NICOTINATE_AND_NICOTINAMIDE_METABOLISM	Nicotinate And Nicotinamide Metabolism
0	KEGG_NITROGEN_METABOLISM	Nitrogen Metabolism
0	KEGG_NOD_LIKE_RECEPTOR_SIGNALING_PATHWAY	Nod Like Receptor Signaling Pathway
0	KEGG_NON_HOMOLOGOUS_END_JOINING	Non Homologous End Joining
0	KEGG_NON_SMALL_CELL_LUNG_CANCER	Non Small Cell Lung Cancer
0	KEGG_NOTCH_SIGNALING_PATHWAY	Notch Signaling Pathway
0	KEGG_NUCLEOTIDE_EXCISION_REPAIR	Nucleotide Excision Repair
0	KEGG_O_GLYCAN_BIOSYNTHESIS	O Glycan Biosynthesis
0	KEGG_OLFACTORY_TRANSDUCTION	Olfactory Transduction
0	KEGG_ONE_CARBON_POOL_BY_FOLATE	One Carbon Pool By Folate
0	KEGG_OOCYTE_MEIOSIS	Oocyte Meiosis
0	KEGG_OTHER_GLYCAN_DEGRADATION	Other Glycan Degradation
0	KEGG_OXIDATIVE_PHOSPHORYLATION	Oxidative Phosphorylation
0	KEGG_P53_SIGNALING_PATHWAY	P53 Signaling Pathway
0	KEGG_PANCREATIC_CANCER	Pancreatic Cancer
0	KEGG_PANTOTHENATE_AND_COA_BIOSYNTHESIS	Pantothenate And Coa Biosynthesis
0	KEGG_PARKINSONS_DISEASE	Parkinsons Disease
0	KEGG_PATHOGENIC_ESCHERICHIA_COLI_INFECTION	Pathogenic Escherichia Coli Infection
0	KEGG_PATHWAYS_IN_CANCER	Pathways In Cancer
0	KEGG_PENTOSE_AND_GLUCURONATE_INTERCONVERSIONS	Pentose And Glucuronate Interconversions
0	KEGG_PENTOSE_PHOSPHATE_PATHWAY	Pentose Phosphate Pathway
0	KEGG_PEROXISOME	Peroxisome
0	KEGG_PHENYLALANINE_METABOLISM	Phenylalanine Metabolism
1	KEGG_PHOSPHATIDYLINOSITOL_SIGNALING_SYSTEM	Phosphatidylinositol Signaling System
0	KEGG_PORPHYRIN_AND_CHLOROPHYLL_METABOLISM	Porphyrin And Chlorophyll Metabolism
0	KEGG_PPAR_SIGNALING_PATHWAY	Ppar Signaling Pathway
0	KEGG_PRIMARY_BILE_ACID_BIOSYNTHESIS	Primary Bile Acid Biosynthesis
0	KEGG_PRIMARY_IMMUNODEFICIENCY	Primary Immunodeficiency
0	KEGG_PRION_DISEASES	Prion Diseases
0	KEGG_PROGESTERONE_MEDIATED_OOCYTE_MATURATION	Progesterone Mediated Oocyte Maturation
0	KEGG_PROPANOATE_METABOLISM	Propanoate Metabolism
0	KEGG_PROSTATE_CANCER	Prostate Cancer
0	KEGG_PROTEASOME	Proteasome
0	KEGG_PROTEIN_EXPORT	Protein Export
0	KEGG_PROXIMAL_TUBULE_BICARBONATE_RECLAMATION	Proximal Tubule Bicarbonate Reclamation
0	KEGG_PURINE_METABOLISM	Purine Metabolism

0	KEGG_PYRIMIDINE_METABOLISM	Pyrimidine Metabolism
0	KEGG_PYRUVATE_METABOLISM	Pyruvate Metabolism
0	KEGG_REGULATION_OF_ACTIN_CYTOSKELETON	Regulation Of Actin Cytoskeleton
0	KEGG_REGULATION_OF_AUTOPHAGY	Regulation Of Autophagy
0	KEGG_RENAL_CELL_CARCINOMA	Renal Cell Carcinoma
0	KEGG_RENIN_ANGIOTENSIN_SYSTEM	Renin Angiotensin System
0	KEGG_RETINOL_METABOLISM	Retinol Metabolism
0	KEGG_RIBOFLAVIN_METABOLISM	Riboflavin Metabolism
0	KEGG_RIBOSOME	Ribosome
0	KEGG_RIG_I_LIKE_RECEPTOR_SIGNALING_PATHWAY	Rig I Like Receptor Signaling Pathway
0	KEGG_RNA_DEGRADATION	Rna Degradation
0	KEGG_RNA_POLYMERASE	Rna Polymerase
0	KEGG_SELENOAMINO_ACID_METABOLISM	Selenoamino Acid Metabolism
0	KEGG_SMALL_CELL_LUNG_CANCER	Small Cell Lung Cancer
0	KEGG_SNARE_INTERACTIONS_IN_VESICULAR_TRANSPORT	Snare Interactions In Vesicular Transport
0	KEGG_SPHINGOLIPID_METABOLISM	Sphingolipid Metabolism
0	KEGG_SPLICEOSOME	Spliceosome
0	KEGG_STARCH_AND_SUCROSE_METABOLISM	Starch And Sucrose Metabolism
0	KEGG_STEROID_BIOSYNTHESIS	Steroid Biosynthesis
0	KEGG_STEROID_HORMONE_BIOSYNTHESIS	Steroid Hormone Biosynthesis
0	KEGG_SULFUR_METABOLISM	Sulfur Metabolism
0	KEGG_SYSTEMIC_LUPUS_ERYTHEMATOSUS	Systemic Lupus Erythematosus
0	KEGG_T_CELL_RECEPTOR_SIGNALING_PATHWAY	T Cell Receptor Signaling Pathway
0	KEGG_TASTE_TRANSDUCTION	Taste Transduction
0	KEGG_TERPENOID_BACKBONE_BIOSYNTHESIS	Terpenoid Backbone Biosynthesis
0	KEGG_TGF_BETA_SIGNALING_PATHWAY	Tgf Beta Signaling Pathway
0	KEGG_THYROID_CANCER	Thyroid Cancer
0	KEGG_TIGHT_JUNCTION	Tight Junction
0	KEGG_TOLL_LIKE_RECEPTOR_SIGNALING_PATHWAY	Toll Like Receptor Signaling Pathway
0	KEGG_TRYPTOPHAN_METABOLISM	Tryptophan Metabolism
0	KEGG_TYPE_I_DIABETES_MELLITUS	Type I Diabetes Mellitus
0	KEGG_TYPE_II_DIABETES_MELLITUS	Type Ii Diabetes Mellitus
0	KEGG_TYROSINE_METABOLISM	Tyrosine Metabolism
0	KEGG_UBIQUITIN_MEDIATED_PROTEOLYSIS	Ubiquitin Mediated Proteolysis
0	KEGG_VALINE_LEUCINE_AND_ISOLEUCINE_BIOSYNTHESIS	Valine Leucine And Isoleucine Biosynthesis
0	KEGG_VALINE_LEUCINE_AND_ISOLEUCINE_DEGRADATION	Valine Leucine And Isoleucine Degradation

0	KEGG_VASCULAR_SMOOTH_MUSCLE_CONTRACTION	Vascular Smooth Muscle Contraction
0	KEGG_VASOPRESSIN_REGULATED_WATER_REABSORPTION	Vasopressin Regulated Water Reabsorption
0	KEGG_VEGF_SIGNALING_PATHWAY	Vegf Signaling Pathway
0	KEGG_VIBRIO_CHOLERAE_INFECTION	Vibrio Cholerae Infection
0	KEGG_VIRAL_MYOCARDITIS	Viral Myocarditis
0	KEGG_WNT_SIGNALING_PATHWAY	Wnt Signaling Pathway