

Transcriptional Profiling in Coronary Artery Disease Indications for Novel Markers of Coronary Collateralization

Thomas W. Chittenden, PhD; Jonathan A. Sherman, MD; Fei Xiong, MEng; Amy E. Hall, BS; Anthony A. Lanahan, PhD; Jennifer M. Taylor, PhD; Hangjun Duan, PhD; Justin D. Pearlman, MD, PhD; Jason H. Moore, PhD; Stephen M. Schwartz, MD, PhD; Michael Simons, MD

Background—The development of collateral circulation plays an important role in protecting tissues from ischemic damage, and its stimulation has emerged as one of principal approaches to therapeutic angiogenesis. Clinical observations have documented substantial differences in the extent of collateralization among patients with coronary artery disease (CAD), with some individuals demonstrating marked abundance and others showing nearly complete absence of these vessels. Recent studies have suggested that circulating monocytes play a major role in collateral growth. The present study was undertaken to determine transcriptional profiles of circulating monocytes in CAD patients with different extents of collateral growth.

Methods and Results—Monocyte transcriptomes from CAD patients with and without collateral vessels were obtained by use of high-throughput expression profiling. Using a newly developed redundancy-based data mining method, we have identified a set of molecular markers characteristic of a “noncollateralgenic” phenotype. Moreover, we show that these transcriptional abnormalities are independent of the severity of CAD or any other known clinical parameter thought to affect collateral development and correlated with protein expression levels in monocytes and plasma.

Conclusions—Monocyte transcription profiling identifies sets of patients with extensive versus poorly developed collateral circulation. Thus, genetic factors may heavily influence coronary collateral vessel growth in CAD and affect prognosis and response to therapeutic interventions. (*Circulation*. 2006;114:1811-1820.)

Key Words: angiogenesis ■ collateral circulation ■ coronary disease ■ genes ■ arteriogenesis

Coronary artery disease (CAD) is the most common cause of morbidity and mortality in industrialized societies. Typically, advancing atherosclerosis leads to narrowing or occlusion of major coronary arteries and their branches, resulting in angina, heart failure, or myocardial infarction. Clinical investigations suggest that a significant minority of CAD patients present with or develop in the course of their illness extra-arterial conduits, termed coronary collaterals, which link proximal and distal parts of the arterial tree bypassing areas of stenosis and/or occlusion.¹ Thus, collateral arteries function as “natural bypasses,” effectively restoring blood flow to compromised tissues. Moreover, the development of collateral circulation has been shown to play an important physiological role in promoting survival and protecting tissues from ischemic damage,^{2,3} and its stimulation has emerged as one of the principal approaches to therapeutic angiogenesis.⁴

Clinical Perspective p 1820

Factors responsible for the presence or absence of collateral circulation are poorly understood. Certain predictors of collateral presence have been proposed, such as a history of angina,⁵ hypercholesterolemia,⁶ plasma levels of homocysteine,⁷ reduced pericardial levels of endostatin,⁸ certain patterns of interindividual heterogeneity in hypoxic response,⁹ a haptoglobin phenotype,¹⁰ and C⁵⁸²-T⁵⁸² HIF-1 α gene polymorphism.¹¹ Little is known about the biology of collateral growth, and considerable disagreement exists as to whether collateral development represents a mere remodeling of the preexisting (but not hitherto detectable) vasculature or is the result of de novo arterial growth or vasculogenesis.^{12–14}

Recent studies have suggested that circulating monocytes may play a major role in the collateral formation.^{15–17} Abnormalities in monocyte function then may be one of the factors responsible for abnormal collateral growth in certain

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From the Angiogenesis Research Center (T.W.C., J.A.S., A.E.H., A.L., J.P., M.S.), Section of Cardiology, Departments of Medicine (T.W.C., J.A.S., A.E.H., A.A.L., J.D.P., M.S.), Pharmacology and Toxicology (M.S.), and Radiology (J.D.P.), and Norris Cotton Cancer Center, Department of Genetics (J.H.M.), Dartmouth Medical School, Hanover, NH; Bioinformatics Programme, Department of Statistics (T.W.C., J.A.S.), and Wellcome Trust Centre for Human Genetics (J.M.T.), University of Oxford, Oxford, UK; Department of Computer Science (F.X., J.D.P.), Dartmouth College, Hanover, NH; and Department of Pathology (H.D., S.M.S.), University of Washington, Seattle.

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Correspondence to Michael Simons, MD, Section of Cardiology, Dartmouth Hitchcock Medical Center, 1 Medical Center Dr, Lebanon, NH 03755. E-mail michael.simons@dartmouth.edu

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patient subsets.⁹ We therefore reasoned that monocyte transcriptome profiling from patients with CAD may shed some light on the differences in extent of collateral circulation in these patients and lead to an improved understanding of biology of arteriogenesis. To this end, we carried out comprehensive characterizations of the molecular determinants of the human CAD monocyte transcriptome using a combination of established supervised machine learning and knowledge-based algorithms, as well as a recently developed, gene redundancy reduction microarray bioinformatics data mining technique.¹⁸ We find that the absence or presence of coronary collaterals is associated with a distinct monocyte gene expression profile.

Methods

Patient Selection

This study was approved by the Committee for Protection of Human Subjects at Dartmouth-Hitchcock Medical Center, and informed consent was obtained from all participants. Patients >18 years of age who were undergoing diagnostic coronary angiography were eligible for entry into the study. Patients were excluded if they had other conditions thought to influence potential neovascularization such as symptomatic peripheral arterial disease, recent ST-segment elevation myocardial infarction (<72 hours before enrollment), increased white blood counts, or a known malignancy in the past 5 years. Cardiac history and risk factors were documented, together with any data known to influence collateral growth, such as the use of medication,^{19–21} age,²² hypercholesterolemia,²³ diabetes,²⁴ and smoking.²⁵ Only patients who had angiographically evident CAD and absent (score 0) or well-developed (score 2) collateral circulations were included in this analysis.

Coronary Angiography and Collateral Scoring

Severity of CAD on x-ray angiography was estimated through the use of a vessel score, defined as the number of vessels with at least one 50% stenosis, and the Gensini scoring system.²⁶ Coronary collateral extent was assessed on the basis of a modified Rentrop scoring system.⁹ Angiograms were reviewed by an experienced angiographer and then by a different angiographer blinded to the initial reading. In cases of disagreement, the angiograms were reviewed by a third angiographer blinded to the initial 2 readings. Clinical and angiographic data were not revealed to those involved in gene expression or monocyte analysis. Left ventricular function was estimated by left ventriculography at the time of cardiac catheterization or by echocardiography performed during the same hospitalization. A total of 100 mL blood was collected from the side arm of the introducer sheath in the femoral artery before angiography and immediately processed for monocyte isolation as described below.

Human Monocyte Cell Separation

Human monocytes were separated from whole blood by standard procedures.²⁷ Briefly, peripheral blood mononuclear cells were isolated by Ficoll density gradient centrifugation and then used immediately for monocyte isolation by positive selection with CD14 antibody-coated microbeads. Cells were then separated by use of autoMACS with the positive selection protocol, and cell collections were made from both positive and negative ports. Stained aliquots of the positive and negative cell fractions were collected and analyzed by flow cytometry to assess purity.

Human Monocyte RNA Extraction, Target Processing, and Labeling

Labeled cRNA was generated with the low-RNA input fluorescent linear amplification kit (Agilent, Santa Clara, Calif). All samples were labeled with cyanine (Cy) 5, and a reference cRNA was generated and labeled with Cy3. To generate a reference cRNA, 500

ng total RNA from each control sample was mixed, and 500 ng mixed total RNA was amplified and labeled with Cy3 (4 reactions were carried out to generate enough Cy3 NC for all 16 hybridizations). The hybridizations for each sample were performed with an Agilent in situ hybridization kit. For each hybridization, 0.75 μ g Cy5-labeled, linearly amplified cRNA from each sample was mixed with equal amounts of Cy3-labeled, linearly amplified reference cRNA. The mixed cRNA was fragmented by incubation with the fragmentation buffer at 60°C for 30 minutes. An equal amount of 2 \times hybridization buffer was added to the fragmented cRNA mixture and hybridized to Agilent human whole-genome oligo array (G4112A) at 60°C for 17 hours. Fluorescent images of hybridized microarrays were obtained with an Agilent DNA microarray scanner and analyzed with Agilent Feature Extraction software, and the data were stored in a database.

Statistical Analyses

Clinical results are reported as mean \pm SD. Analysis between groups for statistically significant differences in categorical data were performed with the χ^2 test and for continuous variables with Student's *t* test (STATA, StataCorp, College Station, Tex).

The primary human monocyte data set was made up of gene expression data from 16 patients: 8 patients with well-developed collateral vessels (score 2) and 8 patients with no collateral vessels (score 0). To assess the possible confounding effects of disease severity, these same subjects were regrouped according to the percentage or degree of occlusion of ≥ 1 coronary vessels to form a secondary data set. In this secondary data set, patients with 2- to 3-vessel disease (n=7) were compared with patients with 1-vessel disease (n=9). The 2 data sets, the first based on collateral vessel scores and the second based on disease severity, were further filtered on the basis of critical probability values ($P \leq 0.05$ and 0.01) as assessed between subjects through Welch approximation of unequal group variances. Significance analysis of microarrays²⁸ was used to determine an approximate false discovery rate of 32% for the primary patient feature selection set.

To improve the accuracy of the 4 statistical classifiers described in the online data supplement, small subsets of top-ranked class membership predictors were generated with the HykGene classification¹⁸ method. GO::TermFinder software (available at <http://go.princeton.edu/cgi-bin/GOTermFinder>) was used to classify data according to biological process, molecular function, and cellular component. Chilibot text mining software (available at <http://www.chilibot.net/>) was used to assess known relationships between angiogenesis and statistically significant differentially expressed genes within the enriched biological process terms of the gene ontology (GO) analysis.²⁹

Quantitative Polymerase Chain Reaction Validation

Total monocyte RNA was isolated and cDNA was synthesized as previously described. Polymerase chain reaction (PCR) amplification was carried out with gene-specific TaqMan-based assays (Applied Biosystems, Foster City, Calif) on a GeneAmp 5700 sequence detection system (Applied Biosystems)—LEPROTL1 (NM_015344; Hs00209745_m1), MAPKAPK-2 (NM_004759; Hs00358962_m1), GRB2-related protein (NM_004810; Hs00191325_m1), inositol polyphosphate-4-phosphatase (NM_003866; Hs00182580_m1), and ARID4B (NM_016374; Hs00249610_m1)—and normalized to ACTB (NM_001615.3; Hs00242273_m1). Relative gene expression was assessed by the 2^{- $\Delta\Delta$ CT} method. Statistical significance was assessed in *R* with 1-sample Wilcoxon signed-rank or 1-sample *t* tests.

Protein Expression Assessment

ELISA Analysis

Human soluble intracellular adhesion molecule (sICAM-1) was analyzed in heparinized plasma with a sICAM-1 ELISA kit (R&D Systems, Inc, Minneapolis, Minn) in 100 μ L diluted plasma (1:20) that was incubated on the ELISA plate for 1.5 hours, then washed and incubated with secondary reagents. Plates were read using a

Multiskan microplate spectrophotometer (Thermo Electron, Waltham, Mass).

Western Blotting

Peripheral blood mononuclear cells from collateral score 0 and 2 patients were placed in pellets at 4°C and resuspended in 200 μ L RIPA buffer. Protein from patients (10 μ g) was resolved on an SDS-PAGE gel, transferred to a polyvinylidene fluoride membrane, and probed with a polyclonal anti-Cdc42 antibody (Cell Signaling Technology, Danvers, Mass) overnight at 4°C. The membrane was incubated with an anti-rabbit antibody conjugated to horseradish peroxidase and detected with the Phototope HRP Western Blot Detection System (Cell Signaling). Human serum albumin was used as a lane-loading marker. Membranes containing plasma proteins were incubated overnight at 4°C with a monoclonal antibody to human serum albumin (Sigma Chemical Corp, St Louis, Mo). The secondary antibody and detection conditions were the same as described for Cdc42.

The authors had full access to the data and take full responsibility for their integrity. All authors have read and agree to the manuscript as written.

Results

To explore the role of monocytes in collateral development in patients with CAD, 16 patients with angiographically evident disease, grouped on the basis of their degree of angiographically detectable collateral circulation, were evaluated in this study. The score 2 group comprised 8 patients with well-developed coronary collaterals; the score 0 group was made up of 8 patients with no angiographically evident collateral circulations. The groups were not statistically different in terms of age, CAD risk factors (such as weight and diabetic status), clinical presentation, indications for coronary angiography, total cholesterol and low-density lipoprotein levels, or past coronary revascularization procedures (Table 1). The only observed difference between groups was the extent of CAD measured by a vessel score and Gensini score (score 2 versus score 0 collaterals groups: 2.4 ± 0.9 versus 1.1 ± 0.12 diseased vessels [$P=0.003$], and 50 ± 23 versus 23 ± 20 Gensini score [$P=0.02$]).

Agilent human whole genome oligonucleotide arrays (G4112A) comprising 44 000 features representing 33 000 unique genes were profiled using total RNA extracted from peripheral blood monocytes. Two subsets of transcripts demonstrating statistically robust differences ($P \leq 0.05$ and 0.01) in abundance between patient groups were identified. An inclusive subset of 1327 transcripts ($P \leq 0.05$) (S1) was used for GO analysis, whereas a more statistically restricted ($P < 0.01$) subset comprising 256 transcripts (S2) was used as a feature set to predict patient class membership via the newly developed redundancy-based HykGene classification¹⁸ method.

The GO analysis (Table 2) shows that after correction for multiple hypothesis testing there are statistically significant enrichments of transcripts within the S1 subset displaying transcriptional activator and transcription cofactor activities. These differences in molecular function also are observed as significant enrichments of transcripts involved in the biological processes of transcription, cell organization and biogenesis, cellular localization, and intracellular transport response to stress, apoptosis, and cell proliferation. Score 0 group patients have significantly elevated expression levels of retinoblastoma 1 (RB1) and cyclin-dependent kinase inhibitor

TABLE 1. Baseline Clinical Characteristics of the Study Population

Variables	Collateral Score 2 (n=8)	Collateral Score 0 (n=8)	P
Age, y	61 \pm 9	57 \pm 7.8	0.38
Men, n	8	8	1.0
Height, m	1.75 \pm 0.05	1.76 \pm 0.05	0.69
Weight, kg	91 \pm 20	99 \pm 26	0.49
BSA, m ²	2.06 \pm 0.22	2.14 \pm 0.25	0.49
BMI, kg/m ²	30 \pm 6	32 \pm 8	0.53
Hypertension, n	7	6	0.52
Hyperlipidemia, n	8	6	0.13
Total cholesterol, mg/dL	173 \pm 36	173 \pm 4	0.98
LDL, mg/dL	96 \pm 43	101 \pm 12	0.82
HDL, mg/dL	47 \pm 14	47 \pm 6	0.77
Triglycerides, mg/dL	198 \pm 106	148 \pm 41	0.40
Diabetes, n	3	1	0.25
Insulin dependent, n	1	0	0.30
Smoking status, n			0.82
Current smoker	3	3	
Ex-smoker	3	2	
Never smoked	2	3	
Family history of CAD, n	4	3	0.61
Previous MI, n	2	2	1.0
Previous PCI, n	2	2	1.0
Previous CABG, n	2	1	0.52
Vessel score	2.4 \pm 0.92	1.1 \pm 0.12	0.003
Gensini score	50 \pm 22	23 \pm 20	0.02
>50% LM stenosis, n	0	1	0.30
Ejection fraction <35%	0	0	1.0
Indication for angiography, n			0.29
Stable angina	6	6	
Unstable angina, troponin -1	1	2	
NSTEMI	1	0	
Medications, n			
Aspirin	8	6	0.13
Clopidigrel	1	1	1.0
ACE-I	4	4	1.0
ARB	1	1	1.0
β -Blockers	8	6	0.13
Calcium channel blockers	3	1	0.25
Diuretics	2	2	1.0
Digitalis	0	1	0.30
Lipid-lowering therapy	7	7	1.0
Nitrates	2	0	0.13
Analgesics	2	1	0.52
Glycoprotein IIb/IIIa inhibitor	1	0	0.31
Anticoagulants	1	1	1.0

BSA indicates bovine serum albumin; BMI, body mass index; LDL, low-density lipoprotein; HDL, high-density lipoprotein; MI, myocardial infarction; PCI, percutaneous coronary intervention; CABG, coronary artery bypass grafting; LM, left main; NSTEMI, non-ST-segment elevation MI; ACE-I, angiotensin-converting enzyme inhibitor; and ARB, angiotensin receptor blocker.

TABLE 2. Generic GO::TermFinder Analysis

GO term	GOID	<i>P</i>	Corrected <i>P</i>	Annotations, n
Biological Process				
Transcription	GO:0006350	1.5×10^{-10}	1.5×10^{-7}	125/3195
Cell organization and biogenesis	GO:0016043	8.6×10^{-9}	8.6×10^{-6}	84/1985
Cellular localization	GO:0051641	4.0×10^{-6}	0.004	42/887
Intracellular transport	GO:0046907	6.7×10^{-6}	0.006	41/875
Response to stress	GO:0006950	3.6×10^{-6}	0.003	53/1230
Apoptosis	GO:0006915	2.5×10^{-8}	2.5×10^{-5}	37/597
Cell proliferation	GO:0008283	1.6×10^{-6}	0.002	31/538
Molecular function				
Protein binding	GO:0005515	3.8×10^{-17}	2.2e-14	196/4994
Transcription factor binding	GO:0008134	4.6×10^{-9}	2.6×10^{-6}	27/323
Transcription cofactor activity	GO:0003712	6.3×10^{-8}	3.6×10^{-5}	23/275
DNA binding	GO:0003677	1.1×10^{-7}	6.5×10^{-5}	110/3020
Transcription regulator activity	GO:0030528	1.7×10^{-8}	9.7×10^{-6}	78/1816
Transcriptional activator activity	GO:0016563	3.1×10^{-6}	0.002	19/247
Cellular component				
Nucleus	GO:0005634	1.0×10^{-20}	2.05×10^{-18}	214/5279
Cytoplasm	GO:0005737	1.7×10^{-7}	3.4×10^{-5}	145/4347
Endosome	GO:0005768	3.7×10^{-6}	0.001	10/71
Golgi stack	GO:0005795	1.2×10^{-5}	0.002	23/373

This is a partial list of biological processes, molecular functions, and cellular component terms from the Generic GO::TermFinder Analysis. See supplemental data for complete GO::TermFinder Analysis. Corrected probability values represent simulation-based analysis for multiple hypothesis correction. The numerator for the number of annotation ratio equates to the number of genes within the parsed data set determined for the statistically significant GO term; the denominator represents the number of current annotations for the GO term.

2D with concomitant decreased expression levels of Cdc42, 3 Kruppel-like transcription factors, and cyclin-dependent kinase inhibitor 2B (Table 3), a profile consistent with transcriptional abnormalities related to apoptosis and cell proliferation. Moreover, the apparently coordinated dysregulation of specific gene families, including the syntaxins, tubulins, Rabs, and adaptor-related protein complex genes, suggests that abnormalities in transcriptional regulation of cellular organization and intracellular transport did not arise by chance (Table 3).

Significant cellular component terms, comprising the nucleus, cytoplasm, endosome, and Golgi stack, support appropriate compartmentalization of the observed biological processes and molecular functions within the S1 transcript list. A partial tabulation of differential S1 transcripts that comprise these GO terms is shown in Table 3. The complete GO analysis is included in the results section in the Data Supplement (available online).

To confirm that these GO terms did not arise by chance, 10 randomly permuted data sets containing the same 16 CAD patients were generated and analyzed in the same manner. The random data permutations resulted in loss of significant associative GO terms (not shown), further indicating that enriched GO terms in the S1 list represent relevant biological differences between patient groups.

Agglomerative hierarchical clustering³⁰ and principal component analysis (PCA)³¹ were used to visualize the 256 ($P \leq 0.01$) transcripts of the S2 subset (Figure 1A and 1B).

Subjects 1 through 8 are from the score 2 coronary collateral vessel group (group 1); subjects 9 through 16 are from the score 0 coronary collateral vessel group (group 2). The heat map in Figure 1A shows strong statistical segregation in expression values between patient groups and demonstrates that the majority of the transcripts in the S2 probe set are significantly upregulated in score 0 group patients.

To confirm these findings, we performed PCA on the S2 transcript list. PCA indicates that the first and second principal components cumulatively explain 77.96% of the variability within the 256 transcripts used for analysis (Figure 1B). Score 2 group subjects form the blue encircled patient cluster; score 0 subjects shape the second red patient cluster. These visualizations support the power of the S2 data set to capture variation in expression relevant to discrimination of patient classes.

Based on expression patterns, K-Nearest Neighbors,³² Support Vector Machines,³³ C4.5,³⁴ and Naïve Bayes/Diagonal Linear Discriminant Analysis³⁵ classification algorithms were used to assess the predictive power of this cluster of transcripts to assign patients to either the score 2 or score 0 group. Leave-one-out cross-validation³⁶ was used to evaluate the efficiency of each classifier (supplemental Table I). Reduction of observation expression redundancy improved K-Nearest Neighbors, Support Vector Machines, and Naïve Bayes/Diagonal Linear Discriminant Analysis but not C4.5 classification accuracy (supplemental Table II).

TABLE 3. Biological Process Transcripts of the S1 Generic GO::TermFinder Analysis

Gene	Gene ID	Description	Fold Change*	P
Transcription				
KLF7	NM_003709	ubiquitous Kruppel-like transcription factor	2.7	0.02
KLF10	NM_005655	Kruppel-like factor 10 / TGFB inducible early growth response	9.8	0.03
KLF11	AK002186	Kruppel-like factor 11/ TGFB inducible early growth response 2	3.1	0.01
CREB1	NM_13442	cAMP responsive element binding protein 1	-2.8	0.02
DRAP1	BC018095	DR1-associated protein 1 (negative cofactor 2 alpha)	2.4	0.04
RREB1	NM_002955	ras responsive element binding protein 1	2.7	0.04
RB1	NM_000321	Retinoblastoma 1	-2.2	0.04
GATA5	NM_080473	GATA binding protein 5	8.9	0.05
RUNX1	X90980	Runt-related transcription factor 1	11.5	0.02
RUNX3	NM_004350	Runt-related transcription factor 3	3.5	0.05
Cell organization and biogenesis and intracellular transport cell				
CDC42	NM_044472	Cell division cycle 42 (GTP binding protein, 25kDa)	4.2	0.04
MYO9B	L29149	Myosin IXB	4.4	0.01
RAB9A	NM_004251	RAB9A, member RAS oncogene family	-3.3	0.01
RAB10	AF297660	RAB10, member RAS oncogene family	-2.6	0.01
AP3M2	NM_006803	Adaptor-related protein complex 3, mu 2 subunit	-2.5	0.02
AP3S2	NM_005829	Adaptor-related protein complex 3, sigma 2 subunit	8.4	0.04
AP4E1	BC015224	Adaptor-related protein complex 4, ε1 subunit	-2.8	0.01
AP4S1	AB030654	Adaptor-related protein complex 4, σ1 subunit	-2.5	0.04
STXBP2	NM_006949	Syntaxin binding protein 2	2.7	0.03
STX6	NM_005819	Syntaxin 6	-2.9	0.02
STX7	NM_003569	Syntaxin 7	-2.8	0.04
TUBA1	NM_006000	Tubulin, α1 (testis specific)	2.1	0.04
H2-ALPHA	AK093116	α-Tubulin isotype H2-α	2.4	0.05
TUBA6	NM_032704	Tubulin, α6	2.8	0.01
TUBB4	AK095202	Tubulin, β4	5.7	0.02
TUBB6	NM_032525	Tubulin, β6	4.0	0.00
Apoptosis				
BAG4	BC038505	BCL2-associated athanogene 4	-6.6	0.04
CARD6	NM_032587	Caspase recruitment domain family, member 6	-5.6	0.02
CASP3	NM_004346	Caspase 3, apoptosis-related cysteine peptidase	-3.6	0.02
CASP10	NM_032977	Caspase 10, apoptosis-related cysteine peptidase	-4.2	0.01
CUL5	NM_003478	Cullin 5	-2.5	0.03
CYCS	NM_018947	Cytochrome c, somatic	-2.7	0.05
IFI16	AK094968	Interferon γ-inducible protein 16	-5.1	0.02
TNFSF10	AI376429	Tumor necrosis factor (ligand) superfamily, member 10	-5.4	0.03
Cell proliferation				
SPHK1	NM_021972	Sphingosine kinase 1	4.3	0.03
EMP1	NM_001423	Epithelial membrane protein 1	9.8	0.02
EMP3	NM_001425	Epithelial membrane protein 3	2.5	0.04
NCK1	NM_006153	NCK adaptor protein 1	-3.0	0.02
PIM1	NM_002648	Pim-1 oncogene	11	0.00
SCGB3A1	NM_052863	Secretoglobin, family 3A, member 1	2.3	0.03
CDKN2D	NM_001800	Cyclin-dependent kinase inhibitor 2D (p19, inhibits CDK4)	4.4	0.03
CDKN2B	NM_078487	Cyclin-dependent kinase inhibitor 2B (p15, inhibits CDK4)	-2.8	0.03

This is a partial list of genes within each significant biological process term derived from the Generic GO::TermFinder Analysis. See supplemental data for complete GO::TermFinder Analysis.

*Relative fold change: ratio of group 1 (collateral score 2) to group 2 (collateral score 0).

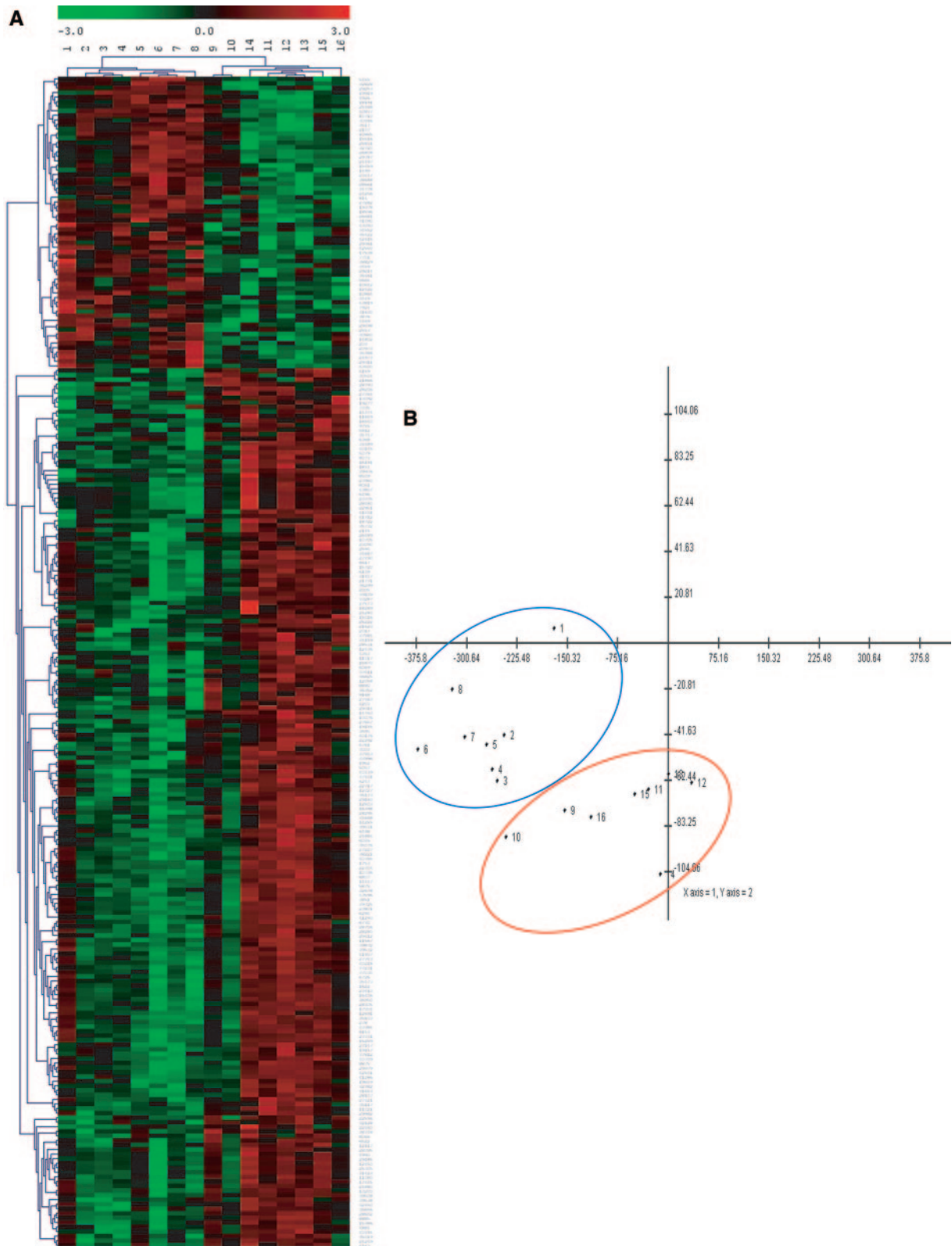


Figure 1. Hierarchical clustering and PCA visualizations of differentially expressed genes between patients with and without collateral vessels. A, The heat map data matrix represents agglomerative hierarchical clustering with Pearson correlation distance and average linkage of the cluster of 256 differentially expressed genes between score 2 and score 0 groups. B, PCA projection of CAD patients resolved over the first and second principal components. Subjects 1 through 8 have angiographically confirmed coronary collateral vessels; subjects 9 through 16 have no angiographically confirmed coronary collateral vessels. Blue circle indicates first cluster containing CAD patients in the score 2 group; red circle, second cluster of CAD patients in the score 0 group.

TABLE 4. qPCR Validation for Both Patient Data Sets

Gene	Gene ID	Microarray Fold Change*	P	qPCR Fold Change*	P
<i>ARID4B</i>	NM_016374	-4.4	0.001	-4.8	0.007
<i>MAPKAPK-2</i>	NM_004759	6.0	0.002	1.2	0.534
<i>LEPROTL1</i>	NM_015344	-5.4	0.001	-3.6	0.001
<i>INPP4B</i>	NM_003866	-7.4	0.007	-9.5	0.008
<i>GRB2-related 2</i>	NM_004810	4.2	0.008	2.4	0.031
Independent patient data set					
<i>ARID4B</i>	NM_016374	NA	NA	-9.6	0.031
<i>MAPKAPK-2</i>	NM_004759	NA	NA	1.7	0.485
<i>LEPROTL1</i>	NM_015344	NA	NA	-7.5	0.031
<i>INPP4B</i>	NM_003866	NA	NA	-11	0.031
<i>GRB2-related 2</i>	NM_004810	NA	NA	1.3	0.618

Comparison of microarray and qPCR results for top HykGene classifiers.

*Relative fold change: ratio of group 1 (collateral score 2) to group 2 (collateral score 0).

After correction for expression redundancy, patient classification accuracy was improved in part by identifying the following transcripts: retinoblastoma binding protein 1-like 1 (*ARID4B*), mitogen-activated protein kinase-activated protein kinase 2 (*MAPKAPK-2*), leptin receptor overlapping transcript-like 1 (*LEPROTL1*), inositol polyphosphate-4-phosphatase, type II (*INPP4B*), and growth factor receptor-binding protein (*GRB2-related 2*). These genes represent a partial consensus of top-ranked HykGene transcripts (Table 4).

To confirm the HykGene findings and to determine the possible effect of a cell-processing bias found in the primary collateral group data set, we carried out quantitative PCR (qPCR) analysis of differential gene expression both between these groups of CAD patients using the original patient population and in 12 additional clinically matched CAD patients with 3-vessel disease (6 patients with collateral score 2, 6 with collateral score 0). In both cases, qPCR confirmed differential abundance of the top HykGene-determined ex-

pression markers (Table 4) between patient classes. Furthermore, qPCR analysis of these 12 additional 3-vessel-disease patients suggests that relative collateral marker expression is not dependent on disease severity.

To demonstrate that transcriptional changes in monocyte gene expression correlated with changes in corresponding protein expression, 2 additional studies were carried out using patient samples that were different from the original 16-patient data set. Chilibot text mining was used to determine whether known relationships existed between angiogenesis, the hypothesized queried term, and statistically significant, differentially expressed genes within the enriched biological process terms of the GO analysis to further narrow the list of candidates for assessment of differential protein expression (Figure 2). On the basis of this analysis, we identified 4 prospective proteins—ICAM-1, Cdc42, osteopontin (SSP1), and RB1—as suitable markers of differences between the score 2 and score 0 collateral groups. In agreement with the

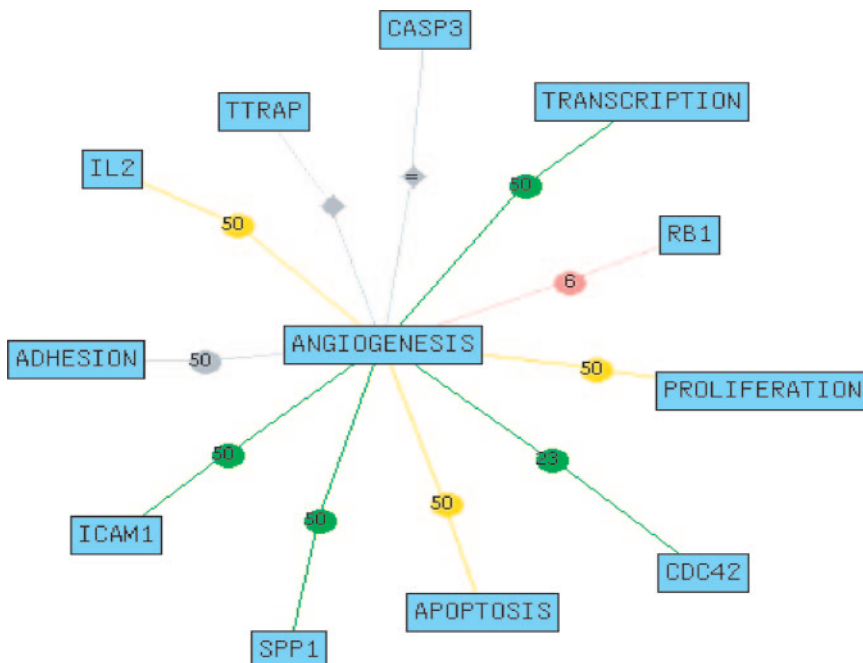


Figure 2. Chilibot text mining analysis of known relationships between angiogenesis and statistically significant differentially expressed genes within enriched biological process terms of the GO analysis, indicating that ICAM-1, Rho family GTPase Cdc42, and SSP1 have stimulatory effects on angiogenesis, whereas RB1 has an inhibitory role in vessel development. Circles represent color-coded interactive relationships: gray is neutral, green is stimulatory, red is inhibitory, and yellow is both stimulatory and inhibitory. The numerical values within each icon present the number of PubMed abstracts used to validate the relationship (default is 50). Icons containing “=” represent parallel relationships, whereas gray rhomboidal icons indicate co-occurrence.

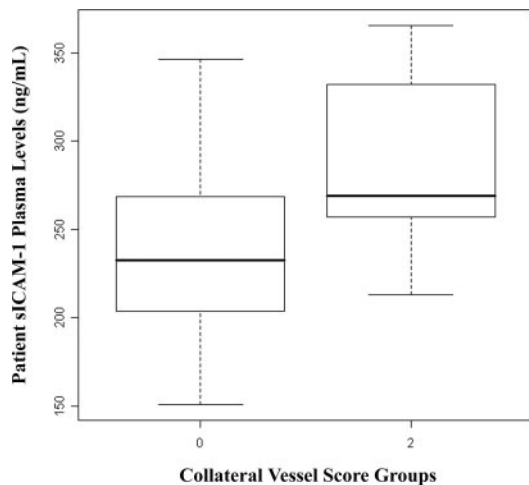


Figure 3. Parallel box plot analysis of sICAM-1 plasma levels in CAD patients with score 0 and score 2 collateral vessels. Note significantly depressed sICAM-1 plasma levels in CAD patients with score 0 collateral vessels relative to CAD patients with score 2 collateral vessels. Each box contains the middle 50% of its relative data distribution. The horizontal line within each box indicates the median value of each data distribution, whereas the upper and lower horizontal lines of each box represent the 75th and 25th percentiles of each data set, respectively. The horizontal lines at the ends of the dotted vertical lines indicate maximum and minimum data points.

microarray analyses, plasma ELISA measurements of circulating sICAM-1 levels in an independent group of 29 patients demonstrated significantly higher levels (287.29 \pm 12.69 versus 235.80 \pm 12.73 ng/mL; $P < 0.01$) in the plasma of patients with score 2 collaterals ($n = 14$) compared with patients with score 0 collaterals ($n = 15$) (Figure 3).

Western blot analysis of Cdc42 expression in circulating monocytes demonstrated, in agreement with the microarray findings, more frequent expression in patients with score 2 collaterals (15 of 17 patients) versus score 0 collaterals (6 of 17 patients, $\chi^2 = 10.1$; $P < 0.01$).

To further assess the possible confounding effects of disease severity on collateral group classification membership, subjects of the initial microarray analysis were then regrouped according to the angiographic extent of coronary disease to form a secondary disease-severity data set. This data set, which represents a reordering of patient class membership, was statistically evaluated in the same manner as the primary collateralization data set. Patients with 2- to 3-vessel disease ($n = 7$) were compared with patients with 1-vessel disease ($n = 9$). As with the primary collateral data set, GO was used to characterize the significance of the statistically assessed disease-severity data set. Unlike the collateral data set, evaluation of the disease-severity groups indicates that the only significant molecular difference resides in protein binding.

Discussion

The differences in the extent of collateral circulation among patients with seemingly similar clinical characteristics raise the possibility that genetic and molecular differences may play a role in collateral development. Because circulating

monocytes are considered the key element in the development of collateral circulation, we set out to uncover novel transcriptional determinants of human coronary collateralization using a combination of established and newly developed microarray bioinformatics analysis techniques. The principal finding of this study is that the monocyte transcriptome of closely matched patients with CAD who possess abundant collateral circulation is significantly different from the transcriptome of collateral-poor CAD subjects. Interestingly, many of the observed changes in gene expression in this study parallel prior observations in a mouse model of hind-limb ischemia.³⁷

The key differences include significant alterations in transcriptional regulation of specific determinants of monocyte biology that can be directly related to abnormalities in intracellular transport, apoptosis, and cell proliferation. These differences were confirmed in independent patient populations using qPCR analysis, Cdc42 protein expression, and plasma sICAM-1 levels.

ICAM-1 is a cell adhesion receptor expressed on a number of cell types, including monocytes and endothelial cells, that is thought to play an important role in the mediation of inflammatory and immune responses. Because arteriogenesis often is viewed as a process dependent on certain immune and inflammatory processes such as activation of specific T-cell³⁸ and mononuclear cell¹⁵ subsets, it is a logical choice for a marker of a collateralgenic phenotype. Therefore, the increased amounts of circulating sICAM-1 in patients with more extensive collateral development may reflect activation of the “inflammatory” state necessary for collateral growth.

Cdc42 is a member of the Rho family of GTPases involved in regulation of cell motility that is required for sensing colony-stimulating factor-1 concentration gradient and directed migration of monocytes/macrophages.³⁹ Increased Cdc42 levels would increase the ability of monocytes to sense and respond to the presence of CSF-1, a step thought to be important in collateral development.⁴⁰ These data point to the underlying differences in monocyte biology that may account for the variable extent of collateral formation in CAD patients and to the utility of comparative GO analysis for the evaluation and discovery of specific determinants of various pathological states.

The collateral-rich and collateral-poor patient populations in the study were carefully matched for all known CAD and collateral development risk factors, with the only significant difference being the angiographic extent of CAD as documented by the Gensini and vessel scoring systems. The severity of CAD has long been considered a predictor of collateral development.^{1,13,41} Another important determinant of the collateral presence is thought to be the gradual development of coronary stenosis rather than a sudden coronary occlusion.^{5,13} To evaluate the potential effect of differences in the severity of CAD on our results, we carried out additional analyses to evaluate the contribution of those differences on the GO class memberships describing differences in monocyte transcriptome. Reordering the data set into 2 classes based on the angiographic extent of CAD resulted in the loss of significant GO feature terms associated with collateral class, indicating the presence of 2 distinct monocyte

transcriptional processes in these patients. This finding also strongly suggests that angiographic CAD extent does not substantially influence transcriptional regulation of coronary collateralization. As a result, human collateral vessel growth and maturation may be influenced to a much greater degree by still-unknown genetic factors, not by the presence and severity of CAD.

Although recent studies have shown the efficacy of high-throughput DNA microarray platforms for phenotypic classification of various pathobiological states, major statistical concerns arise in classification analysis of gene expression data as a result, in part, of the large number of features and the relatively small number of samples. The hybrid HykGene classification system directly addresses this issue and was therefore used to assess the transcriptional correlates of the monocyte phenotype in CAD patients with and without collateral vessels. Applying this new classification method derived small sets of highly statistically significant discriminant marker genes, which were then confirmed in an independent patient data set. Interestingly, these novel collateral vessel markers are involved in the same molecular functions and biological processes proposed by GO analysis. Thus, HykGene classification provided additional statistical confirmation of the GO analysis.

Conclusions

The major findings of this study include the demonstration of collateralgenic monocyte transcription profiles in patients with CAD, delineation of novel transcriptional regulatory determinants of coronary collateralization, and the suggestion that the presence of collateral circulation may be independent of the angiographic extent of CAD. These findings support the contention that genetic factors heavily influence coronary collateral vessel growth and maturation in humans. The identification of such factors may aid in the delineation of patient prognosis and response to therapy.

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Disclosures

None.

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CLINICAL PERSPECTIVE

Collateral circulation develops in some but not all patients with advanced coronary artery disease (CAD). Although the presence of coronary collaterals has been associated with better outcomes in a number of CAD syndromes, it is not clear why collaterals are present in some but not other patients. Recent investigations have suggested that circulating mononuclear cells play a major role in collateral development and that the effect probably is achieved by a paracrine action. The present study was carried out to determine whether there are differences in the transcriptional profile of monocytes from CAD patients with an extensive versus absent collateral circulation. In a group of 16 patients, we have identified a set of molecular markers characteristic of “collateralgenic” versus “noncollateralgenic” phenotypes. Interestingly, the observed transcriptional abnormalities are independent of the severity of CAD, a variable thought to be the main cause of differences in the extent of collateral development. The collateralgenic profile was characterized by activation of molecular pathways involved in cell migration and proliferation; these pathways were suppressed in patients with absent collaterals. Furthermore, there was a significant difference in the plasma level of soluble intracellular adhesion molecule-1, potentially providing a useful biomarker of collateral development. In summary, this study suggests that genetic differences play a major role in determining the presence or absence of collaterals in CAD patients. The presence of collateralgenic biomarkers may identify patients with a more favorable prognosis and may indicate enhanced likelihood of response to therapeutic angiogenesis agents.

Transcriptional Profiling in Coronary Artery Disease: Indications for Novel Markers of Coronary Collateralization

Thomas W. Chittenden, Jonathan A. Sherman, Fei Xiong, Amy E. Hall, Anthony A. Lanahan, Jennifer M. Taylor, Hangjun Duan, Justin D. Pearlman, Jason H. Moore, Stephen M. Schwartz and Michael Simons

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Terms from the process ontology exceeding a pvalue cutoff of 0.01.

The total number of genes used to calculate the background distribution of GO terms is 23531.

-- 1 of 596--

GOID GO:0050789

TERM regulation of biological process

P-VALUE 8.06522576201302e-16

CORRECTED P-VALUE 8.04909531048899e-13

NUM_ANNOTATIONS 184 (of 4703)

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-- 2 of 596--

GOID GO:0050791

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CORRECTED P-VALUE 1.09779504530634e-12

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GOID GO:0051244

TERM regulation of cellular physiological process

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CORRECTED P-VALUE 1.88570751478217e-12

NUM_ANNOTATIONS 169 (of 4207)

ANNOTATED_GENES TNF10_HUMAN, IF16_HUMAN, FAF1_HUMAN, AF17_HUMAN, BIRC3_HUMAN, CCNT2_HUMAN, THA_HUMAN, APC10_HUMAN, SMRCD_HUMAN, ZN408_HUMAN, BNIP2_HUMAN, ZN223_HUMAN, LAT_HUMAN, BMP10_HUMAN, SRTD1_HUMAN, CDR2_HUMAN, ZN492_HUMAN, TERF1_HUMAN, NR1D1_HUMAN, HOP_HUMAN, TNR8_HUMAN, ZN646_HUMAN, SLAP2_HUMAN, ZN264_HUMAN, RUNX3_HUMAN, BAZ1A_HUMAN, ZN174_HUMAN, BCLX_HUMAN, ARF6_HUMAN, BORG1_HUMAN, ZN143_HUMAN, IF4G3_HUMAN, BRCA1_HUMAN, GATA5_HUMAN, ATF2_HUMAN, BCL3_HUMAN, HMG2_HUMAN, ING5_HUMAN, SOCS6_HUMAN, ZN222_HUMAN, ATF4_HUMAN, FOXO1_HUMAN, ATRX_HUMAN, CV106_HUMAN, CAR12_HUMAN, KLF10_HUMAN, ZNF10_HUMAN, SON_HUMAN, TRPS1_HUMAN, ZFHX2_HUMAN, ZN350_HUMAN, BAG4_HUMAN, NARGL_HUMAN, PHTF1_HUMAN, SODM_HUMAN, FIBA_HUMAN, PIM1_HUMAN, IF5_HUMAN, MKL2_HUMAN, UGRP2_HUMAN, NR1H2_HUMAN, SUFU_HUMAN, CDC42_HUMAN, MEF2C_HUMAN, RECK_HUMAN, CRSP6_HUMAN, ZEP2_HUMAN, NF2L1_HUMAN, MAF_HUMAN, CASPA_HUMAN, SMRA3_HUMAN, NRG1_HUMAN, PEPP1_HUMAN, PO6F2_HUMAN, ZBTB3_HUMAN, KLF11_HUMAN, BAZ1B_HUMAN, EPC1_HUMAN, CDN1C_HUMAN, FLI1_HUMAN, TF2H2_HUMAN, MN1_HUMAN, CDN2D_HUMAN, CREB1_HUMAN, DRAP1_HUMAN, ZNF7_HUMAN, KLF7_HUMAN, SCRT2_HUMAN, MTERF_HUMAN, OSTP_HUMAN, ZBTB1_HUMAN, ZFP95_HUMAN, RB_HUMAN, ZN516_HUMAN, ZNF12_HUMAN, ZN189_HUMAN, CYC_HUMAN, PHF20_HUMAN, ID3_HUMAN, ETS2_HUMAN, ZN430_HUMAN, POLH_HUMAN, HEN2_HUMAN, PLK3_HUMAN, CDN2B_HUMAN, EMP3_HUMAN, MSH2_HUMAN, MIZF_HUMAN, TOB2_HUMAN, SMCA5_HUMAN, BRD1_HUMAN, NCK1_HUMAN, RUNX1_HUMAN, SPHK1_HUMAN, RREB1_HUMAN, SPI1_HUMAN, ETV5_HUMAN, ZN202_HUMAN, MDM4_HUMAN, HDAC4_HUMAN, ZFY_HUMAN, ID2_HUMAN, PUM2_HUMAN, ID1_HUMAN, RHG07_HUMAN, SALL3_HUMAN, CARD6_HUMAN, SIP1_HUMAN, ZN133_HUMAN, ZN200_HUMAN, TADBP_HUMAN, TCF7_HUMAN, CASP3_HUMAN, CUL5_HUMAN, TRIP4_HUMAN, VPS4B_HUMAN, ZN397_HUMAN, PSN1_HUMAN, SIRT1_HUMAN, S12A4_HUMAN, SP3_HUMAN, BRD8_HUMAN, ZNF25_HUMAN, T2EA_HUMAN, BIM_HUMAN, CIAS1_HUMAN, FGF18_HUMAN, ZNF79_HUMAN, ZN217_HUMAN, NAMPT_HUMAN, IRF2_HUMAN, ZN286_HUMAN, TBBX_HUMAN, ZNF22_HUMAN, PO5FM_HUMAN, TPPC2_HUMAN, HXA9_HUMAN, PO5FL_HUMAN, ZN161_HUMAN, TF2AA_HUMAN, BB1_HUMAN, IF2P_HUMAN, M3K5_HUMAN, T2FB_HUMAN, EYA1_HUMAN, ZF276_HUMAN, TRI27_HUMAN, DLX2_HUMAN, ELL_HUMAN

-- 4 of 596--

GOID GO:0006366

TERM transcription from RNA polymerase II promoter

P-VALUE 9.65832775085157e-15

CORRECTED P-VALUE 9.63901109534986e-12

NUM_ANNOTATIONS 44 (of 500)

ANNOTATED_GENES TADBP_HUMAN, TCF7_HUMAN, TRIP4_HUMAN, ATF4_HUMAN, NMI_HUMAN, FOXO1_HUMAN, DRAP1_HUMAN, KLF7_HUMAN, BRD8_HUMAN, CCNT2_HUMAN, T2EA_HUMAN, KLF10_HUMAN, THA_HUMAN, RB_HUMAN, TRPS1_HUMAN, ZN189_HUMAN, IRF2_HUMAN, SODM_HUMAN, MKL2_HUMAN, MEF2C_HUMAN, SLAP2_HUMAN, SMCA5_HUMAN, CRSP6_HUMAN, RUNX1_HUMAN, RREB1_HUMAN, RUNX3_HUMAN, SPI1_HUMAN, ZN161_HUMAN, ZN202_HUMAN, ZN174_HUMAN, NF2L1_HUMAN, TF2AA_HUMAN, MDM4_HUMAN, MAF_HUMAN, ZN143_HUMAN, T2FB_HUMAN, RFXAP_HUMAN, BRCA1_HUMAN, ID1_HUMAN, HMG2_HUMAN, ELL_HUMAN, PO6F2_HUMAN, TRIPB_HUMAN, KLF11_HUMAN

Biological Process 01-12-06.txt

-- 5 of 596--

GOID GO:0050794

TERM regulation of cellular process

P-VALUE 9.75532802031456e-15

CORRECTED P-VALUE 9.73581736427393e-12

NUM_ANNOTATIONS 172 (of 4390)

ANNOTATED_GENES TNF10_HUMAN, GIT2_HUMAN, IF16_HUMAN, FAF1_HUMAN, AF17_HUMAN, BIRC3_HUMAN, CCNT2_HUMAN, THA_HUMAN, APC10_HUMAN, SMRCD_HUMAN, ZN408_HUMAN, BNIP2_HUMAN, ZN223_HUMAN, LAT_HUMAN, BMP10_HUMAN, SRTD1_HUMAN, CDR2_HUMAN, ZN492_HUMAN, TERF1_HUMAN, NR1D1_HUMAN, HOP_HUMAN, TNR8_HUMAN, ZN646_HUMAN, SLAP2_HUMAN, ZN264_HUMAN, RUNX3_HUMAN, BAZ1A_HUMAN, ZN174_HUMAN, BCLX_HUMAN, ARF6_HUMAN, BORG1_HUMAN, ZN143_HUMAN, IF4G3_HUMAN, BRCA1_HUMAN, GATA5_HUMAN, ATF2_HUMAN, BCL3_HUMAN, HMG2_HUMAN, ING5_HUMAN, SOCS6_HUMAN, ZN222_HUMAN, ATF4_HUMAN, FOXO1_HUMAN, ATRX_HUMAN, CV106_HUMAN, CAR12_HUMAN, KLF10_HUMAN, ZNF10_HUMAN, SON_HUMAN, TRPS1_HUMAN, ZFH2_HUMAN, ZN350_HUMAN, BAG4_HUMAN, NARGL_HUMAN, PHTF1_HUMAN, SODM_HUMAN, FIBA_HUMAN, PIM1_HUMAN, IF5_HUMAN, MKL2_HUMAN, UGRP2_HUMAN, NR1H2_HUMAN, SUFU_HUMAN, CDC42_HUMAN, MEF2C_HUMAN, RECK_HUMAN, CRSP6_HUMAN, ZEP2_HUMAN, NF2L1_HUMAN, FLNA_HUMAN, MAF_HUMAN, CASPA_HUMAN, SMRA3_HUMAN, NRG1_HUMAN, PEPP1_HUMAN, PO6F2_HUMAN, ZBTB3_HUMAN, KLF11_HUMAN, BAZ1B_HUMAN, EPC1_HUMAN, CDN1C_HUMAN, FLI1_HUMAN, TF2H2_HUMAN, MN1_HUMAN, CDN2D_HUMAN, CREB1_HUMAN, DRAP1_HUMAN, ZNF7_HUMAN, KLF7_HUMAN, SCRT2_HUMAN, MTERF_HUMAN, OSTP_HUMAN, ZBTB1_HUMAN, ZFP95_HUMAN, RB_HUMAN, ZN516_HUMAN, ZNF12_HUMAN, ZN189_HUMAN, CYC_HUMAN, PHF20_HUMAN, ID3_HUMAN, ETS2_HUMAN, ZN430_HUMAN, POLH_HUMAN, HEN2_HUMAN, PLK3_HUMAN, CDN2B_HUMAN, EMP3_HUMAN, MSH2_HUMAN, MIZF_HUMAN, TOB2_HUMAN, SMCA5_HUMAN, BRD1_HUMAN, NCK1_HUMAN, RUNX1_HUMAN, SPHK1_HUMAN, RREB1_HUMAN, SPI1_HUMAN, ETV5_HUMAN, ZN202_HUMAN, MDM4_HUMAN, HDAC4_HUMAN, ZFY_HUMAN, ID2_HUMAN, PUM2_HUMAN, ID1_HUMAN, RHG07_HUMAN, SALL3_HUMAN, CARD6_HUMAN, SIP1_HUMAN, ZN133_HUMAN, ZN200_HUMAN, TADBP_HUMAN, TCF7_HUMAN, CASP3_HUMAN, CUL5_HUMAN, TRIP4_HUMAN, VPS4B_HUMAN, ZN397_HUMAN, PSN1_HUMAN, SIRT1_HUMAN, FKB1A_HUMAN, S12A4_HUMAN, SP3_HUMAN, BRD8_HUMAN, ZNF25_HUMAN, T2EA_HUMAN, BIM_HUMAN, CIAS1_HUMAN, FGF18_HUMAN, ZNF79_HUMAN, ZN217_HUMAN, NAMPT_HUMAN, IRF2_HUMAN, ZN286_HUMAN, TBBX_HUMAN, ZNF22_HUMAN, PO5FM_HUMAN, TPPC2_HUMAN, HXA9_HUMAN, PO5FL_HUMAN, ZN161_HUMAN, TF2AA_HUMAN, BB1_HUMAN, IF2P_HUMAN, M3K5_HUMAN, T2FB_HUMAN, EYA1_HUMAN, ZF276_HUMAN, TRI27_HUMAN, DLX2_HUMAN, ELL_HUMAN

-- 6 of 596--

GOID GO:0006139

TERM nucleobase, nucleoside, nucleotide and nucleic acid metabolism

P-VALUE 1.87829149182768e-12

CORRECTED P-VALUE 1.87453490884402e-09

NUM_ANNOTATIONS 179 (of 4916)

ANNOTATED_GENES PARP4_HUMAN, IF16_HUMAN, AF17_HUMAN, PPIG_HUMAN, RP9_HUMAN, CCNT2_HUMAN, THA_HUMAN, WDR33_HUMAN, SMRCD_HUMAN, ZN408_HUMAN, ZN223_HUMAN, SRTD1_HUMAN, PAPOG_HUMAN, ZN492_HUMAN, TERF1_HUMAN, NR1D1_HUMAN, SYR_HUMAN, HOP_HUMAN, ZN646_HUMAN, FANCA_HUMAN, SLAP2_HUMAN, G6PE_HUMAN, ZN264_HUMAN, RUNX3_HUMAN, TDG_HUMAN, BAZ1A_HUMAN, ZN174_HUMAN, MPP8_HUMAN, KYNU_HUMAN, BLM_HUMAN, ZN143_HUMAN, PURA2_HUMAN, RFXAP_HUMAN, BRCA1_HUMAN, HCA66_HUMAN, GATA5_HUMAN, RPC2_HUMAN, ATF2_HUMAN, BCL3_HUMAN, HMG2_HUMAN, ING5_HUMAN, ZN222_HUMAN, PUR1_HUMAN, ATF4_HUMAN, FOXO1_HUMAN, PYR5_HUMAN, ATRX_HUMAN, CV106_HUMAN, KLF10_HUMAN, ZNF10_HUMAN, TRPS1_HUMAN, ZFH2_HUMAN, ZN350_HUMAN, PYRG_HUMAN, NARGL_HUMAN, PHTF1_HUMAN, NOP56_HUMAN, SEN2_HUMAN, SODM_HUMAN, MKL2_HUMAN, NR1H2_HUMAN, MEF2C_HUMAN, PRP17_HUMAN, PP1RA_HUMAN, UGPA2_HUMAN, MTO1_HUMAN, 5NT1B_HUMAN, CRSP6_HUMAN, ZEP2_HUMAN, NF2L1_HUMAN, MAF_HUMAN, TF3C4_HUMAN, SMRA3_HUMAN, NRG1_HUMAN, PEPP1_HUMAN, PO6F2_HUMAN, ZBTB3_HUMAN, KLF11_HUMAN, BAZ1B_HUMAN, EPC1_HUMAN, FLI1_HUMAN, TF2H2_HUMAN, MK67I_HUMAN, CSTF1_HUMAN, NMI_HUMAN, CREB1_HUMAN, DRAP1_HUMAN, TGDS_HUMAN, ZNF7_HUMAN, KLF7_HUMAN, SCRT2_HUMAN, MTERF_HUMAN, ZBTB1_HUMAN, RPA2_HUMAN, ZFP95_HUMAN, RB_HUMAN, ZN516_HUMAN, ZNF12_HUMAN, ZN189_HUMAN, SPOP_HUMAN, CYC_HUMAN, PHF20_HUMAN, ID3_HUMAN, PLRG1_HUMAN, UBP1_HUMAN, PUS3_HUMAN, NCBP2_HUMAN, ETS2_HUMAN, ZN430_HUMAN, POLH_HUMAN, HEN2_HUMAN, MSH2_HUMAN, SETB1_HUMAN, GEMI6_HUMAN, MIZF_HUMAN, SMCA5_HUMAN, RREB1_HUMAN, BRD1_HUMAN, RUNX1_HUMAN, SPI1_HUMAN, ETV5_HUMAN,

Biological Process 01-12-06.txt

ZN202_HUMAN, RAD18_HUMAN, CB80_HUMAN, MDM4_HUMAN, MSH6_HUMAN, SF3B3_HUMAN, HDAC4_HUMAN, ZFY_HUMAN, SUV91_HUMAN, ID2_HUMAN, ID1_HUMAN, SALL3_HUMAN, MTAP_HUMAN, SIP1_HUMAN, ZN133_HUMAN, ZN200_HUMAN, TADBP_HUMAN, TCF7_HUMAN, DUS11_HUMAN, TRIP4_HUMAN, VPS4B_HUMAN, ZN397_HUMAN, SIRT1_HUMAN, SP3_HUMAN, BRD8_HUMAN, ZNF25_HUMAN, T2EA_HUMAN, REN3B_HUMAN, RN5A_HUMAN, ZNF79_HUMAN, AA2AR_HUMAN, ZN217_HUMAN, NAMPT_HUMAN, IRF2_HUMAN, ZN286_HUMAN, ZNF22_HUMAN, PO5FM_HUMAN, HNRPU_HUMAN, TPPC2_HUMAN, HXA9_HUMAN, PO5FL_HUMAN, ZN161_HUMAN, ADML_HUMAN, TF2AA_HUMAN, DCP1B_HUMAN, FANCE_HUMAN, DNL4_HUMAN, T2FB_HUMAN, EYA1_HUMAN, ZF276_HUMAN, HNRLL_HUMAN, GEMI5_HUMAN, TRI27_HUMAN, EXOS3_HUMAN, DLX2_HUMAN, ELL_HUMAN, TRIPB_HUMAN, CSTF3_HUMAN

-- 7 of 596--

GOID GO:0006350

TERM transcription

P-VALUE 1.51412949605874e-10

CORRECTED P-VALUE 1.51110123706663e-07

NUM_ANNOTATIONS 125 (of 3195)

ANNOTATED_GENES TF2H2_HUMAN, FLI1_HUMAN, MK67I_HUMAN, IF16_HUMAN, AF17_HUMAN, NMI_HUMAN, CREB1_HUMAN, DRAP1_HUMAN, ZNF7_HUMAN, KLF7_HUMAN, CCNT2_HUMAN, MTERF_HUMAN, SCRT2_HUMAN, RPA2_HUMAN, ZBTB1_HUMAN, ZFP95_HUMAN, THA_HUMAN, RB_HUMAN, ZN516_HUMAN, ZNF12_HUMAN, ZN189_HUMAN, SMRCD_HUMAN, ZN408_HUMAN, ID3_HUMAN, ZN223_HUMAN, PHF20_HUMAN, SRTD1_HUMAN, PAPOG_HUMAN, ETS2_HUMAN, ZN492_HUMAN, TERF1_HUMAN, NR1D1_HUMAN, ZN430_HUMAN, HEN2_HUMAN, HOP_HUMAN, ZN646_HUMAN, SLAP2_HUMAN, MIZF_HUMAN, SMCA5_HUMAN, RREB1_HUMAN, RUNX1_HUMAN, ZN264_HUMAN, BRD1_HUMAN, RUNX3_HUMAN, SPI1_HUMAN, BAZ1A_HUMAN, ZN202_HUMAN, ETV5_HUMAN, ZN174_HUMAN, MDM4_HUMAN, ZN143_HUMAN, ZFY_HUMAN, HDAC4_HUMAN, ID2_HUMAN, RFXAP_HUMAN, BRCA1_HUMAN, GATA5_HUMAN, RPC2_HUMAN, ATF2_HUMAN, BCL3_HUMAN, ID1_HUMAN, HMG2_HUMAN, SALL3_HUMAN, ING5_HUMAN, SIP1_HUMAN, ZN133_HUMAN, ZN200_HUMAN, ZN222_HUMAN, TADBP_HUMAN, TCF7_HUMAN, TRIP4_HUMAN, ZN397_HUMAN, VPS4B_HUMAN, ATF4_HUMAN, FOXO1_HUMAN, SIRT1_HUMAN, ATRX_HUMAN, SP3_HUMAN, CV106_HUMAN, BRD8_HUMAN, ZNF25_HUMAN, T2EA_HUMAN, KLF10_HUMAN, ZNF10_HUMAN, TRPS1_HUMAN, ZFH2_HUMAN, ZNF79_HUMAN, ZN350_HUMAN, ZN217_HUMAN, NARGL_HUMAN, PHTF1_HUMAN, IRF2_HUMAN, SODM_HUMAN, ZN286_HUMAN, MKL2_HUMAN, NR1H2_HUMAN, ZNF22_HUMAN, PO5FM_HUMAN, TPPC2_HUMAN, MEF2C_HUMAN, HXA9_HUMAN, PP1RA_HUMAN, PO5FL_HUMAN, CRSP6_HUMAN, ZN161_HUMAN, ZEP2_HUMAN, NF2L1_HUMAN, TF2AA_HUMAN, MAF_HUMAN, TF3C4_HUMAN, T2FB_HUMAN, ZF276_HUMAN, EYA1_HUMAN, TRI27_HUMAN, SMRA3_HUMAN, DLX2_HUMAN, NRG1_HUMAN, PEPP1_HUMAN, ELL_HUMAN, PO6F2_HUMAN, ZBTB3_HUMAN, KLF11_HUMAN, TRIPB_HUMAN, BAZ1B_HUMAN, EPC1_HUMAN

-- 8 of 596--

GOID GO:0050875

TERM cellular physiological process

P-VALUE 2.32310992087056e-10

CORRECTED P-VALUE 2.31846370102882e-07

NUM_ANNOTATIONS 426 (of 15799)

ANNOTATED_GENES TRIM6_HUMAN, TXND5_HUMAN, TNF10_HUMAN, PACE1_HUMAN, IF16_HUMAN, MLP3B_HUMAN, FAF1_HUMAN, APBP2_HUMAN, PPIG_HUMAN, RP9_HUMAN, DYI2_HUMAN, RT18B_HUMAN, IBRD2_HUMAN, AP3M2_HUMAN, BIRC3_HUMAN, CCNT2_HUMAN, WDR33_HUMAN, AP4E1_HUMAN, APC10_HUMAN, DCOR_HUMAN, BNIP2_HUMAN, B3GN1_HUMAN, SRTD1_HUMAN, TBA6_HUMAN, KPVM_HUMAN, TERF1_HUMAN, SYR_HUMAN, HOP_HUMAN, ACHB_HUMAN, HGD_HUMAN, SATT_HUMAN, OSR2_HUMAN, ZN646_HUMAN, FANCA_HUMAN, ZN264_HUMAN, RUNX3_HUMAN, TDG_HUMAN, ZN174_HUMAN, BCLX_HUMAN, UGPA1_HUMAN, APBA2_HUMAN, BLM_HUMAN, ZN143_HUMAN, IF4G3_HUMAN, DHSO_HUMAN, RFXAP_HUMAN, BRCA1_HUMAN, HCA66_HUMAN, ATF2_HUMAN, STX6_HUMAN, STK35_HUMAN, ING5_HUMAN, SOCS6_HUMAN, ZN222_HUMAN, RGR_HUMAN, CCR2_HUMAN, ATF4_HUMAN, FOXO1_HUMAN, ATRX_HUMAN, HCN1_HUMAN, HSP47_HUMAN, CV106_HUMAN, LIPB_HUMAN, KLF10_HUMAN, PDRN4_HUMAN, EZRI_HUMAN, ST1A3_HUMAN, TRPS1_HUMAN, ZFH2_HUMAN, ZN350_HUMAN, RNF6_HUMAN, NARGL_HUMAN, NUPL1_HUMAN, FETA_HUMAN, PHTF1_HUMAN, NISM_HUMAN, TRIM4_HUMAN, SODM_HUMAN, FIBA_HUMAN, RANB9_HUMAN, PIM1_HUMAN, IF5_HUMAN, NECP2_HUMAN, NR1H2_HUMAN, SUFU_HUMAN, CDC42_HUMAN, CERK1_HUMAN, AP4S1_HUMAN, PP1RA_HUMAN, WBS18_HUMAN, MTO1_HUMAN, RECK_HUMAN, CA022_HUMAN, PA24A_HUMAN, PLSB_HUMAN, MAF_HUMAN, TF3C4_HUMAN, TXND9_HUMAN, K2C8_HUMAN, MK06_HUMAN, SMRA3_HUMAN, HAP28_HUMAN, MFN1_HUMAN, ZBTB3_HUMAN, KLF11_HUMAN, FPGT_HUMAN, NIPBL_HUMAN, CDN1C_HUMAN, TF2H2_HUMAN,

Biological Process 01-12-06.txt

MN1_HUMAN, NMI_HUMAN, DRAP1_HUMAN, ZNF7_HUMAN, KLF7_HUMAN, FBX32_HUMAN, RPA2_HUMAN, ZBTB1_HUMAN, ZFP95_HUMAN, SETX_HUMAN, RB_HUMAN, ZNF12_HUMAN, GLYC_HUMAN, SPOP_HUMAN, CBPA1_HUMAN, AT2B2_HUMAN, CYC_HUMAN, STXB2_HUMAN, TR11B_HUMAN, UBP1_HUMAN, NCBP2_HUMAN, ETS2_HUMAN, POLH_HUMAN, RT18C_HUMAN, HEN2_HUMAN, TRI34_HUMAN, RAB10_HUMAN, AGM1_HUMAN, CDN2B_HUMAN, S23IP_HUMAN, EMP3_HUMAN, SETB1_HUMAN, SMCA5_HUMAN, RREB1_HUMAN, TNPO1_HUMAN, ETV5_HUMAN, CLPX_HUMAN, PTH2_HUMAN, ZFY_HUMAN, SUV91_HUMAN, SPEB_HUMAN, PUM2_HUMAN, M4K5_HUMAN, RS10_HUMAN, SALL3_HUMAN, MTAP_HUMAN, FBX38_HUMAN, SIP1_HUMAN, ZN200_HUMAN, TCF7_HUMAN, DUS11_HUMAN, PANK2_HUMAN, SEP10_HUMAN, CASP3_HUMAN, FN14_HUMAN, ZN397_HUMAN, VPS4B_HUMAN, SIRT1_HUMAN, ARD1_HUMAN, AP3S2_HUMAN, C5AR_HUMAN, T2EA_HUMAN, ZCSL3_HUMAN, VAPB_HUMAN, NALDL_HUMAN, RAB9A_HUMAN, TEX10_HUMAN, REN3B_HUMAN, RN5A_HUMAN, EEA1_HUMAN, FGF18_HUMAN, SPH2_HUMAN, AA2AR_HUMAN, ZNF79_HUMAN, ZN217_HUMAN, UT14C_HUMAN, FUT8_HUMAN, IRF2_HUMAN, SIAH1_HUMAN, ZN286_HUMAN, PO5FM_HUMAN, TPPC2_HUMAN, LYST_HUMAN, PO5FL_HUMAN, EMP1_HUMAN, MOB3_HUMAN, TRI32_HUMAN, KELL_HUMAN, ADML_HUMAN, TF2AA_HUMAN, TBB6_HUMAN, BB1_HUMAN, OBP2B_HUMAN, DCP1B_HUMAN, IF2P_HUMAN, ANGL7_HUMAN, FANCE_HUMAN, DHRS3_HUMAN, ICT1_HUMAN, T2FB_HUMAN, SIA10_HUMAN, RN146_HUMAN, ZF276_HUMAN, OST3B_HUMAN, EXOS3_HUMAN, DLX2_HUMAN, S22A3_HUMAN, TRIPB_HUMAN, DNJA1_HUMAN, TBA2_HUMAN, PIM3_HUMAN, CSTF3_HUMAN, MK14_HUMAN, APG5_HUMAN, PARP4_HUMAN, TACD2_HUMAN, SNX27_HUMAN, AF17_HUMAN, ACADM_HUMAN, TRPM3_HUMAN, STRN3_HUMAN, MELPH_HUMAN, PFTA_HUMAN, THA_HUMAN, ARFP1_HUMAN, SMRCD_HUMAN, ZN408_HUMAN, ZN223_HUMAN, LAT_HUMAN, BMP10_HUMAN, DYL2_HUMAN, PAPOG_HUMAN, CDR2_HUMAN, REN1_HUMAN, ZN492_HUMAN, NR1D1_HUMAN, SFTA2_HUMAN, NU160_HUMAN, FBX34_HUMAN, BET1_HUMAN, NUP50_HUMAN, TNR8_HUMAN, SLAP2_HUMAN, G6PE_HUMAN, RM19_HUMAN, BAZ1A_HUMAN, MPP8_HUMAN, KYNU_HUMAN, EAA2_HUMAN, ARF6_HUMAN, STAM1_HUMAN, PPBI_HUMAN, BORG1_HUMAN, PURA2_HUMAN, GATA5_HUMAN, RPC2_HUMAN, RIOK3_HUMAN, BCL3_HUMAN, HMG2_HUMAN, AMFR1_HUMAN, FBX5_HUMAN, LIS1_HUMAN, FTMT_HUMAN, DCMC_HUMAN, AK1C1_HUMAN, PPID_HUMAN, STX7_HUMAN, DAPP1_HUMAN, PUR1_HUMAN, PYR5_HUMAN, CAR12_HUMAN, TBB4_HUMAN, ZNF10_HUMAN, PDPK1_HUMAN, INSI1_HUMAN, SON_HUMAN, AMFR2_HUMAN, PYRG_HUMAN, BAG4_HUMAN, NOP56_HUMAN, SEN2_HUMAN, MKL2_HUMAN, UGRP2_HUMAN, UT14A_HUMAN, GTR3_HUMAN, LDLR_HUMAN, MEF2C_HUMAN, PRP17_HUMAN, UGPA2_HUMAN, HS105_HUMAN, 5NT1B_HUMAN, CRSP6_HUMAN, KCNQ2_HUMAN, ZEP2_HUMAN, BCDO2_HUMAN, NF2L1_HUMAN, NEUL_HUMAN, FLNA_HUMAN, KCMA1_HUMAN, CASPA_HUMAN, CCG1_HUMAN, NRG1_HUMAN, PFTK1_HUMAN, PEPP1_HUMAN, TRI12_HUMAN, PO6F2_HUMAN, CD97_HUMAN, UBP33_HUMAN, BAZ1B_HUMAN, EPC1_HUMAN, FLI1_HUMAN, MK67I_HUMAN, CSTF1_HUMAN, CDN2D_HUMAN, CREB1_HUMAN, TGDS_HUMAN, MTERF_HUMAN, SCRT2_HUMAN, OSTP_HUMAN, CN108_HUMAN, LAMC1_HUMAN, ZN516_HUMAN, ZN189_HUMAN, ACHA_HUMAN, PHF20_HUMAN, ID3_HUMAN, PLRG1_HUMAN, C43BP_HUMAN, PUS3_HUMAN, UB2J1_HUMAN, ZN430_HUMAN, B4GT4_HUMAN, PLK3_HUMAN, CPNE1_HUMAN, MSH2_HUMAN, CO9A3_HUMAN, GEMI6_HUMAN, TOB2_HUMAN, UBP47_HUMAN, MIZF_HUMAN, SPHK1_HUMAN, BRD1_HUMAN, NCK1_HUMAN, RUNX1_HUMAN, STAG2_HUMAN, SPI1_HUMAN, ZN202_HUMAN, SNX18_HUMAN, RAD18_HUMAN, APG7L_HUMAN, PP2CB_HUMAN, RAP2B_HUMAN, NMT1_HUMAN, CB80_HUMAN, MDM4_HUMAN, MSH6_HUMAN, IDS_HUMAN, SF3B3_HUMAN, HDAC4_HUMAN, ID2_HUMAN, ID1_HUMAN, MGAT2_HUMAN, RHG07_HUMAN, OSR11_HUMAN, IRK2_HUMAN, MYO9B_HUMAN, CTNL1_HUMAN, CARD6_HUMAN, KCNG4_HUMAN, SMS2_HUMAN, CAH8_HUMAN, ZN133_HUMAN, GRAN_HUMAN, TADBP_HUMAN, TRIP4_HUMAN, CUL5_HUMAN, PSN1_HUMAN, FKB1A_HUMAN, S12A4_HUMAN, SP3_HUMAN, AXUD1_HUMAN, BRD8_HUMAN, ZNF25_HUMAN, BIM_HUMAN, TOM1_HUMAN, CIAS1_HUMAN, NCKX1_HUMAN, FBX25_HUMAN, CSE1_HUMAN, NAMPT_HUMAN, ZN363_HUMAN, ZNF22_HUMAN, TBBX_HUMAN, FKBP5_HUMAN, HNRPU_HUMAN, IRK3_HUMAN, TBA1_HUMAN, HXA9_HUMAN, RABE1_HUMAN, DYL1_HUMAN, ZN161_HUMAN, ZNT1_HUMAN, PPT2_HUMAN, RRS1_HUMAN, DNL4_HUMAN, M3K5_HUMAN, DET1_HUMAN, EYA1_HUMAN, HNRLL_HUMAN, GEMI5_HUMAN, TRI27_HUMAN, CD1D_HUMAN, ELL_HUMAN, STK39_HUMAN, GA45B_HUMAN, STXB3_HUMAN, CETN3_HUMAN

-- 9 of 596--

GOID GO:0019222

TERM regulation of metabolism

P-VALUE 3.62767403579336e-10

CORRECTED P-VALUE 3.62041868772178e-07

NUM_ANNOTATIONS 127 (of 3310)

ANNOTATED_GENES TF2H2_HUMAN, FLI1_HUMAN, IF16_HUMAN, FAF1_HUMAN, AF17_HUMAN, CREB1_HUMAN, DRAP1_HUMAN, ZNF7_HUMAN, KLF7_HUMAN, CCNT2_HUMAN, MTERF_HUMAN, SCRT2_HUMAN, ZBTB1_HUMAN, ZFP95_HUMAN, THA_HUMAN, RB_HUMAN, ZN516_HUMAN,

Biological Process 01-12-06.txt

ZNF12_HUMAN, ZN189_HUMAN, SMRCD_HUMAN, ZN408_HUMAN, ID3_HUMAN, ZN223_HUMAN, PHF20_HUMAN, SRTD1_HUMAN, CDR2_HUMAN, ETS2_HUMAN, ZN492_HUMAN, TERF1_HUMAN, NR1D1_HUMAN, ZN430_HUMAN, POLH_HUMAN, HEN2_HUMAN, HOP_HUMAN, ZN646_HUMAN, SLAP2_HUMAN, MIZF_HUMAN, SMCA5_HUMAN, RREB1_HUMAN, RUNX1_HUMAN, NCK1_HUMAN, ZN264_HUMAN, BRD1_HUMAN, RUNX3_HUMAN, SPI1_HUMAN, BAZ1A_HUMAN, ZN202_HUMAN, ETV5_HUMAN, ZN174_HUMAN, MDM4_HUMAN, ARF6_HUMAN, BORG1_HUMAN, ZN143_HUMAN, IF4G3_HUMAN, ZFY_HUMAN, HDAC4_HUMAN, ID2_HUMAN, BRCA1_HUMAN, PUM2_HUMAN, GATA5_HUMAN, ATF2_HUMAN, BCL3_HUMAN, ID1_HUMAN, HMG2_HUMAN, SALL3_HUMAN, ING5_HUMAN, SIP1_HUMAN, ZN133_HUMAN, ZN200_HUMAN, ZN222_HUMAN, TADBP_HUMAN, TCF7_HUMAN, TRIP4_HUMAN, ZN397_HUMAN, VPS4B_HUMAN, ATF4_HUMAN, FOXO1_HUMAN, SIRT1_HUMAN, ATRX_HUMAN, SP3_HUMAN, CV106_HUMAN, BRD8_HUMAN, ZNF25_HUMAN, T2EA_HUMAN, KLF10_HUMAN, ZNF10_HUMAN, TRPS1_HUMAN, ZFHX2_HUMAN, ZNF79_HUMAN, ZN350_HUMAN, ZN217_HUMAN, NARGL_HUMAN, PHTF1_HUMAN, IRF2_HUMAN, SODM_HUMAN, ZN286_HUMAN, IF5_HUMAN, MKL2_HUMAN, NR1H2_HUMAN, ZNF22_HUMAN, PO5FM_HUMAN, TPPC2_HUMAN, CDC42_HUMAN, MEF2C_HUMAN, HXA9_HUMAN, PO5FL_HUMAN, CRSP6_HUMAN, ZN161_HUMAN, ZEP2_HUMAN, NF2L1_HUMAN, TF2AA_HUMAN, MAF_HUMAN, IF2P_HUMAN, T2FB_HUMAN, ZF276_HUMAN, EYA1_HUMAN, SMRA3_HUMAN, TRI27_HUMAN, DLX2_HUMAN, NRG1_HUMAN, PEPP1_HUMAN, ELL_HUMAN, PO6F2_HUMAN, ZBTB3_HUMAN, KLF11_HUMAN, BAZ1B_HUMAN, EPC1_HUMAN

-- 10 of 596--

GOID GO:0006351

TERM transcription, DNA-dependent

P-VALUE 4.99009955439855e-10

CORRECTED P-VALUE 4.98011935528975e-07

NUM_ANNOTATIONS 115 (of 2905)

ANNOTATED_GENES TF2H2_HUMAN, FLI1_HUMAN, MK67I_HUMAN, IF16_HUMAN, AF17_HUMAN, NMI_HUMAN, CREB1_HUMAN, DRAP1_HUMAN, ZNF7_HUMAN, KLF7_HUMAN, CCNT2_HUMAN, MTERF_HUMAN, SCRT2_HUMAN, ZBTB1_HUMAN, ZFP95_HUMAN, THA_HUMAN, RB_HUMAN, ZN516_HUMAN, ZNF12_HUMAN, ZN189_HUMAN, ZN408_HUMAN, ZN223_HUMAN, PHF20_HUMAN, SRTD1_HUMAN, ETS2_HUMAN, ZN492_HUMAN, NR1D1_HUMAN, ZN430_HUMAN, HEN2_HUMAN, HOP_HUMAN, ZN646_HUMAN, SLAP2_HUMAN, MIZF_HUMAN, SMCA5_HUMAN, RREB1_HUMAN, RUNX1_HUMAN, ZN264_HUMAN, BRD1_HUMAN, RUNX3_HUMAN, SPI1_HUMAN, BAZ1A_HUMAN, ZN202_HUMAN, ETV5_HUMAN, ZN174_HUMAN, MDM4_HUMAN, ZN143_HUMAN, ZFY_HUMAN, HDAC4_HUMAN, RFXAP_HUMAN, BRCA1_HUMAN, GATA5_HUMAN, ATF2_HUMAN, BCL3_HUMAN, ID1_HUMAN, HMG2_HUMAN, SALL3_HUMAN, ING5_HUMAN, SIP1_HUMAN, ZN133_HUMAN, ZN200_HUMAN, ZN222_HUMAN, TADBP_HUMAN, TCF7_HUMAN, TRIP4_HUMAN, ZN397_HUMAN, VPS4B_HUMAN, ATF4_HUMAN, FOXO1_HUMAN, SIRT1_HUMAN, ATRX_HUMAN, SP3_HUMAN, BRD8_HUMAN, ZNF25_HUMAN, T2EA_HUMAN, KLF10_HUMAN, ZNF10_HUMAN, TRPS1_HUMAN, ZFHX2_HUMAN, ZNF79_HUMAN, ZN350_HUMAN, ZN217_HUMAN, NARGL_HUMAN, PHTF1_HUMAN, IRF2_HUMAN, SODM_HUMAN, ZN286_HUMAN, MKL2_HUMAN, NR1H2_HUMAN, ZNF22_HUMAN, PO5FM_HUMAN, TPPC2_HUMAN, MEF2C_HUMAN, HXA9_HUMAN, PO5FL_HUMAN, CRSP6_HUMAN, ZN161_HUMAN, ZEP2_HUMAN, NF2L1_HUMAN, TF2AA_HUMAN, MAF_HUMAN, TF3C4_HUMAN, T2FB_HUMAN, ZF276_HUMAN, EYA1_HUMAN, SMRA3_HUMAN, TRI27_HUMAN, DLX2_HUMAN, PEPP1_HUMAN, ELL_HUMAN, PO6F2_HUMAN, ZBTB3_HUMAN, KLF11_HUMAN, TRIPB_HUMAN, BAZ1B_HUMAN, EPC1_HUMAN

-- 11 of 596--

GOID GO:0006357

TERM regulation of transcription from RNA polymerase II promoter

P-VALUE 7.70272363132352e-10

CORRECTED P-VALUE 7.68731818406087e-07

NUM_ANNOTATIONS 26 (of 277)

ANNOTATED_GENES TCF7_HUMAN, SLAP2_HUMAN, ATF4_HUMAN, FOXO1_HUMAN, SMCA5_HUMAN, DRAP1_HUMAN, CRSP6_HUMAN, RUNX1_HUMAN, SPI1_HUMAN, ZN161_HUMAN, BRD8_HUMAN, KLF7_HUMAN, ZN202_HUMAN, ZN174_HUMAN, KLF10_HUMAN, MDM4_HUMAN, ZN143_HUMAN, RB_HUMAN, ZN189_HUMAN, BRCA1_HUMAN, ID1_HUMAN, HMG2_HUMAN, IRF2_HUMAN, SODM_HUMAN, KLF11_HUMAN, MKL2_HUMAN

-- 12 of 596--

GOID GO:0008219

TERM cell death

P-VALUE 8.6282069006952e-10

Biological Process 01-12-06.txt

CORRECTED P-VALUE 8.61095048689381e-07

NUM_ANNOTATIONS 41 (of 626)

ANNOTATED_GENES APG5_HUMAN, PARP4_HUMAN, TNF10_HUMAN, CUL5_HUMAN, CASP3_HUMAN, FN14_HUMAN, IF16_HUMAN, PSN1_HUMAN, FAF1_HUMAN, FOXO1_HUMAN, SIRT1_HUMAN, AXUD1_HUMAN, CAR12_HUMAN, BIRC3_HUMAN, BIM_HUMAN, OSTP_HUMAN, CIAS1_HUMAN, SON_HUMAN, SETX_HUMAN, AA2AR_HUMAN, BAG4_HUMAN, CSE1_HUMAN, CYC_HUMAN, BNIP2_HUMAN, TR11B_HUMAN, SIAH1_HUMAN, PIM1_HUMAN, TBBX_HUMAN, EMP3_HUMAN, RAB1_HUMAN, EMP1_HUMAN, SPHK1_HUMAN, BCLX_HUMAN, MDM4_HUMAN, PTH2_HUMAN, M3K5_HUMAN, CASPA_HUMAN, BRCA1_HUMAN, GA45B_HUMAN, CTNL1_HUMAN, CARD6_HUMAN

-- 13 of 596--

GOID GO:0051243

TERM negative regulation of cellular physiological process

P-VALUE 1.00858899528296e-09

CORRECTED P-VALUE 1.00657181729239e-06

NUM_ANNOTATIONS 42 (of 655)

ANNOTATED_GENES CDN1C_HUMAN, MN1_HUMAN, CUL5_HUMAN, PSN1_HUMAN, FAF1_HUMAN, FOXO1_HUMAN, SIRT1_HUMAN, CDN2D_HUMAN, DRAP1_HUMAN, BIRC3_HUMAN, OSTP_HUMAN, KLF10_HUMAN, SON_HUMAN, RB_HUMAN, ZN189_HUMAN, BAG4_HUMAN, BNIP2_HUMAN, IRF2_HUMAN, PIM1_HUMAN, UGRP2_HUMAN, SUFU_HUMAN, CDN2B_HUMAN, TNR8_HUMAN, MSH2_HUMAN, EMP3_HUMAN, SLAP2_HUMAN, RECK_HUMAN, TOB2_HUMAN, SPHK1_HUMAN, SPI1_HUMAN, ZN202_HUMAN, ZN174_HUMAN, BCLX_HUMAN, MDM4_HUMAN, ARF6_HUMAN, BRCA1_HUMAN, NRG1_HUMAN, BCL3_HUMAN, RHG07_HUMAN, ING5_HUMAN, KLF11_HUMAN, SIP1_HUMAN

-- 14 of 596--

GOID GO:0016265

TERM death

P-VALUE 1.04033101931202e-09

CORRECTED P-VALUE 1.0382503572734e-06

NUM_ANNOTATIONS 41 (of 630)

ANNOTATED_GENES APG5_HUMAN, PARP4_HUMAN, TNF10_HUMAN, CUL5_HUMAN, CASP3_HUMAN, FN14_HUMAN, IF16_HUMAN, PSN1_HUMAN, FAF1_HUMAN, FOXO1_HUMAN, SIRT1_HUMAN, AXUD1_HUMAN, CAR12_HUMAN, BIRC3_HUMAN, BIM_HUMAN, OSTP_HUMAN, CIAS1_HUMAN, SON_HUMAN, SETX_HUMAN, AA2AR_HUMAN, BAG4_HUMAN, CSE1_HUMAN, CYC_HUMAN, BNIP2_HUMAN, TR11B_HUMAN, SIAH1_HUMAN, PIM1_HUMAN, TBBX_HUMAN, EMP3_HUMAN, RAB1_HUMAN, EMP1_HUMAN, SPHK1_HUMAN, BCLX_HUMAN, MDM4_HUMAN, PTH2_HUMAN, M3K5_HUMAN, CASPA_HUMAN, BRCA1_HUMAN, GA45B_HUMAN, CTNL1_HUMAN, CARD6_HUMAN

-- 15 of 596--

GOID GO:0031323

TERM regulation of cellular metabolism

P-VALUE 2.21462596371323e-09

CORRECTED P-VALUE 2.21019671178581e-06

NUM_ANNOTATIONS 122 (of 3228)

ANNOTATED_GENES TF2H2_HUMAN, FLI1_HUMAN, IF16_HUMAN, AF17_HUMAN, CREB1_HUMAN, DRAP1_HUMAN, ZNF7_HUMAN, KLF7_HUMAN, CCNT2_HUMAN, MTERF_HUMAN, SCRT2_HUMAN, ZBTB1_HUMAN, ZFP95_HUMAN, THA_HUMAN, RB_HUMAN, ZN516_HUMAN, ZNF12_HUMAN, ZN189_HUMAN, SMRCD_HUMAN, ZN408_HUMAN, ID3_HUMAN, ZN223_HUMAN, PHF20_HUMAN, SRTD1_HUMAN, CDR2_HUMAN, ETS2_HUMAN, ZN492_HUMAN, TERF1_HUMAN, NR1D1_HUMAN, ZN430_HUMAN, POLH_HUMAN, HEN2_HUMAN, HOP_HUMAN, ZN646_HUMAN, SLAP2_HUMAN, MIZF_HUMAN, SMCA5_HUMAN, RREB1_HUMAN, RUNX1_HUMAN, ZN264_HUMAN, BRD1_HUMAN, RUNX3_HUMAN, SPI1_HUMAN, BAZ1A_HUMAN, ZN202_HUMAN, ETV5_HUMAN, ZN174_HUMAN, MDM4_HUMAN, ZN143_HUMAN, IF4G3_HUMAN, ZFY_HUMAN, HDAC4_HUMAN, ID2_HUMAN, BRCA1_HUMAN, PUM2_HUMAN, GATA5_HUMAN, ATF2_HUMAN, BCL3_HUMAN, ID1_HUMAN, HMG2_HUMAN, SALL3_HUMAN, ING5_HUMAN, SIP1_HUMAN, ZN133_HUMAN, ZN200_HUMAN, ZN222_HUMAN, TADBP_HUMAN, TCF7_HUMAN, TRIP4_HUMAN, ZN397_HUMAN, VPS4B_HUMAN, ATF4_HUMAN, FOXO1_HUMAN, SIRT1_HUMAN, ATRX_HUMAN, SP3_HUMAN, CV106_HUMAN, BRD8_HUMAN, ZNF25_HUMAN, T2EA_HUMAN, KLF10_HUMAN, ZNF10_HUMAN, TRPS1_HUMAN, ZFH2_HUMAN, ZNF79_HUMAN, ZN350_HUMAN, ZN217_HUMAN, NARG1_HUMAN, PHTF1_HUMAN, IRF2_HUMAN, SODM_HUMAN, ZN286_HUMAN, IF5_HUMAN, MKL2_HUMAN, NR1H2_HUMAN, ZNF22_HUMAN, PO5FM_HUMAN, TPPC2_HUMAN, MEF2C_HUMAN, HXA9_HUMAN, PO5FL_HUMAN, CRSP6_HUMAN, ZN161_HUMAN, ZEP2_HUMAN, NF2L1_HUMAN, TF2AA_HUMAN, MAF_HUMAN, IF2P_HUMAN, T2FB_HUMAN, ZF276_HUMAN, EYA1_HUMAN, SMRA3_HUMAN, TRI27_HUMAN, DLX2_HUMAN,

Biological Process 01-12-06.txt

NRG1_HUMAN, PEPP1_HUMAN, ELL_HUMAN, PO6F2_HUMAN, ZBTB3_HUMAN, KLF11_HUMAN, BAZ1B_HUMAN, EPC1_HUMAN

-- 16 of 596--

GOID GO:0006355

TERM regulation of transcription, DNA-dependent

P-VALUE 3.75970814083212e-09

CORRECTED P-VALUE 3.75218872455046e-06

NUM_ANNOTATIONS 110 (of 2832)

ANNOTATED_GENES TF2H2_HUMAN, FLI1_HUMAN, IF16_HUMAN, AF17_HUMAN, CREB1_HUMAN, DRAP1_HUMAN, ZNF7_HUMAN, KLF7_HUMAN, CCNT2_HUMAN, MTERF_HUMAN, SCRT2_HUMAN, ZBTB1_HUMAN, ZFP95_HUMAN, THA_HUMAN, RB_HUMAN, ZN516_HUMAN, ZNF12_HUMAN, ZN189_HUMAN, ZN408_HUMAN, ZN223_HUMAN, PHF20_HUMAN, SRTD1_HUMAN, ETS2_HUMAN, ZN492_HUMAN, NR1D1_HUMAN, ZN430_HUMAN, HEN2_HUMAN, HOP_HUMAN, ZN646_HUMAN, SLAP2_HUMAN, MIZF_HUMAN, SMCA5_HUMAN, RREB1_HUMAN, RUNX1_HUMAN, ZN264_HUMAN, BRD1_HUMAN, RUNX3_HUMAN, SPI1_HUMAN, BAZ1A_HUMAN, ZN202_HUMAN, ETV5_HUMAN, ZN174_HUMAN, MDM4_HUMAN, ZN143_HUMAN, ZFY_HUMAN, HDAC4_HUMAN, BRCA1_HUMAN, GATA5_HUMAN, ATF2_HUMAN, BCL3_HUMAN, ID1_HUMAN, HMG2_HUMAN, SALL3_HUMAN, ING5_HUMAN, SIP1_HUMAN, ZN133_HUMAN, ZN200_HUMAN, ZN222_HUMAN, TADBP_HUMAN, TCF7_HUMAN, TRIP4_HUMAN, ZN397_HUMAN, VPS4B_HUMAN, ATF4_HUMAN, FOXO1_HUMAN, SIRT1_HUMAN, ATRX_HUMAN, SP3_HUMAN, BRD8_HUMAN, ZNF25_HUMAN, T2EA_HUMAN, KLF10_HUMAN, ZNF10_HUMAN, TRPS1_HUMAN, ZFH2_HUMAN, ZNF79_HUMAN, ZN350_HUMAN, ZN217_HUMAN, NARGL_HUMAN, PHTF1_HUMAN, IRF2_HUMAN, SODM_HUMAN, ZN286_HUMAN, MKL2_HUMAN, NR1H2_HUMAN, ZNF22_HUMAN, PO5FM_HUMAN, TTPC2_HUMAN, MEF2C_HUMAN, HXA9_HUMAN, PO5FL_HUMAN, CRSP6_HUMAN, ZN161_HUMAN, ZEP2_HUMAN, NF2L1_HUMAN, TF2AA_HUMAN, MAF_HUMAN, T2FB_HUMAN, ZF276_HUMAN, EYA1_HUMAN, SMRA3_HUMAN, TRI27_HUMAN, DLX2_HUMAN, PEPP1_HUMAN, ELL_HUMAN, PO6F2_HUMAN, ZBTB3_HUMAN, KLF11_HUMAN, BAZ1B_HUMAN, EPC1_HUMAN

-- 17 of 596--

GOID GO:0043118

TERM negative regulation of physiological process

P-VALUE 4.66646074942243e-09

CORRECTED P-VALUE 4.65712782792358e-06

NUM_ANNOTATIONS 42 (of 690)

ANNOTATED_GENES CDN1C_HUMAN, MN1_HUMAN, CUL5_HUMAN, PSN1_HUMAN, FAF1_HUMAN, FOXO1_HUMAN, SIRT1_HUMAN, CDN2D_HUMAN, DRAP1_HUMAN, BIRC3_HUMAN, OSTP_HUMAN, KLF10_HUMAN, SON_HUMAN, RB_HUMAN, ZN189_HUMAN, BAG4_HUMAN, BNIP2_HUMAN, IRF2_HUMAN, PIM1_HUMAN, UGRP2_HUMAN, SUFU_HUMAN, CDN2B_HUMAN, TNR8_HUMAN, MSH2_HUMAN, EMP3_HUMAN, SLAP2_HUMAN, RECK_HUMAN, TOB2_HUMAN, SPHK1_HUMAN, SPI1_HUMAN, ZN202_HUMAN, ZN174_HUMAN, BCLX_HUMAN, MDM4_HUMAN, ARF6_HUMAN, BRCA1_HUMAN, NRG1_HUMAN, BCL3_HUMAN, RHG07_HUMAN, ING5_HUMAN, KLF11_HUMAN, SIP1_HUMAN

-- 18 of 596--

GOID GO:0019219

TERM regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolism

P-VALUE 4.9107107652334e-09

CORRECTED P-VALUE 4.90088934370293e-06

NUM_ANNOTATIONS 117 (of 3093)

ANNOTATED_GENES TF2H2_HUMAN, FLI1_HUMAN, IF16_HUMAN, AF17_HUMAN, CREB1_HUMAN, DRAP1_HUMAN, ZNF7_HUMAN, KLF7_HUMAN, CCNT2_HUMAN, MTERF_HUMAN, SCRT2_HUMAN, ZBTB1_HUMAN, ZFP95_HUMAN, THA_HUMAN, RB_HUMAN, ZN516_HUMAN, ZNF12_HUMAN, ZN189_HUMAN, SMRCD_HUMAN, ZN408_HUMAN, ID3_HUMAN, ZN223_HUMAN, PHF20_HUMAN, SRTD1_HUMAN, ETS2_HUMAN, ZN492_HUMAN, TERF1_HUMAN, NR1D1_HUMAN, ZN430_HUMAN, POLH_HUMAN, HEN2_HUMAN, HOP_HUMAN, ZN646_HUMAN, SLAP2_HUMAN, MIZF_HUMAN, SMCA5_HUMAN, RREB1_HUMAN, RUNX1_HUMAN, ZN264_HUMAN, BRD1_HUMAN, RUNX3_HUMAN, SPI1_HUMAN, BAZ1A_HUMAN, ZN202_HUMAN, ETV5_HUMAN, ZN174_HUMAN, MDM4_HUMAN, ZN143_HUMAN, ZFY_HUMAN, HDAC4_HUMAN, ID2_HUMAN, BRCA1_HUMAN, GATA5_HUMAN, ATF2_HUMAN, BCL3_HUMAN, ID1_HUMAN, HMG2_HUMAN, SALL3_HUMAN, ING5_HUMAN, SIP1_HUMAN, ZN133_HUMAN, ZN200_HUMAN, ZN222_HUMAN, TADBP_HUMAN, TCF7_HUMAN, TRIP4_HUMAN, ZN397_HUMAN, VPS4B_HUMAN, ATF4_HUMAN, FOXO1_HUMAN, SIRT1_HUMAN, ATRX_HUMAN, SP3_HUMAN, CV106_HUMAN, BRD8_HUMAN, ZNF25_HUMAN, T2EA_HUMAN, KLF10_HUMAN, ZNF10_HUMAN, TRPS1_HUMAN, ZFH2_HUMAN, ZNF79_HUMAN, ZN350_HUMAN, ZN217_HUMAN,

Biological Process 01-12-06.txt

NARGL_HUMAN, PHTF1_HUMAN, IRF2_HUMAN, SODM_HUMAN, ZN286_HUMAN, MKL2_HUMAN, NR1H2_HUMAN, ZNF22_HUMAN, PO5FM_HUMAN, TPPC2_HUMAN, MEF2C_HUMAN, HXA9_HUMAN, PO5FL_HUMAN, CRSP6_HUMAN, ZN161_HUMAN, ZEP2_HUMAN, NF2L1_HUMAN, TF2AA_HUMAN, MAF_HUMAN, T2FB_HUMAN, ZF276_HUMAN, EYA1_HUMAN, SMRA3_HUMAN, TRI27_HUMAN, DLX2_HUMAN, NRG1_HUMAN, PEPP1_HUMAN, ELL_HUMAN, PO6F2_HUMAN, ZBTB3_HUMAN, KLF11_HUMAN, BAZ1B_HUMAN, EPC1_HUMAN

-- 19 of 596--

GOID GO:0045449

TERM regulation of transcription

P-VALUE 4.95873375309256e-09

CORRECTED P-VALUE 4.94881628558638e-06

NUM_ANNOTATIONS 116 (of 3058)

ANNOTATED_GENES TF2H2_HUMAN, FLI1_HUMAN, IF16_HUMAN, AF17_HUMAN, CREB1_HUMAN, DRAP1_HUMAN, ZNF7_HUMAN, KLF7_HUMAN, CCNT2_HUMAN, MTERF_HUMAN, SCRT2_HUMAN, ZBTB1_HUMAN, ZFP95_HUMAN, THA_HUMAN, RB_HUMAN, ZN516_HUMAN, ZNF12_HUMAN, ZN189_HUMAN, SMRCD_HUMAN, ZN408_HUMAN, ID3_HUMAN, ZN223_HUMAN, PHF20_HUMAN, SRTD1_HUMAN, ETS2_HUMAN, ZN492_HUMAN, TERF1_HUMAN, NR1D1_HUMAN, ZN430_HUMAN, HEN2_HUMAN, HOP_HUMAN, ZN646_HUMAN, SLAP2_HUMAN, MIZF_HUMAN, SMCA5_HUMAN, RREB1_HUMAN, RUNX1_HUMAN, ZN264_HUMAN, BRD1_HUMAN, RUNX3_HUMAN, SPI1_HUMAN, BAZ1A_HUMAN, ZN202_HUMAN, ETV5_HUMAN, ZN174_HUMAN, MDM4_HUMAN, ZN143_HUMAN, ZFY_HUMAN, HDAC4_HUMAN, ID2_HUMAN, BRCA1_HUMAN, GATA5_HUMAN, ATF2_HUMAN, BCL3_HUMAN, ID1_HUMAN, HMG2_HUMAN, SALL3_HUMAN, ING5_HUMAN, SIP1_HUMAN, ZN133_HUMAN, ZN200_HUMAN, ZN222_HUMAN, TADBP_HUMAN, TCF7_HUMAN, TRIP4_HUMAN, ZN397_HUMAN, VPS4B_HUMAN, ATF4_HUMAN, FOXO1_HUMAN, SIRT1_HUMAN, ATRX_HUMAN, SP3_HUMAN, CV106_HUMAN, BRD8_HUMAN, ZNF25_HUMAN, T2EA_HUMAN, KLF10_HUMAN, ZNF10_HUMAN, TRPS1_HUMAN, ZFHX2_HUMAN, ZNF79_HUMAN, ZN350_HUMAN, ZN217_HUMAN, NARGL_HUMAN, PHTF1_HUMAN, IRF2_HUMAN, SODM_HUMAN, ZN286_HUMAN, MKL2_HUMAN, NR1H2_HUMAN, ZNF22_HUMAN, PO5FM_HUMAN, TPPC2_HUMAN, MEF2C_HUMAN, HXA9_HUMAN, PO5FL_HUMAN, CRSP6_HUMAN, ZN161_HUMAN, ZEP2_HUMAN, NF2L1_HUMAN, TF2AA_HUMAN, MAF_HUMAN, T2FB_HUMAN, ZF276_HUMAN, EYA1_HUMAN, SMRA3_HUMAN, TRI27_HUMAN, DLX2_HUMAN, NRG1_HUMAN, PEPP1_HUMAN, ELL_HUMAN, PO6F2_HUMAN, ZBTB3_HUMAN, KLF11_HUMAN, BAZ1B_HUMAN, EPC1_HUMAN

-- 20 of 596--

GOID GO:0048523

TERM negative regulation of cellular process

P-VALUE 6.54353432512948e-09

CORRECTED P-VALUE 6.53044725647922e-06

NUM_ANNOTATIONS 43 (of 725)

ANNOTATED_GENES CDN1C_HUMAN, MN1_HUMAN, CUL5_HUMAN, PSN1_HUMAN, FAF1_HUMAN, FOXO1_HUMAN, SIRT1_HUMAN, CDN2D_HUMAN, DRAP1_HUMAN, BIRC3_HUMAN, OSTP_HUMAN, KLF10_HUMAN, SON_HUMAN, RB_HUMAN, ZN189_HUMAN, BAG4_HUMAN, BNIP2_HUMAN, IRF2_HUMAN, PIM1_HUMAN, UGRP2_HUMAN, SUFU_HUMAN, CDN2B_HUMAN, TNR8_HUMAN, MSH2_HUMAN, EMP3_HUMAN, SLAP2_HUMAN, RECK_HUMAN, TOB2_HUMAN, SPHK1_HUMAN, SPI1_HUMAN, ZN202_HUMAN, ZN174_HUMAN, BCLX_HUMAN, MDM4_HUMAN, ARF6_HUMAN, BRCA1_HUMAN, NRG1_HUMAN, BCL3_HUMAN, RHG07_HUMAN, ING5_HUMAN, SOCS6_HUMAN, KLF11_HUMAN, SIP1_HUMAN

-- 21 of 596--

GOID GO:0016043

TERM cell organization and biogenesis

P-VALUE 8.65020930660272e-09

CORRECTED P-VALUE 8.63290888798951e-06

NUM_ANNOTATIONS 84 (of 1985)

ANNOTATED_GENES FAF1_HUMAN, APBP2_HUMAN, DYI2_HUMAN, AP3M2_HUMAN, MELPH_HUMAN, CN108_HUMAN, ARFP1_HUMAN, AP4E1_HUMAN, SMRCD_HUMAN, STXB2_HUMAN, DYL2_HUMAN, TBA6_HUMAN, NCBP2_HUMAN, TERF1_HUMAN, RAB10_HUMAN, NU160_HUMAN, BET1_HUMAN, NUP50_HUMAN, S23IP_HUMAN, EMP3_HUMAN, SETB1_HUMAN, SMCA5_HUMAN, SPHK1_HUMAN, TNPO1_HUMAN, NCK1_HUMAN, MPP8_HUMAN, APG7L_HUMAN, CB80_HUMAN, ARF6_HUMAN, STAM1_HUMAN, BORG1_HUMAN, HDAC4_HUMAN, SUV91_HUMAN, BRCA1_HUMAN, STX6_HUMAN, BCL3_HUMAN, HMG2_HUMAN, RHG07_HUMAN, SOCS6_HUMAN, MYO9B_HUMAN, LIS1_HUMAN, STX7_HUMAN, GRAN_HUMAN, VPS4B_HUMAN, PSN1_HUMAN, SIRT1_HUMAN, ATRX_HUMAN,

Biological Process 01-12-06.txt

BRD8_HUMAN, AP3S2_HUMAN, TOM1_HUMAN, TBB4_HUMAN, PDPK1_HUMAN, RAB9A_HUMAN, EZRI_HUMAN, REN3B_HUMAN, TRPS1_HUMAN, EEA1_HUMAN, CSE1_HUMAN, UT14C_HUMAN, NOP56_HUMAN, SIAH1_HUMAN, RANB9_HUMAN, UGRP2_HUMAN, UT14A_HUMAN, TBBX_HUMAN, TPPC2_HUMAN, CDC42_HUMAN, LYST_HUMAN, AP4S1_HUMAN, TBA1_HUMAN, RABE1_HUMAN, EMP1_HUMAN, DYLL1_HUMAN, TBB6_HUMAN, BB1_HUMAN, FLNA_HUMAN, RRS1_HUMAN, K2C8_HUMAN, SMRA3_HUMAN, EXOS3_HUMAN, MFN1_HUMAN, TBA2_HUMAN, CETN3_HUMAN, EPC1_HUMAN

-- 22 of 596--

GOID GO:0048519
TERM negative regulation of biological process
P-VALUE 1.13999722698473e-08
CORRECTED P-VALUE 1.13771723253076e-05
NUM_ANNOTATIONS 45 (of 794)

ANNOTATED_GENES CDN1C_HUMAN, MN1_HUMAN, CUL5_HUMAN, CCR2_HUMAN, PSN1_HUMAN, FAF1_HUMAN, FOXO1_HUMAN, SIRT1_HUMAN, CDN2D_HUMAN, DRAP1_HUMAN, BIRC3_HUMAN, OSTP_HUMAN, MGR7_HUMAN, KLF10_HUMAN, SON_HUMAN, RB_HUMAN, ZN189_HUMAN, BAG4_HUMAN, BNIP2_HUMAN, IRF2_HUMAN, PIM1_HUMAN, UGRP2_HUMAN, SUFU_HUMAN, CDN2B_HUMAN, TNR8_HUMAN, MSH2_HUMAN, EMP3_HUMAN, SLAP2_HUMAN, RECK_HUMAN, TOB2_HUMAN, SPHK1_HUMAN, SPI1_HUMAN, ZN202_HUMAN, ZN174_HUMAN, BCLX_HUMAN, MDM4_HUMAN, ARF6_HUMAN, BRCA1_HUMAN, NRG1_HUMAN, BCL3_HUMAN, RHG07_HUMAN, ING5_HUMAN, SOCS6_HUMAN, KLF11_HUMAN, SIP1_HUMAN

-- 23 of 596--

GOID GO:0006915
TERM apoptosis
P-VALUE 2.47560234819913e-08
CORRECTED P-VALUE 2.47065114350273e-05
NUM_ANNOTATIONS 37 (of 597)

ANNOTATED_GENES APG5_HUMAN, TNF10_HUMAN, CUL5_HUMAN, CASP3_HUMAN, FN14_HUMAN, IF16_HUMAN, PSN1_HUMAN, FAF1_HUMAN, FOXO1_HUMAN, SIRT1_HUMAN, AXUD1_HUMAN, CAR12_HUMAN, BIRC3_HUMAN, BIM_HUMAN, OSTP_HUMAN, CIAS1_HUMAN, SON_HUMAN, AA2AR_HUMAN, BAG4_HUMAN, CSE1_HUMAN, CYC_HUMAN, BNIP2_HUMAN, TR11B_HUMAN, SIAH1_HUMAN, PIM1_HUMAN, TBBX_HUMAN, RABE1_HUMAN, SPHK1_HUMAN, BCLX_HUMAN, MDM4_HUMAN, PTH2_HUMAN, M3K5_HUMAN, CASPA_HUMAN, BRCA1_HUMAN, GA45B_HUMAN, CTN1L_HUMAN, CARD6_HUMAN

-- 24 of 596--

GOID GO:0012501
TERM programmed cell death
P-VALUE 2.8168477143143e-08
CORRECTED P-VALUE 2.81121401888568e-05
NUM_ANNOTATIONS 37 (of 600)

ANNOTATED_GENES APG5_HUMAN, TNF10_HUMAN, CUL5_HUMAN, CASP3_HUMAN, FN14_HUMAN, IF16_HUMAN, PSN1_HUMAN, FAF1_HUMAN, FOXO1_HUMAN, SIRT1_HUMAN, AXUD1_HUMAN, CAR12_HUMAN, BIRC3_HUMAN, BIM_HUMAN, OSTP_HUMAN, CIAS1_HUMAN, SON_HUMAN, AA2AR_HUMAN, BAG4_HUMAN, CSE1_HUMAN, CYC_HUMAN, BNIP2_HUMAN, TR11B_HUMAN, SIAH1_HUMAN, PIM1_HUMAN, TBBX_HUMAN, RABE1_HUMAN, SPHK1_HUMAN, BCLX_HUMAN, MDM4_HUMAN, PTH2_HUMAN, M3K5_HUMAN, CASPA_HUMAN, BRCA1_HUMAN, GA45B_HUMAN, CTN1L_HUMAN, CARD6_HUMAN

-- 25 of 596--

GOID GO:0048518
TERM positive regulation of biological process
P-VALUE 1.61675801668977e-07
CORRECTED P-VALUE 0.000161352450065639
NUM_ANNOTATIONS 37 (of 643)

ANNOTATED_GENES TNF10_HUMAN, CUL5_HUMAN, CASP3_HUMAN, IF16_HUMAN, PSN1_HUMAN, FAF1_HUMAN, ATF4_HUMAN, FKB1A_HUMAN, C5AR_HUMAN, BIM_HUMAN, OSTP_HUMAN, CIAS1_HUMAN, RB_HUMAN, FGF18_HUMAN, AA2AR_HUMAN, NARGL_HUMAN, SMRCD_HUMAN, NAMPT_HUMAN, CYC_HUMAN, SRTD1_HUMAN, FIBA_HUMAN, MKL2_HUMAN, TBBX_HUMAN, NCK1_HUMAN, CRSP6_HUMAN, RUNX1_HUMAN, SPHK1_HUMAN, ARF6_HUMAN, FLNA_HUMAN, BORG1_HUMAN, M3K5_HUMAN, CASPA_HUMAN, M4K5_HUMAN, BRCA1_HUMAN, GATA5_HUMAN, CD1D_HUMAN, GA45B_HUMAN

Biological Process 01-12-06.txt

-- 26 of 596--

GOID GO:0044238

TERM primary metabolism

P-VALUE 2.6800841246326e-07

CORRECTED P-VALUE 0.000267472395638333

NUM_ANNOTATIONS 307 (of 11066)

ANNOTATED_GENES TRIM6_HUMAN, PACE1_HUMAN, IF16_HUMAN, MLP3B_HUMAN, FAF1_HUMAN, PPIG_HUMAN, RP9_HUMAN, RT18B_HUMAN, IBRD2_HUMAN, BIRC3_HUMAN, CCNT2_HUMAN, WDR33_HUMAN, APC10_HUMAN, DCOR_HUMAN, B3GN1_HUMAN, SRTD1_HUMAN, TBA6_HUMAN, KP YM_HUMAN, TERF1_HUMAN, SYR_HUMAN, HOP_HUMAN, HGD_HUMAN, OSR2_HUMAN, ZN646_HUMAN, FANCA_HUMAN, ZN264_HUMAN, RUNX3_HUMAN, TDG_HUMAN, ZN174_HUMAN, BLM_HUMAN, ZN143_HUMAN, IF4G3_HUMAN, DHSO_HUMAN, RFXAP_HUMAN, BRCA1_HUMAN, HCA66_HUMAN, ATF2_HUMAN, STK35_HUMAN, ING5_HUMAN, ZN222_HUMAN, RGR_HUMAN, ATF4_HUMAN, FOXO1_HUMAN, ATRX_HUMAN, HSP47_HUMAN, CV106_HUMAN, LIPB_HUMAN, KLF10_HUMAN, PDRN4_HUMAN, ST1A3_HUMAN, TRPS1_HUMAN, ZFHX2_HUMAN, ZN350_HUMAN, RNF6_HUMAN, NARGL_HUMAN, PHTF1_HUMAN, TRIM4_HUMAN, SODM_HUMAN, PIM1_HUMAN, IF5_HUMAN, NR1H2_HUMAN, SUFU_HUMAN, CDC42_HUMAN, CERK1_HUMAN, PP1RA_HUMAN, WBS18_HUMAN, MTO1_HUMAN, CA022_HUMAN, PA24A_HUMAN, PLSB_HUMAN, MAF_HUMAN, TF3C4_HUMAN, MK06_HUMAN, SMRA3_HUMAN, ZBTB3_HUMAN, KLF11_HUMAN, FPGT_HUMAN, TF2H2_HUMAN, NMI_HUMAN, DRAP1_HUMAN, ZNF7_HUMAN, KLF7_HUMAN, FBX32_HUMAN, RPA2_HUMAN, ZBTB1_HUMAN, ZFP95_HUMAN, RB_HUMAN, ZNF12_HUMAN, GLYC_HUMAN, SPOP_HUMAN, CBPA1_HUMAN, CYC_HUMAN, UBP1_HUMAN, NCBP2_HUMAN, ETS2_HUMAN, POLH_HUMAN, RT18C_HUMAN, HEN2_HUMAN, TRI34_HUMAN, AGM1_HUMAN, SETB1_HUMAN, SMCA5_HUMAN, RREB1_HUMAN, ETV5_HUMAN, CLPX_HUMAN, ZFY_HUMAN, SUV91_HUMAN, SPEB_HUMAN, PUM2_HUMAN, M4K5_HUMAN, RS10_HUMAN, SALL3_HUMAN, MTAP_HUMAN, FBX38_HUMAN, SIP1_HUMAN, ZN200_HUMAN, TCF7_HUMAN, DUS11_HUMAN, CASP3_HUMAN, ZN397_HUMAN, VPS4B_HUMAN, SIRT1_HUMAN, ARD1_HUMAN, T2EA_HUMAN, ZCSL3_HUMAN, VAPB_HUMAN, NALDL_HUMAN, REN3B_HUMAN, RN5A_HUMAN, SPH2_HUMAN, AA2AR_HUMAN, ZNF79_HUMAN, ZN217_HUMAN, FUT8_HUMAN, IRF2_HUMAN, SIAH1_HUMAN, ZN286_HUMAN, PO5FM_HUMAN, TPPC2_HUMAN, PO5FL_HUMAN, TRI32_HUMAN, KELL_HUMAN, ADML_HUMAN, TF2AA_HUMAN, TBB6_HUMAN, DCP1B_HUMAN, PRS10_HUMAN, IF2P_HUMAN, FANCE_HUMAN, DHRS3_HUMAN, ICT1_HUMAN, T2FB_HUMAN, SIA10_HUMAN, RN146_HUMAN, ZF276_HUMAN, OST3B_HUMAN, EXOS3_HUMAN, DLX2_HUMAN, DNJA1_HUMAN, TRIPB_HUMAN, TBA2_HUMAN, PIM3_HUMAN, CSTF3_HUMAN, MK14_HUMAN, PARP4_HUMAN, AF17_HUMAN, ACADM_HUMAN, PFTA_HUMAN, THA_HUMAN, SMRCD_HUMAN, ZN408_HUMAN, ZN223_HUMAN, PAPOG_HUMAN, CDR2_HUMAN, REN1_HUMAN, NR1D1_HUMAN, ZN492_HUMAN, FBX34_HUMAN, G6PE_HUMAN, SLAP2_HUMAN, RM19_HUMAN, BAZ1A_HUMAN, MPP8_HUMAN, KYNU_HUMAN, ARF6_HUMAN, BORG1_HUMAN, PURA2_HUMAN, GATA5_HUMAN, RPC2_HUMAN, RIOK3_HUMAN, BCL3_HUMAN, HMG2_HUMAN, FBX5_HUMAN, LIS1_HUMAN, PPID_HUMAN, DCMC_HUMAN, DAPP1_HUMAN, PUR1_HUMAN, PYR5_HUMAN, PLPL4_HUMAN, TBB4_HUMAN, ZNF10_HUMAN, PDPK1_HUMAN, AMFR2_HUMAN, PYRG_HUMAN, BAG4_HUMAN, NOP56_HUMAN, SEN2_HUMAN, MKL2_HUMAN, GTR3_HUMAN, LDLR_HUMAN, MEF2C_HUMAN, PRP17_HUMAN, UGPA2_HUMAN, HS105_HUMAN, 5NT1B_HUMAN, CRSP6_HUMAN, ZEP2_HUMAN, BCDO2_HUMAN, NF2L1_HUMAN, NEUL_HUMAN, CASPA_HUMAN, NRG1_HUMAN, PFTK1_HUMAN, PEPP1_HUMAN, TRI12_HUMAN, PO6F2_HUMAN, UBP33_HUMAN, BAZ1B_HUMAN, EPC1_HUMAN, FLI1_HUMAN, MK67I_HUMAN, CSTF1_HUMAN, CREB1_HUMAN, GUSL3_HUMAN, TGDS_HUMAN, MTERF_HUMAN, SCRT2_HUMAN, LAMC1_HUMAN, ZN516_HUMAN, ZN189_HUMAN, PHF20_HUMAN, ID3_HUMAN, GUSL2_HUMAN, PLRG1_HUMAN, C43BP_HUMAN, PUS3_HUMAN, UB2J1_HUMAN, ZN430_HUMAN, B4GT4_HUMAN, PLK3_HUMAN, CPNE1_HUMAN, MSH2_HUMAN, UBP47_HUMAN, MIZF_HUMAN, GEMI6_HUMAN, BRD1_HUMAN, NCK1_HUMAN, RUNX1_HUMAN, SPHK1_HUMAN, SPI1_HUMAN, ZN202_HUMAN, RAD18_HUMAN, APG7L_HUMAN, PP2CB_HUMAN, CB80_HUMAN, NMT1_HUMAN, MDM4_HUMAN, SF3B3_HUMAN, MSH6_HUMAN, IDS_HUMAN, HDAC4_HUMAN, ID2_HUMAN, ID1_HUMAN, MGAT2_HUMAN, OSR11_HUMAN, SMS2_HUMAN, ZN133_HUMAN, TADBP_HUMAN, CUL5_HUMAN, TRIP4_HUMAN, PSN1_HUMAN, FKB1A_HUMAN, SP3_HUMAN, BRD8_HUMAN, ZNF25_HUMAN, FBX25_HUMAN, NAMPT_HUMAN, ZN363_HUMAN, TBBX_HUMAN, ZNF22_HUMAN, FKBP5_HUMAN, HNRPU_HUMAN, TBA1_HUMAN, HXA9_HUMAN, ZN161_HUMAN, GALT3_HUMAN, PPT2_HUMAN, DNL4_HUMAN, M3K5_HUMAN, DET1_HUMAN, EYA1_HUMAN, GEMI5_HUMAN, TRI27_HUMAN, HNRL1_HUMAN, ELL_HUMAN, STK39_HUMAN

-- 27 of 596--

GOID GO:0007582

TERM physiological process

P-VALUE 3.27836205280687e-07

CORRECTED P-VALUE 0.000327180532870125

Biological Process 01-12-06.txt

NUM_ANNOTATIONS 458 (of 18034)

ANNOTATED_GENES TRIM6_HUMAN, TXND5_HUMAN, TNF10_HUMAN, PACE1_HUMAN, IF16_HUMAN, MLP3B_HUMAN, FAF1_HUMAN, APBP2_HUMAN, PPIG_HUMAN, RP9_HUMAN, DYI2_HUMAN, RT18B_HUMAN, IBRD2_HUMAN, AP3M2_HUMAN, BIRC3_HUMAN, CCNT2_HUMAN, IFIT2_HUMAN, WDR33_HUMAN, HA25_HUMAN, AP4E1_HUMAN, APC10_HUMAN, DCOR_HUMAN, BNIP2_HUMAN, B3GN1_HUMAN, SRTD1_HUMAN, TBA6_HUMAN, KPYM_HUMAN, TERF1_HUMAN, SYR_HUMAN, HOP_HUMAN, TPM3_HUMAN, ACHB_HUMAN, HGD_HUMAN, SATT_HUMAN, OSR2_HUMAN, ZN646_HUMAN, FANCA_HUMAN, ZN264_HUMAN, RUNX3_HUMAN, TDG_HUMAN, ZN174_HUMAN, BCLX_HUMAN, UGPA1_HUMAN, APBA2_HUMAN, BLM_HUMAN, ZN143_HUMAN, IF4G3_HUMAN, DHSO_HUMAN, RFXAP_HUMAN, BRCA1_HUMAN, HCA66_HUMAN, ATF2_HUMAN, STX6_HUMAN, STK35_HUMAN, ING5_HUMAN, SOCS6_HUMAN, ZN222_HUMAN, RGR_HUMAN, CCR2_HUMAN, ATF4_HUMAN, FOXO1_HUMAN, MYPT1_HUMAN, ATRX_HUMAN, HCN1_HUMAN, HSP47_HUMAN, CV106_HUMAN, LIPB_HUMAN, KLF10_HUMAN, PDRN4_HUMAN, EMD_HUMAN, EZRI_HUMAN, ST1A3_HUMAN, TRPS1_HUMAN, ZFH2_HUMAN, ZN350_HUMAN, FA8_HUMAN, RNF6_HUMAN, NARGL_HUMAN, NUPL1_HUMAN, FETA_HUMAN, PHTF1_HUMAN, NISM_HUMAN, TRIM4_HUMAN, SODM_HUMAN, FIBA_HUMAN, RANB9_HUMAN, PIM1_HUMAN, IF5_HUMAN, NECP2_HUMAN, NR1H2_HUMAN, SUFU_HUMAN, CDC42_HUMAN, CERK1_HUMAN, AP4S1_HUMAN, PP1RA_HUMAN, WBS18_HUMAN, ATRN_HUMAN, MTO1_HUMAN, RECK_HUMAN, CA022_HUMAN, PA24A_HUMAN, PLSB_HUMAN, MAF_HUMAN, TF3C4_HUMAN, TXND9_HUMAN, K2C8_HUMAN, MK06_HUMAN, SMRA3_HUMAN, HAP28_HUMAN, MFN1_HUMAN, ZBTB3_HUMAN, KLF11_HUMAN, FPGT_HUMAN, NIPBL_HUMAN, CDN1C_HUMAN, TF2H2_HUMAN, MN1_HUMAN, NMI_HUMAN, DRAP1_HUMAN, ZNF7_HUMAN, KLF7_HUMAN, FBX32_HUMAN, MUTA_HUMAN, PTAFR_HUMAN, RPA2_HUMAN, ZBTB1_HUMAN, ZFP95_HUMAN, SETX_HUMAN, RB_HUMAN, ZNF12_HUMAN, WHRN_HUMAN, GLYC_HUMAN, SPOP_HUMAN, CBPA1_HUMAN, AT2B2_HUMAN, GSTA5_HUMAN, CYC_HUMAN, STXB2_HUMAN, TREM1_HUMAN, TR11B_HUMAN, NCBP2_HUMAN, UBP1_HUMAN, ETS2_HUMAN, POLH_HUMAN, RT18C_HUMAN, HEN2_HUMAN, TRI34_HUMAN, RAB10_HUMAN, AGM1_HUMAN, HA22_HUMAN, CDN2B_HUMAN, S23IP_HUMAN, EMP3_HUMAN, SETB1_HUMAN, SMCA5_HUMAN, RREB1_HUMAN, TNPO1_HUMAN, ETV5_HUMAN, CLPX_HUMAN, PTH2_HUMAN, ZFY_HUMAN, SUV91_HUMAN, SPEB_HUMAN, PUM2_HUMAN, M4K5_HUMAN, RS10_HUMAN, SALL3_HUMAN, MTAP_HUMAN, FBX38_HUMAN, SIP1_HUMAN, ZN200_HUMAN, TCF7_HUMAN, DUS11_HUMAN, PANK2_HUMAN, SEP10_HUMAN, CASP3_HUMAN, FN14_HUMAN, ZN397_HUMAN, VPS4B_HUMAN, SIRT1_HUMAN, ARD1_HUMAN, AP3S2_HUMAN, C5AR_HUMAN, T2EA_HUMAN, ZCSL3_HUMAN, VAPB_HUMAN, CBLN1_HUMAN, RAB9A_HUMAN, NALDL_HUMAN, TEX10_HUMAN, REN3B_HUMAN, RN5A_HUMAN, EEA1_HUMAN, FGF18_HUMAN, SPH2_HUMAN, AA2AR_HUMAN, ZNF79_HUMAN, ZN217_HUMAN, UT14C_HUMAN, FUT8_HUMAN, IRF2_HUMAN, SIAH1_HUMAN, ZN286_HUMAN, PO5FM_HUMAN, TPPC2_HUMAN, LYST_HUMAN, PO5FL_HUMAN, EMP1_HUMAN, MOB3_HUMAN, TRI32_HUMAN, KELL_HUMAN, ADML_HUMAN, TF2AA_HUMAN, TBB6_HUMAN, BB1_HUMAN, OBP2B_HUMAN, DCP1B_HUMAN, PRS10_HUMAN, IF2P_HUMAN, ANGL7_HUMAN, FANCE_HUMAN, DHRS3_HUMAN, ICT1_HUMAN, T2FB_HUMAN, SIA10_HUMAN, RN146_HUMAN, ZF276_HUMAN, OST3B_HUMAN, EXOS3_HUMAN, DLX2_HUMAN, S22A3_HUMAN, TRIPB_HUMAN, DNJA1_HUMAN, TBA2_HUMAN, PIM3_HUMAN, CSTF3_HUMAN, MK14_HUMAN, APG5_HUMAN, PARP4_HUMAN, TACD2_HUMAN, SNX27_HUMAN, AF17_HUMAN, ACADM_HUMAN, TRPM3_HUMAN, STRN3_HUMAN, MELPH_HUMAN, PFTA_HUMAN, THA_HUMAN, ARFP1_HUMAN, SMRCD_HUMAN, ZN408_HUMAN, ZN223_HUMAN, LAT_HUMAN, BMP10_HUMAN, DYL2_HUMAN, PAPOG_HUMAN, CDR2_HUMAN, RENT1_HUMAN, ZN492_HUMAN, NR1D1_HUMAN, SFTA2_HUMAN, NU160_HUMAN, FBX34_HUMAN, BET1_HUMAN, NUP50_HUMAN, TNR8_HUMAN, SLAP2_HUMAN, G6PE_HUMAN, RM19_HUMAN, BAZ1A_HUMAN, MPP8_HUMAN, KYNU_HUMAN, EAA2_HUMAN, ARF6_HUMAN, STAM1_HUMAN, PPBI_HUMAN, BORG1_HUMAN, PURA2_HUMAN, GATA5_HUMAN, RPC2_HUMAN, RIOK3_HUMAN, BCL3_HUMAN, HMG2_HUMAN, AMFR1_HUMAN, FBX5_HUMAN, TSG6_HUMAN, LIS1_HUMAN, FTMT_HUMAN, DCMC_HUMAN, AK1C1_HUMAN, PPID_HUMAN, STX7_HUMAN, DAPP1_HUMAN, PUR1_HUMAN, PYR5_HUMAN, PLPL4_HUMAN, CAR12_HUMAN, TBB4_HUMAN, ZNF10_HUMAN, PDPK1_HUMAN, INSI1_HUMAN, SON_HUMAN, AMFR2_HUMAN, PYRG_HUMAN, BAG4_HUMAN, NOP56_HUMAN, SEN2_HUMAN, IL16_HUMAN, MKL2_HUMAN, UGRP2_HUMAN, UT14A_HUMAN, GTR3_HUMAN, LDLR_HUMAN, MEF2C_HUMAN, PRP17_HUMAN, UGPA2_HUMAN, HS105_HUMAN, 5NT1B_HUMAN, PPBT_HUMAN, CRSP6_HUMAN, KCNQ2_HUMAN, RDH14_HUMAN, ZEP2_HUMAN, BCDO2_HUMAN, NF2L1_HUMAN, NEUL_HUMAN, FLNA_HUMAN, KCMA1_HUMAN, CASPA_HUMAN, CCG1_HUMAN, NRG1_HUMAN, PFTK1_HUMAN, VNN3_HUMAN, PEPP1_HUMAN, TRI12_HUMAN, PO6F2_HUMAN, CD97_HUMAN, UBP33_HUMAN, BAZ1B_HUMAN, EPC1_HUMAN, FLI1_HUMAN, MK67I_HUMAN, CSTF1_HUMAN, GUSL3_HUMAN, ICOS_HUMAN, CREB1_HUMAN, CDN2D_HUMAN, TGDS_HUMAN, MTERF_HUMAN, SCRT2_HUMAN, OSTP_HUMAN, CN108_HUMAN, LAMC1_HUMAN, ZN516_HUMAN, ZN189_HUMAN, GUSL2_HUMAN, ACHA_HUMAN, PHF20_HUMAN, ID3_HUMAN, PLRG1_HUMAN, C43BP_HUMAN, PUS3_HUMAN, UB2J1_HUMAN, ZN430_HUMAN, B4GT4_HUMAN, PLK3_HUMAN, CPNE1_HUMAN, MSH2_HUMAN, CO9A3_HUMAN, TLR7_HUMAN, GEMI6_HUMAN, TOB2_HUMAN, UBP47_HUMAN, MIZF_HUMAN, FCAR_HUMAN, SPHK1_HUMAN, BRD1_HUMAN, NCK1_HUMAN,

Biological Process 01-12-06.txt

RUNX1_HUMAN, STAG2_HUMAN, SPI1_HUMAN, ZN202_HUMAN, SNX18_HUMAN, RAD18_HUMAN, APG7L_HUMAN, PP2CB_HUMAN, RAP2B_HUMAN, NMT1_HUMAN, CB80_HUMAN, MDM4_HUMAN, MSH6_HUMAN, IDS_HUMAN, SF3B3_HUMAN, HDAC4_HUMAN, ID2_HUMAN, ID1_HUMAN, MGAT2_HUMAN, RHG07_HUMAN, OSR1_HUMAN, IRK2_HUMAN, MYO9B_HUMAN, CTNL1_HUMAN, CARD6_HUMAN, ARY1_HUMAN, KCNG4_HUMAN, SMS2_HUMAN, CAH8_HUMAN, ZN133_HUMAN, GRAN_HUMAN, TADBP_HUMAN, TRIP4_HUMAN, CUL5_HUMAN, PSN1_HUMAN, FKB1A_HUMAN, S12A4_HUMAN, GRAP2_HUMAN, SP3_HUMAN, AXUD1_HUMAN, BRD8_HUMAN, ZNF25_HUMAN, BIM_HUMAN, TOM1_HUMAN, MGR7_HUMAN, CIAS1_HUMAN, GSTM4_HUMAN, NCKX1_HUMAN, NAMPT_HUMAN, FBX25_HUMAN, CSE1_HUMAN, ZN363_HUMAN, ZNF22_HUMAN, TBBX_HUMAN, FKBP5_HUMAN, HNRPU_HUMAN, IRK3_HUMAN, TBA1_HUMAN, HXA9_HUMAN, RABE1_HUMAN, DYL1_HUMAN, ZN161_HUMAN, GALT3_HUMAN, ZNT1_HUMAN, PPT2_HUMAN, RRS1_HUMAN, DNL4_HUMAN, M3K5_HUMAN, DET1_HUMAN, EYA1_HUMAN, HNRL1_HUMAN, GEMI5_HUMAN, TRI27_HUMAN, CD1D_HUMAN, ELL_HUMAN, STK39_HUMAN, GA45B_HUMAN, STXB3_HUMAN, CETN3_HUMAN, AADAT_HUMAN

-- 28 of 596--

GOID GO:0007275
TERM development
P-VALUE 5.30087764127439e-07
CORRECTED P-VALUE 0.000529027588599184
NUM_ANNOTATIONS 80 (of 2045)

ANNOTATED_GENES FLI1_HUMAN, IF16_HUMAN, ZNF7_HUMAN, NINJ1_HUMAN, OSTP_HUMAN, ANGP2_HUMAN, LAMC1_HUMAN, PKD1_HUMAN, GUSL2_HUMAN, ID3_HUMAN, BMP10_HUMAN, TR11B_HUMAN, ETS2_HUMAN, HEN2_HUMAN, HOP_HUMAN, TPM3_HUMAN, EMP3_HUMAN, SMDF_HUMAN, RREB1_HUMAN, SPHK1_HUMAN, RUNX1_HUMAN, POGZ_HUMAN, ARF6_HUMAN, APBA2_HUMAN, BORG1_HUMAN, HDAC4_HUMAN, ID2_HUMAN, ID1_HUMAN, RHG07_HUMAN, FZD1_HUMAN, SOCS6_HUMAN, LIS1_HUMAN, SIP1_HUMAN, FN14_HUMAN, SIRT1_HUMAN, ATRX_HUMAN, WNT7B_HUMAN, BRD8_HUMAN, KLF10_HUMAN, ANGL2_HUMAN, CBLN1_HUMAN, TAGL2_HUMAN, EMD_HUMAN, EZRI_HUMAN, FGF18_HUMAN, TRPS1_HUMAN, AA2AR_HUMAN, UT14C_HUMAN, JERKL_HUMAN, FUT8_HUMAN, SIAH1_HUMAN, PIM1_HUMAN, SPNXB_HUMAN, MKL2_HUMAN, UGRP2_HUMAN, ZNF22_HUMAN, SUFU_HUMAN, TPPC2_HUMAN, MEF2C_HUMAN, CDC42_HUMAN, HXA9_HUMAN, ATRN_HUMAN, EMP1_HUMAN, IDD_HUMAN, AGGF1_HUMAN, PPBT_HUMAN, KCNQ2_HUMAN, NF2L1_HUMAN, BB1_HUMAN, FLNA_HUMAN, CYTM_HUMAN, EYA1_HUMAN, DLX2_HUMAN, FZD2_HUMAN, NRG1_HUMAN, PEPP1_HUMAN, CD1D_HUMAN, GA45B_HUMAN, PO6F2_HUMAN, EPC1_HUMAN

-- 29 of 596--

GOID GO:0000122
TERM negative regulation of transcription from RNA polymerase II promoter
P-VALUE 6.90252024556312e-07
CORRECTED P-VALUE 0.000688871520507199
NUM_ANNOTATIONS 11 (of 74)
ANNOTATED_GENES MDM4_HUMAN, RB_HUMAN, ZN189_HUMAN, SLAP2_HUMAN, DRAP1_HUMAN, IRF2_HUMAN, SPI1_HUMAN, ZN202_HUMAN, KLF11_HUMAN, ZN174_HUMAN, KLF10_HUMAN

-- 30 of 596--

GOID GO:0043119
TERM positive regulation of physiological process
P-VALUE 8.88375908521214e-07
CORRECTED P-VALUE 0.000886599156704171
NUM_ANNOTATIONS 29 (of 470)
ANNOTATED_GENES TBBX_HUMAN, TNF10_HUMAN, CUL5_HUMAN, CASP3_HUMAN, IF16_HUMAN, FAF1_HUMAN, ATF4_HUMAN, SPHK1_HUMAN, RUNX1_HUMAN, CRSP6_HUMAN, NCK1_HUMAN, BIM_HUMAN, OSTP_HUMAN, CIAS1_HUMAN, ARF6_HUMAN, RB_HUMAN, BORG1_HUMAN, M3K5_HUMAN, FGF18_HUMAN, CASPA_HUMAN, BRCA1_HUMAN, GATA5_HUMAN, NARGL_HUMAN, SMRCD_HUMAN, NAMPT_HUMAN, CD1D_HUMAN, SRTD1_HUMAN, FIBA_HUMAN, MKL2_HUMAN

-- 31 of 596--

GOID GO:0009987
TERM cellular process
P-VALUE 1.56027957215125e-06
CORRECTED P-VALUE 0.00155715901300695
NUM_ANNOTATIONS 471 (of 18836)
ANNOTATED_GENES TRIM6_HUMAN, TXND5_HUMAN, TNF10_HUMAN, PACE1_HUMAN, IF16_HUMAN, MLP3B_HUMAN, FAF1_HUMAN, APBP2_HUMAN, PPIG_HUMAN, RP9_HUMAN, DYI2_HUMAN,

Biological Process 01-12-06.txt

RT18B_HUMAN, IBRD2_HUMAN, AP3M2_HUMAN, BIRC3_HUMAN, CCNT2_HUMAN, ANGP2_HUMAN, WDR33_HUMAN, AP4E1_HUMAN, PKD1_HUMAN, APC10_HUMAN, DCOR_HUMAN, BNIP2_HUMAN, B3GN1_HUMAN, LIPB2_HUMAN, SRTD1_HUMAN, TBA6_HUMAN, KP YM_HUMAN, TERF1_HUMAN, SYR_HUMAN, HOP_HUMAN, ACHB_HUMAN, HGD_HUMAN, SATT_HUMAN, OSR2_HUMAN, ZN646_HUMAN, FANCA_HUMAN, ZN264_HUMAN, RUNX3_HUMAN, TDG_HUMAN, ZN174_HUMAN, BCLX_HUMAN, UGPA1_HUMAN, APBA2_HUMAN, BLM_HUMAN, ZN143_HUMAN, IF4G3_HUMAN, DHSO_HUMAN, RFXAP_HUMAN, BRCA1_HUMAN, HCA66_HUMAN, ATF2_HUMAN, STX6_HUMAN, STK35_HUMAN, ING5_HUMAN, SOCS6_HUMAN, PCDG3_HUMAN, ZN222_HUMAN, RGR_HUMAN, CCR2_HUMAN, ATF4_HUMAN, FOXO1_HUMAN, ATRX_HUMAN, HCN1_HUMAN, HSP47_HUMAN, CV106_HUMAN, LIPB_HUMAN, PCDG2_HUMAN, KLF10_HUMAN, PDRN4_HUMAN, EZRI_HUMAN, ST1A3_HUMAN, TRPS1_HUMAN, ZFH2_HUMAN, ZN350_HUMAN, FA8_HUMAN, RNF6_HUMAN, NARGL_HUMAN, NUPL1_HUMAN, FETA_HUMAN, PHTF1_HUMAN, NISM_HUMAN, TRIM4_HUMAN, SODM_HUMAN, FIBA_HUMAN, RANB9_HUMAN, PIM1_HUMAN, IF5_HUMAN, NECP2_HUMAN, NR1H2_HUMAN, SUFU_HUMAN, CDC42_HUMAN, CERK1_HUMAN, AP4S1_HUMAN, PP1RA_HUMAN, WBS18_HUMAN, MTO1_HUMAN, RECK_HUMAN, CA022_HUMAN, PA24A_HUMAN, PLSB_HUMAN, MAF_HUMAN, TF3C4_HUMAN, TXND9_HUMAN, K2C8_HUMAN, MK06_HUMAN, PDE4A_HUMAN, SMRA3_HUMAN, HAP28_HUMAN, MFN1_HUMAN, ZBTB3_HUMAN, KLF11_HUMAN, FPGT_HUMAN, NIPBL_HUMAN, CDN1C_HUMAN, TF2H2_HUMAN, MN1_HUMAN, NMI_HUMAN, DRAP1_HUMAN, ZNF7_HUMAN, NINJ1_HUMAN, KLF7_HUMAN, FBX32_HUMAN, PTAFR_HUMAN, RPA2_HUMAN, ZBTB1_HUMAN, ZFP95_HUMAN, SETX_HUMAN, RB_HUMAN, ZNF12_HUMAN, GLYC_HUMAN, RASA1_HUMAN, SPOP_HUMAN, CBPA1_HUMAN, AT2B2_HUMAN, GNDS_HUMAN, CYC_HUMAN, STXB2_HUMAN, DOK1_HUMAN, TREM1_HUMAN, TR11B_HUMAN, NCBP2_HUMAN, UBP1_HUMAN, ETS2_HUMAN, POLH_HUMAN, RT18C_HUMAN, HEN2_HUMAN, TRI34_HUMAN, RAB10_HUMAN, AGM1_HUMAN, CDN2B_HUMAN, S23IP_HUMAN, EMP3_HUMAN, SETB1_HUMAN, SMCA5_HUMAN, RREB1_HUMAN, TNPO1_HUMAN, ETV5_HUMAN, CLPX_HUMAN, PTH2_HUMAN, ZFY_HUMAN, SUV91_HUMAN, SPEB_HUMAN, PUM2_HUMAN, M4K5_HUMAN, RS10_HUMAN, SALL3_HUMAN, MTAP_HUMAN, FZD1_HUMAN, FBX38_HUMAN, SIP1_HUMAN, ZN200_HUMAN, TCF7_HUMAN, DUS11_HUMAN, PANK2_HUMAN, SEP10_HUMAN, CASP3_HUMAN, FN14_HUMAN, ZN397_HUMAN, VPS4B_HUMAN, SIRT1_HUMAN, ARD1_HUMAN, AP3S2_HUMAN, C5AR_HUMAN, T2EA_HUMAN, ZCSL3_HUMAN, VAPB_HUMAN, CBLN1_HUMAN, RAB9A_HUMAN, NALDL_HUMAN, TEX10_HUMAN, REN3B_HUMAN, RN5A_HUMAN, EEA1_HUMAN, FGF18_HUMAN, SPH2_HUMAN, AA2AR_HUMAN, ZNF79_HUMAN, ZN217_HUMAN, UT14C_HUMAN, FUT8_HUMAN, IRF2_HUMAN, SIAH1_HUMAN, CAD22_HUMAN, ZN286_HUMAN, PO5FM_HUMAN, TPPC2_HUMAN, LYST_HUMAN, PO5FL_HUMAN, EMP1_HUMAN, MOB3_HUMAN, IDD_HUMAN, GPR86_HUMAN, TRI32_HUMAN, KELL_HUMAN, AFAD_HUMAN, ADML_HUMAN, TBB6_HUMAN, TF2AA_HUMAN, BB1_HUMAN, DCP1B_HUMAN, OBP2B_HUMAN, IF2P_HUMAN, ANGL7_HUMAN, FANCE_HUMAN, DHRS3_HUMAN, ICT1_HUMAN, T2FB_HUMAN, SIA10_HUMAN, RN146_HUMAN, ZF276_HUMAN, OST3B_HUMAN, PCDGB_HUMAN, GPR18_HUMAN, EXOS3_HUMAN, DLX2_HUMAN, S22A3_HUMAN, TRIPB_HUMAN, DNJA1_HUMAN, TBA2_HUMAN, PIM3_HUMAN, CSTF3_HUMAN, MK14_HUMAN, APG5_HUMAN, PARP4_HUMAN, TACD2_HUMAN, GIT2_HUMAN, SNX27_HUMAN, AF17_HUMAN, ACADM_HUMAN, TRPM3_HUMAN, STRN3_HUMAN, MELPH_HUMAN, PFTA_HUMAN, THA_HUMAN, ARFP1_HUMAN, SMRCD_HUMAN, ZN408_HUMAN, ZN223_HUMAN, LAT_HUMAN, BMP10_HUMAN, DYL2_HUMAN, P2Y14_HUMAN, PAPOG_HUMAN, CDR2_HUMAN, REN1_HUMAN, ZN492_HUMAN, NR1D1_HUMAN, SFTA2_HUMAN, NU160_HUMAN, FBX34_HUMAN, BET1_HUMAN, NUP50_HUMAN, TNR8_HUMAN, SLAP2_HUMAN, G6PE_HUMAN, RM19_HUMAN, BAZ1A_HUMAN, MPP8_HUMAN, KYNU_HUMAN, EAA2_HUMAN, ARF6_HUMAN, STAM1_HUMAN, PPBI_HUMAN, BORG1_HUMAN, PURA2_HUMAN, CADH4_HUMAN, GATA5_HUMAN, RPC2_HUMAN, RIOK3_HUMAN, BCL3_HUMAN, HMG2_HUMAN, AMFR1_HUMAN, FBX5_HUMAN, TSG6_HUMAN, LIS1_HUMAN, FTMT_HUMAN, DCMC_HUMAN, AK1C1_HUMAN, PPID_HUMAN, STX7_HUMAN, DAPP1_HUMAN, PUR1_HUMAN, PYR5_HUMAN, GPR83_HUMAN, WNT7B_HUMAN, CAR12_HUMAN, TBB4_HUMAN, PE2R2_HUMAN, ZNF10_HUMAN, PDPK1_HUMAN, INSI1_HUMAN, SON_HUMAN, AMFR2_HUMAN, PYRG_HUMAN, BAG4_HUMAN, NOP56_HUMAN, SEN2_HUMAN, SPNXB_HUMAN, MKL2_HUMAN, BCL9_HUMAN, UGRP2_HUMAN, UT14A_HUMAN, GTR3_HUMAN, LDLR_HUMAN, MEF2C_HUMAN, PRP17_HUMAN, UGPA2_HUMAN, HS105_HUMAN, AGGF1_HUMAN, WSB1_HUMAN, 5NT1B_HUMAN, CRSP6_HUMAN, KCNQ2_HUMAN, ZEP2_HUMAN, BCDO2_HUMAN, NF2L1_HUMAN, NEUL_HUMAN, PARVG_HUMAN, FLNA_HUMAN, KCMA1_HUMAN, ICAM1_HUMAN, CASPA_HUMAN, PCDGA_HUMAN, CCG1_HUMAN, NRG1_HUMAN, PFTK1_HUMAN, P2RY5_HUMAN, PEPP1_HUMAN, TRI12_HUMAN, PO6F2_HUMAN, CD97_HUMAN, UBP33_HUMAN, PCDG8_HUMAN, BAZ1B_HUMAN, EPC1_HUMAN, FLI1_HUMAN, MK67I_HUMAN, CSTF1_HUMAN, CREB1_HUMAN, CDN2D_HUMAN, TGDS_HUMAN, MTERF_HUMAN, SCRT2_HUMAN, OSTP_HUMAN, CN108_HUMAN, LAMC1_HUMAN, MPRB_HUMAN, ZN516_HUMAN, TTRAP_HUMAN, ZN189_HUMAN, ACHA_HUMAN, PHF20_HUMAN, ID3_HUMAN, PLRG1_HUMAN, C43BP_HUMAN, PUS3_HUMAN, UB2J1_HUMAN, ZN430_HUMAN, B4GT4_HUMAN, PLK3_HUMAN, INGR1_HUMAN, CPNE1_HUMAN, MSH2_HUMAN, CO9A3_HUMAN, GEMI6_HUMAN, TOB2_HUMAN, UBP47_HUMAN, MIZF_HUMAN, SPHK1_HUMAN, BRD1_HUMAN, NCK1_HUMAN, RUNX1_HUMAN,

Biological Process 01-12-06.txt

STAG2_HUMAN, SPI1_HUMAN, ZN202_HUMAN, SNX18_HUMAN, RAD18_HUMAN, APG7L_HUMAN, PP2CB_HUMAN, RAP2B_HUMAN, NMT1_HUMAN, CB80_HUMAN, MDM4_HUMAN, MSH6_HUMAN, IDS_HUMAN, SF3B3_HUMAN, HDAC4_HUMAN, ID2_HUMAN, ID1_HUMAN, MGAT2_HUMAN, RHG07_HUMAN, OSR11_HUMAN, IRK2_HUMAN, MYO9B_HUMAN, CTNL1_HUMAN, CARD6_HUMAN, KCNG4_HUMAN, SMS2_HUMAN, CAH8_HUMAN, ZN133_HUMAN, GRAN_HUMAN, TADBP_HUMAN, TRIP4_HUMAN, CUL5_HUMAN, PSN1_HUMAN, FKB1A_HUMAN, S12A4_HUMAN, GRAP2_HUMAN, SP3_HUMAN, AXUD1_HUMAN, BRD8_HUMAN, ZNF25_HUMAN, BIM_HUMAN, TOM1_HUMAN, MGR7_HUMAN, CIAS1_HUMAN, NCKX1_HUMAN, NAMPT_HUMAN, FBX25_HUMAN, CSE1_HUMAN, ZN363_HUMAN, PLAK_HUMAN, ZNF22_HUMAN, TBBX_HUMAN, FKBP5_HUMAN, HNRPU_HUMAN, IRK3_HUMAN, TBA1_HUMAN, HXA9_HUMAN, RAB1_HUMAN, DYL1_HUMAN, ZN161_HUMAN, ZNT1_HUMAN, PPT2_HUMAN, RRS1_HUMAN, DNL4_HUMAN, M3K5_HUMAN, DET1_HUMAN, EYA1_HUMAN, HNRL1_HUMAN, GEMI5_HUMAN, TRI27_HUMAN, FZD2_HUMAN, RGP2_HUMAN, CD1D_HUMAN, ELL_HUMAN, STK39_HUMAN, GA45B_HUMAN, STXB3_HUMAN, CETN3_HUMAN

-- 32 of 596--

GOID GO:0008283
TERM cell proliferation
P-VALUE 1.59258203397796e-06
CORRECTED P-VALUE 0.00158939686991
NUM_ANNOTATIONS 31 (of 538)
ANNOTATED_GENES CDN1C_HUMAN, TACD2_HUMAN, CUL5_HUMAN, TNFR8_HUMAN, CDN2B_HUMAN, EMP3_HUMAN, IF16_HUMAN, EMP1_HUMAN, TOB2_HUMAN, CDN2D_HUMAN, SPHK1_HUMAN, NCK1_HUMAN, RUNX3_HUMAN, OSTP_HUMAN, KLF10_HUMAN, INSI1_HUMAN, MDM4_HUMAN, FGF18_HUMAN, BRCA1_HUMAN, NAMPT_HUMAN, CSE1_HUMAN, TRI27_HUMAN, BMP10_HUMAN, IRF2_HUMAN, HAP28_HUMAN, ING5_HUMAN, SRTD1_HUMAN, FIBA_HUMAN, KLF11_HUMAN, PIM1_HUMAN, UGRP2_HUMAN

-- 33 of 596--

GOID GO:0042127
TERM regulation of cell proliferation
P-VALUE 2.07980767978865e-06
CORRECTED P-VALUE 0.00207564806442908
NUM_ANNOTATIONS 21 (of 287)
ANNOTATED_GENES CDN1C_HUMAN, CUL5_HUMAN, TNFR8_HUMAN, CDN2B_HUMAN, EMP3_HUMAN, TOB2_HUMAN, CDN2D_HUMAN, SPHK1_HUMAN, NCK1_HUMAN, OSTP_HUMAN, KLF10_HUMAN, MDM4_HUMAN, FGF18_HUMAN, BRCA1_HUMAN, NAMPT_HUMAN, BMP10_HUMAN, ING5_HUMAN, SRTD1_HUMAN, FIBA_HUMAN, KLF11_HUMAN, UGRP2_HUMAN

-- 34 of 596--

GOID GO:0042981
TERM regulation of apoptosis
P-VALUE 2.86969737276697e-06
CORRECTED P-VALUE 0.00286395797802144
NUM_ANNOTATIONS 24 (of 367)
ANNOTATED_GENES TBBX_HUMAN, TNF10_HUMAN, CUL5_HUMAN, CASP3_HUMAN, IF16_HUMAN, PSN1_HUMAN, FAF1_HUMAN, FOXO1_HUMAN, SPHK1_HUMAN, CAR12_HUMAN, BIRC3_HUMAN, BIM_HUMAN, OSTP_HUMAN, BCLX_HUMAN, CIAS1_HUMAN, SON_HUMAN, M3K5_HUMAN, CASPA_HUMAN, BAG4_HUMAN, BRCA1_HUMAN, CYC_HUMAN, BNIP2_HUMAN, CARD6_HUMAN, PIM1_HUMAN

-- 35 of 596--

GOID GO:0043067
TERM regulation of programmed cell death
P-VALUE 3.30060679881348e-06
CORRECTED P-VALUE 0.00329400558521585
NUM_ANNOTATIONS 24 (of 370)
ANNOTATED_GENES TBBX_HUMAN, TNF10_HUMAN, CUL5_HUMAN, CASP3_HUMAN, IF16_HUMAN, PSN1_HUMAN, FAF1_HUMAN, FOXO1_HUMAN, SPHK1_HUMAN, CAR12_HUMAN, BIRC3_HUMAN, BIM_HUMAN, OSTP_HUMAN, BCLX_HUMAN, CIAS1_HUMAN, SON_HUMAN, M3K5_HUMAN, CASPA_HUMAN, BAG4_HUMAN, BRCA1_HUMAN, CYC_HUMAN, BNIP2_HUMAN, CARD6_HUMAN, PIM1_HUMAN

-- 36 of 596--

GOID GO:0051649
TERM establishment of cellular localization

Biological Process 01-12-06.txt

P-VALUE 3.48654209773677e-06
CORRECTED P-VALUE 0.00347956901354129
NUM_ANNOTATIONS 42 (of 882)
ANNOTATED_GENES STX7_HUMAN, VPS4B_HUMAN, FAF1_HUMAN, APBP2_HUMAN, DYI2_HUMAN, AP3M2_HUMAN, AP3S2_HUMAN, TBB4_HUMAN, TOM1_HUMAN, MELPH_HUMAN, CN108_HUMAN, RAB9A_HUMAN, ARFP1_HUMAN, REN3B_HUMAN, EEA1_HUMAN, TRPS1_HUMAN, AP4E1_HUMAN, CSE1_HUMAN, STXB2_HUMAN, DYL2_HUMAN, TBA6_HUMAN, NCBP2_HUMAN, TBBX_HUMAN, RAB10_HUMAN, TPPC2_HUMAN, NU160_HUMAN, BET1_HUMAN, NUP50_HUMAN, LYST_HUMAN, AP4S1_HUMAN, TBA1_HUMAN, S23IP_HUMAN, TNPO1_HUMAN, TBB6_HUMAN, CB80_HUMAN, ARF6_HUMAN, STAM1_HUMAN, BCL3_HUMAN, STX6_HUMAN, MYO9B_HUMAN, LIS1_HUMAN, TBA2_HUMAN

-- 37 of 596--

GOID GO:0006950
TERM response to stress
P-VALUE 3.56049154524857e-06
CORRECTED P-VALUE 0.00355337056215808
NUM_ANNOTATIONS 53 (of 1230)
ANNOTATED_GENES MK14_HUMAN, PARP4_HUMAN, TF2H2_HUMAN, CCR2_HUMAN, IF16_HUMAN, ATF4_HUMAN, NMI_HUMAN, ATRX_HUMAN, GRAP2_HUMAN, NINJ1_HUMAN, HSP47_HUMAN, C5AR_HUMAN, OSTP_HUMAN, PTAFR_HUMAN, CIAS1_HUMAN, WDR33_HUMAN, SPH2_HUMAN, AA2AR_HUMAN, FA8_HUMAN, SODM_HUMAN, TREM1_HUMAN, FIBA_HUMAN, UBP1_HUMAN, POLH_HUMAN, INGR1_HUMAN, LYST_HUMAN, SNN_HUMAN, MSH2_HUMAN, ATRN_HUMAN, FANCA_HUMAN, HS105_HUMAN, SLAP2_HUMAN, TLR7_HUMAN, TDG_HUMAN, ZN161_HUMAN, ADML_HUMAN, RAD18_HUMAN, NF2L1_HUMAN, MSH6_HUMAN, ANGL7_HUMAN, BLM_HUMAN, FANCE_HUMAN, DNL4_HUMAN, M3K5_HUMAN, HDAC4_HUMAN, BRCA1_HUMAN, M4K5_HUMAN, HMG2_HUMAN, TSG6_HUMAN, STK39_HUMAN, GA45B_HUMAN, DNJA1_HUMAN, CD97_HUMAN

-- 38 of 596--

GOID GO:0051641
TERM cellular localization
P-VALUE 4.00838863429694e-06
CORRECTED P-VALUE 0.00400037185702834
NUM_ANNOTATIONS 42 (of 887)
ANNOTATED_GENES STX7_HUMAN, VPS4B_HUMAN, FAF1_HUMAN, APBP2_HUMAN, DYI2_HUMAN, AP3M2_HUMAN, AP3S2_HUMAN, TBB4_HUMAN, TOM1_HUMAN, MELPH_HUMAN, CN108_HUMAN, RAB9A_HUMAN, ARFP1_HUMAN, REN3B_HUMAN, EEA1_HUMAN, TRPS1_HUMAN, AP4E1_HUMAN, CSE1_HUMAN, STXB2_HUMAN, DYL2_HUMAN, TBA6_HUMAN, NCBP2_HUMAN, TBBX_HUMAN, RAB10_HUMAN, TPPC2_HUMAN, NU160_HUMAN, BET1_HUMAN, NUP50_HUMAN, LYST_HUMAN, AP4S1_HUMAN, TBA1_HUMAN, S23IP_HUMAN, TNPO1_HUMAN, TBB6_HUMAN, CB80_HUMAN, ARF6_HUMAN, STAM1_HUMAN, BCL3_HUMAN, STX6_HUMAN, MYO9B_HUMAN, LIS1_HUMAN, TBA2_HUMAN

-- 39 of 596--

GOID GO:0046907
TERM intracellular transport
P-VALUE 6.71647056803164e-06
CORRECTED P-VALUE 0.00670303762689558
NUM_ANNOTATIONS 41 (of 875)
ANNOTATED_GENES STX7_HUMAN, VPS4B_HUMAN, FAF1_HUMAN, APBP2_HUMAN, DYI2_HUMAN, AP3M2_HUMAN, AP3S2_HUMAN, TBB4_HUMAN, TOM1_HUMAN, MELPH_HUMAN, CN108_HUMAN, RAB9A_HUMAN, ARFP1_HUMAN, REN3B_HUMAN, EEA1_HUMAN, TRPS1_HUMAN, AP4E1_HUMAN, CSE1_HUMAN, STXB2_HUMAN, DYL2_HUMAN, TBA6_HUMAN, NCBP2_HUMAN, TBBX_HUMAN, RAB10_HUMAN, TPPC2_HUMAN, NU160_HUMAN, BET1_HUMAN, NUP50_HUMAN, LYST_HUMAN, AP4S1_HUMAN, TBA1_HUMAN, S23IP_HUMAN, TNPO1_HUMAN, TBB6_HUMAN, CB80_HUMAN, ARF6_HUMAN, STAM1_HUMAN, BCL3_HUMAN, STX6_HUMAN, MYO9B_HUMAN, TBA2_HUMAN

Cellular Component.txt

Terms from the component ontology exceeding a pvalue cutoff of 0.01.

The total number of genes used to calculate the background distribution of GO terms is 28042.

-- 1 of 115--

GOID GO:0043231

TERM intracellular membrane-bound organelle

P-VALUE 1.6311971352621e-27

CORRECTED P-VALUE 3.29501821322945e-25

NUM_ANNOTATIONS 285 (of 7253)

ANNOTATED_GENES TXND5_HUMAN, PACE1_HUMAN, IF16_HUMAN, MLP3B_HUMAN, FAF1_HUMAN, APBP2_HUMAN, PPIG_HUMAN, RP9_HUMAN, RT18B_HUMAN, AP3M2_HUMAN, CCNT2_HUMAN, WDR33_HUMAN, AP4E1_HUMAN, APC10_HUMAN, B3GN1_HUMAN, TERF1_HUMAN, HOP_HUMAN, ZN646_HUMAN, FANCA_HUMAN, ZN264_HUMAN, RUNX3_HUMAN, TDG_HUMAN, ZN174_HUMAN, BCLX_HUMAN, BLM_HUMAN, ZN143_HUMAN, RFXAP_HUMAN, BRCA1_HUMAN, HCA66_HUMAN, ATF2_HUMAN, STX6_HUMAN, STK35_HUMAN, ZN222_HUMAN, ATF4_HUMAN, FOXO1_HUMAN, ATRX_HUMAN, HSP47_HUMAN, CV106_HUMAN, LIPB_HUMAN, KLF10_HUMAN, LBR_HUMAN, EMD_HUMAN, TRPS1_HUMAN, ZFH2_HUMAN, ZN350_HUMAN, NARGL_HUMAN, NUPL1_HUMAN, PHTF1_HUMAN, JERKL_HUMAN, NISM_HUMAN, SODM_HUMAN, RANB9_HUMAN, PIM1_HUMAN, NECP2_HUMAN, NR1H2_HUMAN, SUFU_HUMAN, RBM12_HUMAN, AP4S1_HUMAN, PP1RA_HUMAN, YPEL2_HUMAN, MTO1_HUMAN, T103_HUMAN, CA022_HUMAN, PLSB_HUMAN, MAF_HUMAN, TF3C4_HUMAN, SMRA3_HUMAN, MFN1_HUMAN, ZBTB3_HUMAN, SK2L2_HUMAN, KLF11_HUMAN, G6B_HUMAN, NIPBL_HUMAN, CDN1C_HUMAN, TF2H2_HUMAN, ANM6_HUMAN, DRAP1_HUMAN, ZNF7_HUMAN, KLF7_HUMAN, MUTA_HUMAN, RPA2_HUMAN, ZBTB1_HUMAN, ZFP95_HUMAN, SETX_HUMAN, GIMA1_HUMAN, RB_HUMAN, ZNF12_HUMAN, SPOP_HUMAN, CYC_HUMAN, DDX31_HUMAN, UBP1_HUMAN, NCBP2_HUMAN, ETS2_HUMAN, POLH_HUMAN, RT18C_HUMAN, HEN2_HUMAN, S23IP_HUMAN, SETB1_HUMAN, SMCA5_HUMAN, RREB1_HUMAN, TNPO1_HUMAN, ETV5_HUMAN, CLPX_HUMAN, PTH2_HUMAN, ZFY_HUMAN, SUV91_HUMAN, SPEB_HUMAN, SALL3_HUMAN, FBX38_HUMAN, SIP1_HUMAN, ZN200_HUMAN, TCF7_HUMAN, DUS11_HUMAN, SEP10_HUMAN, ZN397_HUMAN, VPS4B_HUMAN, SIRT1_HUMAN, ARD1_HUMAN, AP3S2_HUMAN, T2EA_HUMAN, RT27_HUMAN, RAB9A_HUMAN, TEX10_HUMAN, REN3B_HUMAN, RM46_HUMAN, EEA1_HUMAN, SPH2_HUMAN, ZNF79_HUMAN, ZN217_HUMAN, UT14C_HUMAN, FUT8_HUMAN, IRF2_HUMAN, SIAH1_HUMAN, ZN286_HUMAN, PO5FM_HUMAN, TPPC2_HUMAN, LYST_HUMAN, PO5FL_HUMAN, MOB3_HUMAN, TRI32_HUMAN, TF2AA_HUMAN, DCP1B_HUMAN, PRS10_HUMAN, FANCE_HUMAN, SIA10_HUMAN, T2FB_HUMAN, ZF276_HUMAN, OST3B_HUMAN, EXOS3_HUMAN, HUCE1_HUMAN, DLX2_HUMAN, RM35_HUMAN, TRIPB_HUMAN, CSTF3_HUMAN, APG5_HUMAN, MK14_HUMAN, PARP4_HUMAN, AF17_HUMAN, ACADM_HUMAN, STRN3_HUMAN, THA_HUMAN, GIMA5_HUMAN, ARFP1_HUMAN, SMRCD_HUMAN, ZN223_HUMAN, ZN408_HUMAN, DYI3_HUMAN, PAPOG_HUMAN, CDR2_HUMAN, NR1D1_HUMAN, ZN492_HUMAN, NU160_HUMAN, BET1_HUMAN, NUP50_HUMAN, G6PE_HUMAN, SLAP2_HUMAN, RM19_HUMAN, BAZ1A_HUMAN, MPP8_HUMAN, MOL1A_HUMAN, ARF6_HUMAN, RPC2_HUMAN, GATA5_HUMAN, BCL3_HUMAN, HMG2_HUMAN, LIS1_HUMAN, FTMT_HUMAN, DCMC_HUMAN, STX7_HUMAN, K0690_HUMAN, ZNF10_HUMAN, SON_HUMAN, AMFR2_HUMAN, NOP56_HUMAN, GLI4_HUMAN, SEN2_HUMAN, MKL2_HUMAN, BCL9_HUMAN, SPNXB_HUMAN, UT14A_HUMAN, MEF2C_HUMAN, PRP17_HUMAN, CRSP6_HUMAN, ANR12_HUMAN, ZEP2_HUMAN, NF2L1_HUMAN, NEUL_HUMAN, WDR3_HUMAN, PFTK1_HUMAN, PEPP1_HUMAN, PO6F2_HUMAN, BAZ1B_HUMAN, EPC1_HUMAN, FLI1_HUMAN, MK67I_HUMAN, CSTF1_HUMAN, ZCHC6_HUMAN, DDX52_HUMAN, CDN2D_HUMAN, CREB1_HUMAN, MTERF_HUMAN, SCRT2_HUMAN, CN108_HUMAN, ZN516_HUMAN, TTRAP_HUMAN, ZN189_HUMAN, PHF20_HUMAN, ID3_HUMAN, PLRG1_HUMAN, PUS3_HUMAN, UB2J1_HUMAN, ZN430_HUMAN, B4GT4_HUMAN, MSH2_HUMAN, MIZF_HUMAN, TOB2_HUMAN, GEMI6_HUMAN, BRD1_HUMAN, RUNX1_HUMAN, STAG2_HUMAN, POGZ_HUMAN, SPI1_HUMAN, ZN202_HUMAN, SNX18_HUMAN, RAD18_HUMAN, CB80_HUMAN, MDM4_HUMAN, SF3B3_HUMAN, MSH6_HUMAN, IDS_HUMAN, HDAC4_HUMAN, ID2_HUMAN, MGAT2_HUMAN, ID1_HUMAN, SMS2_HUMAN, ZN133_HUMAN, TADBP_HUMAN, TRIP4_HUMAN, PSN1_HUMAN, SP3_HUMAN, AXUD1_HUMAN, BRD8_HUMAN, ZNF25_HUMAN, TOM1_HUMAN, CSE1_HUMAN, TDIF1_HUMAN, CSR2B_HUMAN, ZNF22_HUMAN, FKBP5_HUMAN, HNRPU_HUMAN, HXA9_HUMAN, RABE1_HUMAN, RT31_HUMAN, GALT3_HUMAN, ZN161_HUMAN, PPT2_HUMAN, RRS1_HUMAN, DNL4_HUMAN, DET1_HUMAN, EYA1_HUMAN, GEMI5_HUMAN, TRI27_HUMAN, HNRLL_HUMAN, ELL_HUMAN, STK39_HUMAN

-- 2 of 115--

GOID GO:0043227

TERM membrane-bound organelle

P-VALUE 1.83781266803964e-27

CORRECTED P-VALUE 3.71238158944008e-25

Cellular Component.txt

NUM_ANNOTATIONS 285 (of 7258)

ANNOTATED_GENES TXND5_HUMAN, PACE1_HUMAN, IF16_HUMAN, MLP3B_HUMAN, FAF1_HUMAN, APBP2_HUMAN, PPIG_HUMAN, RP9_HUMAN, RT18B_HUMAN, AP3M2_HUMAN, CCNT2_HUMAN, WDR33_HUMAN, AP4E1_HUMAN, APC10_HUMAN, B3GN1_HUMAN, TERF1_HUMAN, HOP_HUMAN, ZN646_HUMAN, FANCA_HUMAN, ZN264_HUMAN, RUNX3_HUMAN, TDG_HUMAN, ZN174_HUMAN, BCLX_HUMAN, BLM_HUMAN, ZN143_HUMAN, RFXAP_HUMAN, BRCA1_HUMAN, HCA66_HUMAN, ATF2_HUMAN, STX6_HUMAN, STK35_HUMAN, ZN222_HUMAN, ATF4_HUMAN, FOXO1_HUMAN, ATRX_HUMAN, HSP47_HUMAN, CV106_HUMAN, LIPB_HUMAN, KLF10_HUMAN, LBR_HUMAN, EMD_HUMAN, TRPS1_HUMAN, ZFHX2_HUMAN, ZN350_HUMAN, NARGL_HUMAN, NUPL1_HUMAN, PHTF1_HUMAN, JERKL_HUMAN, NISM_HUMAN, SODM_HUMAN, RANB9_HUMAN, PIM1_HUMAN, NECP2_HUMAN, NR1H2_HUMAN, SUFU_HUMAN, RBM12_HUMAN, AP4S1_HUMAN, PP1RA_HUMAN, YPEL2_HUMAN, MTO1_HUMAN, T103_HUMAN, CA022_HUMAN, PLSB_HUMAN, MAF_HUMAN, TF3C4_HUMAN, SMRA3_HUMAN, MFN1_HUMAN, ZBTB3_HUMAN, SK2L2_HUMAN, KLF11_HUMAN, G6B_HUMAN, NIPBL_HUMAN, CDN1C_HUMAN, TF2H2_HUMAN, ANM6_HUMAN, DRAP1_HUMAN, ZNF7_HUMAN, KLF7_HUMAN, MUTA_HUMAN, RPA2_HUMAN, ZBTB1_HUMAN, ZFP95_HUMAN, SETX_HUMAN, GIMA1_HUMAN, RB_HUMAN, ZNF12_HUMAN, SPOP_HUMAN, CYC_HUMAN, DDX31_HUMAN, UBP1_HUMAN, NCBP2_HUMAN, ETS2_HUMAN, POLH_HUMAN, RT18C_HUMAN, HEN2_HUMAN, S23IP_HUMAN, SETB1_HUMAN, SMCA5_HUMAN, RREB1_HUMAN, TNPO1_HUMAN, ETV5_HUMAN, CLPX_HUMAN, PTH2_HUMAN, ZFY_HUMAN, SUV91_HUMAN, SPEB_HUMAN, SALL3_HUMAN, FBX38_HUMAN, SIP1_HUMAN, ZN200_HUMAN, TCF7_HUMAN, DUS11_HUMAN, SEP10_HUMAN, ZN397_HUMAN, VPS4B_HUMAN, SIRT1_HUMAN, ARD1_HUMAN, AP3S2_HUMAN, T2EA_HUMAN, RT27_HUMAN, RAB9A_HUMAN, TEX10_HUMAN, REN3B_HUMAN, RM46_HUMAN, EEA1_HUMAN, SPH2_HUMAN, ZNF79_HUMAN, ZN217_HUMAN, UT14C_HUMAN, FUT8_HUMAN, IRF2_HUMAN, SIAH1_HUMAN, ZN286_HUMAN, PO5FM_HUMAN, TPPC2_HUMAN, LYST_HUMAN, PO5FL_HUMAN, MOB3_HUMAN, TRI32_HUMAN, TF2AA_HUMAN, DCP1B_HUMAN, PRS10_HUMAN, FANCE_HUMAN, SIA10_HUMAN, T2FB_HUMAN, ZF276_HUMAN, OST3B_HUMAN, EXOS3_HUMAN, HUCE1_HUMAN, DLX2_HUMAN, RM35_HUMAN, TRIPB_HUMAN, CSTF3_HUMAN, APG5_HUMAN, MK14_HUMAN, PARP4_HUMAN, AF17_HUMAN, ACADM_HUMAN, STRN3_HUMAN, THA_HUMAN, GIMA5_HUMAN, ARFP1_HUMAN, SMRCD_HUMAN, ZN223_HUMAN, ZN408_HUMAN, DYI3_HUMAN, PAPOG_HUMAN, CDR2_HUMAN, NR1D1_HUMAN, ZN492_HUMAN, NU160_HUMAN, BET1_HUMAN, NUP50_HUMAN, G6PE_HUMAN, SLAP2_HUMAN, RM19_HUMAN, BAZ1A_HUMAN, MPP8_HUMAN, MOL1A_HUMAN, ARF6_HUMAN, RPC2_HUMAN, GATA5_HUMAN, BCL3_HUMAN, HMG2_HUMAN, LIS1_HUMAN, FTMT_HUMAN, DCMC_HUMAN, STX7_HUMAN, K0690_HUMAN, ZNF10_HUMAN, SON_HUMAN, AMFR2_HUMAN, NOP56_HUMAN, GLI4_HUMAN, SEN2_HUMAN, MKL2_HUMAN, BCL9_HUMAN, SPNXB_HUMAN, UT14A_HUMAN, MEF2C_HUMAN, PRP17_HUMAN, CRSP6_HUMAN, ANR12_HUMAN, ZEP2_HUMAN, NF2L1_HUMAN, NEUL_HUMAN, WDR3_HUMAN, PFTK1_HUMAN, PEPP1_HUMAN, PO6F2_HUMAN, BAZ1B_HUMAN, EPC1_HUMAN, FLI1_HUMAN, MK67I_HUMAN, CSTF1_HUMAN, ZCHC6_HUMAN, DDX52_HUMAN, CDN2D_HUMAN, CREB1_HUMAN, MTERF_HUMAN, SCRT2_HUMAN, CN108_HUMAN, ZN516_HUMAN, TTRAP_HUMAN, ZN189_HUMAN, PHF20_HUMAN, ID3_HUMAN, PLRG1_HUMAN, PUS3_HUMAN, UB2J1_HUMAN, ZN430_HUMAN, B4GT4_HUMAN, MSH2_HUMAN, MIZF_HUMAN, TOB2_HUMAN, GEMI6_HUMAN, BRD1_HUMAN, RUNX1_HUMAN, STAG2_HUMAN, POGZ_HUMAN, SPI1_HUMAN, ZN202_HUMAN, SNX18_HUMAN, RAD18_HUMAN, CB80_HUMAN, MDM4_HUMAN, SF3B3_HUMAN, MSH6_HUMAN, IDS_HUMAN, HDAC4_HUMAN, ID2_HUMAN, MGAT2_HUMAN, ID1_HUMAN, SMS2_HUMAN, ZN133_HUMAN, TADBP_HUMAN, TRIP4_HUMAN, PSN1_HUMAN, SP3_HUMAN, AXUD1_HUMAN, BRD8_HUMAN, ZNF25_HUMAN, TOM1_HUMAN, CSE1_HUMAN, TDIF1_HUMAN, CSR2B_HUMAN, ZNF22_HUMAN, FKBP5_HUMAN, HNRPU_HUMAN, HXA9_HUMAN, RABE1_HUMAN, RT31_HUMAN, GALT3_HUMAN, ZN161_HUMAN, PPT2_HUMAN, RRS1_HUMAN, DNL4_HUMAN, DET1_HUMAN, EYA1_HUMAN, GEMI5_HUMAN, TRI27_HUMAN, HNRL1_HUMAN, ELL_HUMAN, STK39_HUMAN

-- 3 of 115--

GOID GO:0043229

TERM intracellular organelle

P-VALUE 2.21978712575292e-22

CORRECTED P-VALUE 4.4839699940209e-20

NUM_ANNOTATIONS 313 (of 8909)

ANNOTATED_GENES TXND5_HUMAN, PACE1_HUMAN, IF16_HUMAN, MLP3B_HUMAN, FAF1_HUMAN, APBP2_HUMAN, PPIG_HUMAN, RP9_HUMAN, DYI2_HUMAN, RT18B_HUMAN, AP3M2_HUMAN, CCNT2_HUMAN, WDR33_HUMAN, AP4E1_HUMAN, APC10_HUMAN, B3GN1_HUMAN, TBA6_HUMAN, TERF1_HUMAN, HOP_HUMAN, TPM3_HUMAN, ZN646_HUMAN, FANCA_HUMAN, ZN264_HUMAN, RUNX3_HUMAN, TDG_HUMAN, ZN174_HUMAN, BCLX_HUMAN, BLM_HUMAN, ZN143_HUMAN, RFXAP_HUMAN, BRCA1_HUMAN, HCA66_HUMAN, ATF2_HUMAN, STX6_HUMAN, STK35_HUMAN, ZN222_HUMAN, ATF4_HUMAN, FOXO1_HUMAN, MYPT1_HUMAN, ATRX_HUMAN, HSP47_HUMAN, CV106_HUMAN, LIPB_HUMAN, KLF10_HUMAN, LBR_HUMAN, EMD_HUMAN, EZRI_HUMAN, TRPS1_HUMAN,

Cellular Component.txt

ZFH2_HUMAN, ZN350_HUMAN, NARGL_HUMAN, NUPL1_HUMAN, PHTF1_HUMAN, JERKL_HUMAN, NISM_HUMAN, SODM_HUMAN, RANB9_HUMAN, PIM1_HUMAN, NECP2_HUMAN, NR1H2_HUMAN, SUFU_HUMAN, RBM12_HUMAN, AP4S1_HUMAN, PP1RA_HUMAN, YPEL2_HUMAN, MTO1_HUMAN, T103_HUMAN, CA022_HUMAN, PLSB_HUMAN, MAF_HUMAN, TF3C4_HUMAN, K2C8_HUMAN, SMRA3_HUMAN, MFN1_HUMAN, ZBTB3_HUMAN, SK2L2_HUMAN, KLF11_HUMAN, NIPBL_HUMAN, G6B_HUMAN, CDN1C_HUMAN, TF2H2_HUMAN, ANM6_HUMAN, DRAP1_HUMAN, ZNF7_HUMAN, KLF7_HUMAN, MUTA_HUMAN, RPA2_HUMAN, ZBTB1_HUMAN, ZFP95_HUMAN, SETX_HUMAN, GIM1_HUMAN, RB_HUMAN, ZNF12_HUMAN, SPOP_HUMAN, CYC_HUMAN, DDX31_HUMAN, UBP1_HUMAN, NCBP2_HUMAN, ETS2_HUMAN, SYNE2_HUMAN, POLH_HUMAN, RT18C_HUMAN, HEN2_HUMAN, S23IP_HUMAN, SETB1_HUMAN, SMCA5_HUMAN, RREB1_HUMAN, TNPO1_HUMAN, ETV5_HUMAN, CLPX_HUMAN, PTH2_HUMAN, ZFY_HUMAN, SUV91_HUMAN, SPEB_HUMAN, RS10_HUMAN, SALL3_HUMAN, FBX38_HUMAN, SIP1_HUMAN, ZN200_HUMAN, TCF7_HUMAN, DUS11_HUMAN, SEP10_HUMAN, ZN397_HUMAN, VPS4B_HUMAN, SIRT1_HUMAN, ARD1_HUMAN, AP3S2_HUMAN, T2EA_HUMAN, RT27_HUMAN, RAB9A_HUMAN, TEX10_HUMAN, REN3B_HUMAN, RM46_HUMAN, EEA1_HUMAN, SPH2_HUMAN, ZNF79_HUMAN, ZN217_HUMAN, UT14C_HUMAN, FUT8_HUMAN, IRF2_HUMAN, SIAH1_HUMAN, ZN286_HUMAN, PO5FM_HUMAN, TPPC2_HUMAN, LYST_HUMAN, PO5FL_HUMAN, MOB3_HUMAN, TRI32_HUMAN, KELL_HUMAN, AFAD_HUMAN, TF2AA_HUMAN, TBB6_HUMAN, DCP1B_HUMAN, PRS10_HUMAN, FANCE_HUMAN, T2FB_HUMAN, SIA10_HUMAN, ZF276_HUMAN, OST3B_HUMAN, EXOS3_HUMAN, HUCE1_HUMAN, DLX2_HUMAN, RM35_HUMAN, TRIPB_HUMAN, TBA2_HUMAN, CSTF3_HUMAN, APG5_HUMAN, MK14_HUMAN, PARP4_HUMAN, AF17_HUMAN, ACADM_HUMAN, STRN3_HUMAN, THA_HUMAN, GIMA5_HUMAN, ARFP1_HUMAN, SMRCD_HUMAN, ZN408_HUMAN, ZN223_HUMAN, DYL2_HUMAN, DYI3_HUMAN, PAPOG_HUMAN, CDR2_HUMAN, NR1D1_HUMAN, ZN492_HUMAN, NU160_HUMAN, BET1_HUMAN, NUP50_HUMAN, G6PE_HUMAN, SLAP2_HUMAN, RM19_HUMAN, BAZ1A_HUMAN, MPP8_HUMAN, MOL1A_HUMAN, ARF6_HUMAN, BORG1_HUMAN, GATA5_HUMAN, RPC2_HUMAN, BCL3_HUMAN, HMG2_HUMAN, LIS1_HUMAN, FTMT_HUMAN, DCMC_HUMAN, STX7_HUMAN, K0690_HUMAN, KLC8_HUMAN, TBB4_HUMAN, ZNF10_HUMAN, SON_HUMAN, AMFR2_HUMAN, NOP56_HUMAN, GLI4_HUMAN, SEN2_HUMAN, SPNXB_HUMAN, MKL2_HUMAN, BCL9_HUMAN, UT14A_HUMAN, MEF2C_HUMAN, PRP17_HUMAN, CRSP6_HUMAN, ANR12_HUMAN, ZEP2_HUMAN, NF2L1_HUMAN, NEUL_HUMAN, PARVG_HUMAN, FLNA_HUMAN, WDR3_HUMAN, PFTK1_HUMAN, PEPP1_HUMAN, PO6F2_HUMAN, BAZ1B_HUMAN, EPC1_HUMAN, FLI1_HUMAN, MK67I_HUMAN, CSTF1_HUMAN, ZCHC6_HUMAN, DDX52_HUMAN, CDN2D_HUMAN, CREB1_HUMAN, MTERF_HUMAN, SCRT2_HUMAN, CN108_HUMAN, ZN516_HUMAN, TTRAP_HUMAN, ZN189_HUMAN, PHF20_HUMAN, ID3_HUMAN, PLRG1_HUMAN, PUS3_HUMAN, UB2J1_HUMAN, ZN430_HUMAN, B4GT4_HUMAN, MSH2_HUMAN, MIZF_HUMAN, TOB2_HUMAN, GEMI6_HUMAN, BRD1_HUMAN, RUNX1_HUMAN, STAG2_HUMAN, POGZ_HUMAN, SPI1_HUMAN, ZN202_HUMAN, SNX18_HUMAN, RAD18_HUMAN, CB80_HUMAN, MDM4_HUMAN, SF3B3_HUMAN, MSH6_HUMAN, IDS_HUMAN, HDAC4_HUMAN, ID2_HUMAN, ID1_HUMAN, MGAT2_HUMAN, MYO9B_HUMAN, CTNL1_HUMAN, SMS2_HUMAN, ZN133_HUMAN, TADBP_HUMAN, TRIP4_HUMAN, PSN1_HUMAN, ARP6_HUMAN, SP3_HUMAN, AXUD1_HUMAN, BRD8_HUMAN, ZNF25_HUMAN, TOM1_HUMAN, DYLX_HUMAN, CSE1_HUMAN, TDIF1_HUMAN, CSR2B_HUMAN, PLAK_HUMAN, TBBX_HUMAN, ZNF22_HUMAN, FKBP5_HUMAN, HNRPU_HUMAN, ADDB_HUMAN, TBA1_HUMAN, HXA9_HUMAN, RT31_HUMAN, RAB1_HUMAN, DYL1_HUMAN, ZN161_HUMAN, GALT3_HUMAN, PPT2_HUMAN, RRS1_HUMAN, DNL4_HUMAN, DET1_HUMAN, EYA1_HUMAN, GEMI5_HUMAN, TRI27_HUMAN, HNRL1_HUMAN, ELL_HUMAN, STK39_HUMAN, CETN3_HUMAN

-- 4 of 115--

GOID GO:0043226

TERM organelle

P-VALUE 2.44840261102742e-22

CORRECTED P-VALUE 4.94577327427539e-20

NUM_ANNOTATIONS 313 (of 8914)

ANNOTATED_GENES TXND5_HUMAN, PACE1_HUMAN, IF16_HUMAN, MLP3B_HUMAN, FAF1_HUMAN, APBP2_HUMAN, PPIG_HUMAN, RP9_HUMAN, DYI2_HUMAN, RT18B_HUMAN, AP3M2_HUMAN, CCNT2_HUMAN, WDR33_HUMAN, AP4E1_HUMAN, APC10_HUMAN, B3GN1_HUMAN, TBA6_HUMAN, TERF1_HUMAN, HOP_HUMAN, TPM3_HUMAN, ZN646_HUMAN, FANCA_HUMAN, ZN264_HUMAN, RUNX3_HUMAN, TDG_HUMAN, ZN174_HUMAN, BCLX_HUMAN, BLM_HUMAN, ZN143_HUMAN, RFXAP_HUMAN, BRCA1_HUMAN, HCA66_HUMAN, ATF2_HUMAN, STX6_HUMAN, STK35_HUMAN, ZN222_HUMAN, ATF4_HUMAN, FOXO1_HUMAN, MYPT1_HUMAN, ATRX_HUMAN, HSP47_HUMAN, CV106_HUMAN, LIPB_HUMAN, KLF10_HUMAN, LBR_HUMAN, EMD_HUMAN, EZRI_HUMAN, TRPS1_HUMAN, ZFH2_HUMAN, ZN350_HUMAN, NARGL_HUMAN, NUPL1_HUMAN, PHTF1_HUMAN, JERKL_HUMAN, NISM_HUMAN, SODM_HUMAN, RANB9_HUMAN, PIM1_HUMAN, NECP2_HUMAN, NR1H2_HUMAN, SUFU_HUMAN, RBM12_HUMAN, AP4S1_HUMAN, PP1RA_HUMAN, YPEL2_HUMAN, MTO1_HUMAN, T103_HUMAN, CA022_HUMAN, PLSB_HUMAN, MAF_HUMAN, TF3C4_HUMAN, K2C8_HUMAN,

Cellular Component.txt

SMRA3_HUMAN, MFN1_HUMAN, ZBTB3_HUMAN, SK2L2_HUMAN, KLF11_HUMAN, NIPBL_HUMAN, G6B_HUMAN, CDN1C_HUMAN, TF2H2_HUMAN, ANM6_HUMAN, DRAP1_HUMAN, ZNF7_HUMAN, KLF7_HUMAN, MUTA_HUMAN, RPA2_HUMAN, ZBTB1_HUMAN, ZFP95_HUMAN, SETX_HUMAN, GIM1_HUMAN, RB_HUMAN, ZNF12_HUMAN, SPOP_HUMAN, CYC_HUMAN, DDX31_HUMAN, UBP1_HUMAN, NCBP2_HUMAN, ETS2_HUMAN, SYNE2_HUMAN, POLH_HUMAN, RT18C_HUMAN, HEN2_HUMAN, S23IP_HUMAN, SETB1_HUMAN, SMCA5_HUMAN, RREB1_HUMAN, TNPO1_HUMAN, ETV5_HUMAN, CLPX_HUMAN, PTH2_HUMAN, ZFY_HUMAN, SUV91_HUMAN, SPEB_HUMAN, RS10_HUMAN, SALL3_HUMAN, FBX38_HUMAN, SIP1_HUMAN, ZN200_HUMAN, TCF7_HUMAN, DUS11_HUMAN, SEP10_HUMAN, ZN397_HUMAN, VPS4B_HUMAN, SIRT1_HUMAN, ARD1_HUMAN, AP3S2_HUMAN, T2EA_HUMAN, RT27_HUMAN, RAB9A_HUMAN, TEX10_HUMAN, REN3B_HUMAN, RM46_HUMAN, EEA1_HUMAN, SPH2_HUMAN, ZNF79_HUMAN, ZN217_HUMAN, UT14C_HUMAN, FUT8_HUMAN, IRF2_HUMAN, SIAH1_HUMAN, ZN286_HUMAN, PO5FM_HUMAN, TPPC2_HUMAN, LYST_HUMAN, PO5FL_HUMAN, MOB3_HUMAN, TRI32_HUMAN, KELL_HUMAN, AFAD_HUMAN, TF2AA_HUMAN, TBB6_HUMAN, DCP1B_HUMAN, PRS10_HUMAN, FANCE_HUMAN, T2FB_HUMAN, SIA10_HUMAN, ZF276_HUMAN, OST3B_HUMAN, EXOS3_HUMAN, HUCE1_HUMAN, DLX2_HUMAN, RM35_HUMAN, TRIPB_HUMAN, TBA2_HUMAN, CSTF3_HUMAN, APG5_HUMAN, MK14_HUMAN, PARP4_HUMAN, AF17_HUMAN, ACADM_HUMAN, STRN3_HUMAN, THA_HUMAN, GIMA5_HUMAN, ARFP1_HUMAN, SMRCD_HUMAN, ZN408_HUMAN, ZN223_HUMAN, DYL2_HUMAN, DYI3_HUMAN, PAPOG_HUMAN, CDR2_HUMAN, NR1D1_HUMAN, ZN492_HUMAN, NU160_HUMAN, BET1_HUMAN, NUP50_HUMAN, G6PE_HUMAN, SLAP2_HUMAN, RM19_HUMAN, BAZ1A_HUMAN, MPP8_HUMAN, MOL1A_HUMAN, ARF6_HUMAN, BORG1_HUMAN, GATA5_HUMAN, RPC2_HUMAN, BCL3_HUMAN, HMG2_HUMAN, LIS1_HUMAN, FTMT_HUMAN, DCMC_HUMAN, STX7_HUMAN, K0690_HUMAN, KLC8_HUMAN, TBB4_HUMAN, ZNF10_HUMAN, SON_HUMAN, AMFR2_HUMAN, NOP56_HUMAN, GLI4_HUMAN, SEN2_HUMAN, SPNXB_HUMAN, MKL2_HUMAN, BCL9_HUMAN, UT14A_HUMAN, MEF2C_HUMAN, PRP17_HUMAN, CRSP6_HUMAN, ANR12_HUMAN, ZEP2_HUMAN, NF2L1_HUMAN, NEUL_HUMAN, PARVG_HUMAN, FLNA_HUMAN, WDR3_HUMAN, PFTK1_HUMAN, PEPP1_HUMAN, PO6F2_HUMAN, BAZ1B_HUMAN, EPC1_HUMAN, FLI1_HUMAN, MK67I_HUMAN, CSTF1_HUMAN, ZCHC6_HUMAN, DDX52_HUMAN, CDN2D_HUMAN, CREB1_HUMAN, MTERF_HUMAN, SCRT2_HUMAN, CN108_HUMAN, ZN516_HUMAN, TTRAP_HUMAN, ZN189_HUMAN, PHF20_HUMAN, ID3_HUMAN, PLRG1_HUMAN, PUS3_HUMAN, UB2J1_HUMAN, ZN430_HUMAN, B4GT4_HUMAN, MSH2_HUMAN, MIZF_HUMAN, TOB2_HUMAN, GEMI6_HUMAN, BRD1_HUMAN, RUNX1_HUMAN, STAG2_HUMAN, POGZ_HUMAN, SPI1_HUMAN, ZN202_HUMAN, SNX18_HUMAN, RAD18_HUMAN, CB80_HUMAN, MDM4_HUMAN, SF3B3_HUMAN, MSH6_HUMAN, IDS_HUMAN, HDAC4_HUMAN, ID2_HUMAN, ID1_HUMAN, MGAT2_HUMAN, MYO9B_HUMAN, CTNLI1_HUMAN, SMS2_HUMAN, ZN133_HUMAN, TADBP_HUMAN, TRIP4_HUMAN, PSN1_HUMAN, ARP6_HUMAN, SP3_HUMAN, AXUD1_HUMAN, BRD8_HUMAN, ZNF25_HUMAN, TOM1_HUMAN, DYLX_HUMAN, CSE1_HUMAN, TDIF1_HUMAN, CSR2B_HUMAN, PLAK_HUMAN, TBBX_HUMAN, ZNF22_HUMAN, FKBP5_HUMAN, HNRPU_HUMAN, ADDB_HUMAN, TBA1_HUMAN, HXA9_HUMAN, RT31_HUMAN, RAB1_HUMAN, DYL1_HUMAN, ZN161_HUMAN, GALT3_HUMAN, PPT2_HUMAN, RRS1_HUMAN, DNL4_HUMAN, DET1_HUMAN, EYA1_HUMAN, GEMI5_HUMAN, TRI27_HUMAN, HNRLL_HUMAN, ELL_HUMAN, STK39_HUMAN, CETN3_HUMAN

-- 5 of 115--

GOID GO:0005622

TERM intracellular

P-VALUE 8.13796012210764e-22

CORRECTED P-VALUE 1.64386794466574e-19

NUM_ANNOTATIONS 362 (of 11046)

ANNOTATED_GENES TRIM6_HUMAN, TXND5_HUMAN, PACE1_HUMAN, IF16_HUMAN, MLP3B_HUMAN, FAF1_HUMAN, APBP2_HUMAN, PPIG_HUMAN, RP9_HUMAN, DYI2_HUMAN, RT18B_HUMAN, IBRD2_HUMAN, AP3M2_HUMAN, BIRC3_HUMAN, CCNT2_HUMAN, WDR33_HUMAN, AP4E1_HUMAN, APC10_HUMAN, BNIP2_HUMAN, B3GN1_HUMAN, LIPB2_HUMAN, TBA6_HUMAN, KPYM_HUMAN, TERF1_HUMAN, SYR_HUMAN, HOP_HUMAN, TPM3_HUMAN, ZN646_HUMAN, FANCA_HUMAN, ZN264_HUMAN, RUNX3_HUMAN, TDG_HUMAN, ZN174_HUMAN, BCLX_HUMAN, UGPA1_HUMAN, BLM_HUMAN, ZN143_HUMAN, IF4G3_HUMAN, CSKI2_HUMAN, RFXAP_HUMAN, BRCA1_HUMAN, HCA66_HUMAN, ATF2_HUMAN, STX6_HUMAN, STK35_HUMAN, SOCS6_HUMAN, ZN222_HUMAN, ATF4_HUMAN, FOXO1_HUMAN, MYPT1_HUMAN, ATRX_HUMAN, HSP47_HUMAN, CV106_HUMAN, LIPB_HUMAN, KLF10_HUMAN, PDRN4_HUMAN, LBR_HUMAN, EMD_HUMAN, EZRI_HUMAN, ST1A3_HUMAN, TRPS1_HUMAN, ZFHX2_HUMAN, ZN350_HUMAN, RNF6_HUMAN, NARGL_HUMAN, NUPL1_HUMAN, PHTF1_HUMAN, JERKL_HUMAN, NISM_HUMAN, TRIM4_HUMAN, SODM_HUMAN, RANB9_HUMAN, PIM1_HUMAN, IF5_HUMAN, NECP2_HUMAN, NR1H2_HUMAN, SUFU_HUMAN, RBM12_HUMAN, CDC42_HUMAN, AP4S1_HUMAN, PP1RA_HUMAN, YPEL2_HUMAN, MTO1_HUMAN, T103_HUMAN, CA022_HUMAN, PL24A_HUMAN, PLSB_HUMAN, MAF_HUMAN, TF3C4_HUMAN, K2C8_HUMAN, SMRA3_HUMAN, MFN1_HUMAN, ZBTB3_HUMAN, SK2L2_HUMAN, KLF11_HUMAN, FPGT_HUMAN,

Cellular Component.txt

NIPBL_HUMAN, G6B_HUMAN, CDN1C_HUMAN, TF2H2_HUMAN, ANM6_HUMAN, NMI_HUMAN, DRAP1_HUMAN, ZNF7_HUMAN, KLF7_HUMAN, MUTA_HUMAN, RPA2_HUMAN, ZBTB1_HUMAN, ZFP95_HUMAN, SETX_HUMAN, GIMA1_HUMAN, RB_HUMAN, ZNF12_HUMAN, GLYC_HUMAN, SPOP_HUMAN, CYC_HUMAN, DDX31_HUMAN, UBP1_HUMAN, NCBP2_HUMAN, ETS2_HUMAN, SYNE2_HUMAN, POLH_HUMAN, RT18C_HUMAN, HEN2_HUMAN, TRI34_HUMAN, S23IP_HUMAN, SETB1_HUMAN, SMCA5_HUMAN, RREB1_HUMAN, TNPO1_HUMAN, ETV5_HUMAN, CLPX_HUMAN, PTH2_HUMAN, ZFY_HUMAN, SUV91_HUMAN, SPEB_HUMAN, M4K5_HUMAN, RS10_HUMAN, SALL3_HUMAN, FBX38_HUMAN, SIP1_HUMAN, ZN200_HUMAN, TCF7_HUMAN, DUS11_HUMAN, SEP10_HUMAN, ZN397_HUMAN, VPS4B_HUMAN, SIRT1_HUMAN, ARD1_HUMAN, AP3S2_HUMAN, T2EA_HUMAN, RT27_HUMAN, RAB9A_HUMAN, TEX10_HUMAN, REN3B_HUMAN, RM46_HUMAN, EEA1_HUMAN, SPH2_HUMAN, ZNF79_HUMAN, ZN217_HUMAN, UT14C_HUMAN, FUT8_HUMAN, IRF2_HUMAN, SIAH1_HUMAN, ZN286_HUMAN, PO5FM_HUMAN, TPPC2_HUMAN, LYST_HUMAN, PO5FL_HUMAN, MOB3_HUMAN, TRI32_HUMAN, KELL_HUMAN, AFAD_HUMAN, TF2AA_HUMAN, TBB6_HUMAN, DCP1B_HUMAN, PRS10_HUMAN, ANGL7_HUMAN, FANCE_HUMAN, T2FB_HUMAN, SIA10_HUMAN, RN146_HUMAN, ZF276_HUMAN, OST3B_HUMAN, EXOS3_HUMAN, HUCE1_HUMAN, DLX2_HUMAN, RM35_HUMAN, TRIPB_HUMAN, TBA2_HUMAN, CSTF3_HUMAN, MK14_HUMAN, APG5_HUMAN, PARP4_HUMAN, TACD2_HUMAN, AF17_HUMAN, ACADM_HUMAN, STRN3_HUMAN, PFTA_HUMAN, THA_HUMAN, GIMA5_HUMAN, ARFP1_HUMAN, SMRCD_HUMAN, ZN408_HUMAN, ZN223_HUMAN, DYL2_HUMAN, DYI3_HUMAN, PAPOG_HUMAN, CDR2_HUMAN, ZN492_HUMAN, NR1D1_HUMAN, SFTA2_HUMAN, NU160_HUMAN, BET1_HUMAN, NUP50_HUMAN, G6PE_HUMAN, SLAP2_HUMAN, RM19_HUMAN, BAZ1A_HUMAN, MPP8_HUMAN, MOL1A_HUMAN, KYNU_HUMAN, ARF6_HUMAN, BORG1_HUMAN, GATA5_HUMAN, RPC2_HUMAN, BCL3_HUMAN, HMG2_HUMAN, LIS1_HUMAN, FTMT_HUMAN, AK1C1_HUMAN, DCMC_HUMAN, STX7_HUMAN, DAPP1_HUMAN, K0690_HUMAN, KLC8_HUMAN, CAR12_HUMAN, TBB4_HUMAN, ZNF10_HUMAN, PDPK1_HUMAN, SON_HUMAN, AMFR2_HUMAN, NOP56_HUMAN, GLI4_HUMAN, SEN2_HUMAN, SPNXB_HUMAN, MKL2_HUMAN, BCL9_HUMAN, UT14A_HUMAN, MEF2C_HUMAN, PRP17_HUMAN, HS105_HUMAN, AGGF1_HUMAN, 5NT1B_HUMAN, CRSP6_HUMAN, ANR12_HUMAN, ZEP2_HUMAN, BCDO2_HUMAN, NF2L1_HUMAN, NEUL_HUMAN, PARVG_HUMAN, FLNA_HUMAN, WDR3_HUMAN, PFTK1_HUMAN, PEPP1_HUMAN, TRI12_HUMAN, PO6F2_HUMAN, UBP33_HUMAN, BAZ1B_HUMAN, EPC1_HUMAN, FLI1_HUMAN, MK67I_HUMAN, CSTF1_HUMAN, ZCHC6_HUMAN, DDX52_HUMAN, CDN2D_HUMAN, CREB1_HUMAN, MTERF_HUMAN, SCRT2_HUMAN, CN108_HUMAN, ZN516_HUMAN, TTRAP_HUMAN, ZN189_HUMAN, PHF20_HUMAN, ID3_HUMAN, PLRG1_HUMAN, PUS3_HUMAN, UB2J1_HUMAN, ZN430_HUMAN, B4GT4_HUMAN, MSH2_HUMAN, CO9A3_HUMAN, GEMI6_HUMAN, MIZF_HUMAN, TOB2_HUMAN, BRD1_HUMAN, NCK1_HUMAN, RUNX1_HUMAN, SPHK1_HUMAN, STAG2_HUMAN, POGZ_HUMAN, SPI1_HUMAN, ZN202_HUMAN, SNX18_HUMAN, RAD18_HUMAN, APG7L_HUMAN, CB80_HUMAN, MDM4_HUMAN, MSH6_HUMAN, IDS_HUMAN, SF3B3_HUMAN, HDAC4_HUMAN, ID2_HUMAN, ID1_HUMAN, MGAT2_HUMAN, RHG07_HUMAN, MYO9B_HUMAN, CTNL1_HUMAN, CARD6_HUMAN, SMS2_HUMAN, ZN133_HUMAN, GRAN_HUMAN, TADBP_HUMAN, TRIP4_HUMAN, PSN1_HUMAN, ARP6_HUMAN, GRAP2_HUMAN, SP3_HUMAN, AXUD1_HUMAN, BRD8_HUMAN, ZNF25_HUMAN, TOM1_HUMAN, DYLG_HUMAN, FBX25_HUMAN, CSE1_HUMAN, TDIF1_HUMAN, ZN363_HUMAN, CSR2B_HUMAN, PLAK_HUMAN, TBBX_HUMAN, ZNF22_HUMAN, FKBP5_HUMAN, HNRPU_HUMAN, ADDB_HUMAN, TBA1_HUMAN, HXA9_HUMAN, RT31_HUMAN, RABE1_HUMAN, DYL1_HUMAN, ZN161_HUMAN, GALT3_HUMAN, PPT2_HUMAN, RRS1_HUMAN, DNL4_HUMAN, DET1_HUMAN, EYA1_HUMAN, HNRL1_HUMAN, GEMI5_HUMAN, TRI27_HUMAN, ELL_HUMAN, STK39_HUMAN, CETN3_HUMAN

-- 6 of 115--

GOID GO:0005634

TERM nucleus

P-VALUE 1.01539301274456e-20

CORRECTED P-VALUE 2.051093885744e-18

NUM_ANNOTATIONS 214 (of 5279)

ANNOTATED_GENES MK14_HUMAN, PARP4_HUMAN, IF16_HUMAN, FAF1_HUMAN, AF17_HUMAN, APBP2_HUMAN, PPIG_HUMAN, RP9_HUMAN, STRN3_HUMAN, CCNT2_HUMAN, THA_HUMAN, WDR33_HUMAN, APC10_HUMAN, SMRCD_HUMAN, ZN408_HUMAN, ZN223_HUMAN, CDR2_HUMAN, PAPOG_HUMAN, ZN492_HUMAN, TERF1_HUMAN, NR1D1_HUMAN, NU160_HUMAN, HOP_HUMAN, NUP50_HUMAN, ZN646_HUMAN, FANCA_HUMAN, ZN264_HUMAN, RUNX3_HUMAN, TDG_HUMAN, BAZ1A_HUMAN, ZN174_HUMAN, MPP8_HUMAN, MOL1A_HUMAN, BLM_HUMAN, ZN143_HUMAN, RFXAP_HUMAN, BRCA1_HUMAN, HCA66_HUMAN, GATA5_HUMAN, ATF2_HUMAN, RPC2_HUMAN, BCL3_HUMAN, STK35_HUMAN, HMG2_HUMAN, LIS1_HUMAN, ZN222_HUMAN, K0690_HUMAN, ATF4_HUMAN, FOXO1_HUMAN, ATRX_HUMAN, CV106_HUMAN, KLF10_HUMAN, ZNF10_HUMAN, SON_HUMAN, LBR_HUMAN, EMD_HUMAN, TRPS1_HUMAN, ZFH2_HUMAN, ZN350_HUMAN, NARGL_HUMAN, NUPL1_HUMAN, PHTF1_HUMAN, JERKL_HUMAN, GLI4_HUMAN, NOP56_HUMAN, SEN2_HUMAN, RANB9_HUMAN, PIM1_HUMAN, SPNXB_HUMAN, BCL9_HUMAN, MKL2_HUMAN, NR1H2_HUMAN,

Cellular Component.txt

SUFU_HUMAN, UT14A_HUMAN, RBM12_HUMAN, MEF2C_HUMAN, PRP17_HUMAN, PP1RA_HUMAN, YPEL2_HUMAN, CRSP6_HUMAN, ANR12_HUMAN, ZEP2_HUMAN, T103_HUMAN, NF2L1_HUMAN, MAF_HUMAN, WDR3_HUMAN, TF3C4_HUMAN, SMRA3_HUMAN, PFTK1_HUMAN, PEPP1_HUMAN, PO6F2_HUMAN, ZBTB3_HUMAN, SK2L2_HUMAN, KLF11_HUMAN, BAZ1B_HUMAN, NIPBL_HUMAN, EPC1_HUMAN, CDN1C_HUMAN, FLI1_HUMAN, TF2H2_HUMAN, MK67I_HUMAN, ANM6_HUMAN, CSTF1_HUMAN, ZCHC6_HUMAN, CREB1_HUMAN, DDX52_HUMAN, CDN2D_HUMAN, DRAP1_HUMAN, ZNF7_HUMAN, KLF7_HUMAN, SCRT2_HUMAN, ZBTB1_HUMAN, RPA2_HUMAN, ZFP95_HUMAN, SETX_HUMAN, RB_HUMAN, ZN516_HUMAN, ZNF12_HUMAN, TTRAP_HUMAN, ZN189_HUMAN, SPOP_HUMAN, PHF20_HUMAN, ID3_HUMAN, PLRG1_HUMAN, DDX31_HUMAN, UBP1_HUMAN, PUS3_HUMAN, NCBP2_HUMAN, ETS2_HUMAN, ZN430_HUMAN, POLH_HUMAN, HEN2_HUMAN, MSH2_HUMAN, SETB1_HUMAN, GEMI6_HUMAN, TOB2_HUMAN, MIZF_HUMAN, SMCA5_HUMAN, RREB1_HUMAN, BRD1_HUMAN, TNPO1_HUMAN, RUNX1_HUMAN, STAG2_HUMAN, POGZ_HUMAN, SPI1_HUMAN, ZN202_HUMAN, ETV5_HUMAN, RAD18_HUMAN, CB80_HUMAN, MDM4_HUMAN, MSH6_HUMAN, SF3B3_HUMAN, HDAC4_HUMAN, ZFY_HUMAN, ID2_HUMAN, SUV91_HUMAN, ID1_HUMAN, SALL3_HUMAN, FBX38_HUMAN, SIP1_HUMAN, ZN133_HUMAN, ZN200_HUMAN, TADBP_HUMAN, TCF7_HUMAN, DUS11_HUMAN, TRIP4_HUMAN, SEP10_HUMAN, ZN397_HUMAN, PSN1_HUMAN, SIRT1_HUMAN, SP3_HUMAN, AXUD1_HUMAN, BRD8_HUMAN, ZNF25_HUMAN, T2EA_HUMAN, TEX10_HUMAN, REN3B_HUMAN, EEA1_HUMAN, ZNF79_HUMAN, ZN217_HUMAN, CSE1_HUMAN, UT14C_HUMAN, TDIF1_HUMAN, IRF2_HUMAN, CSR2B_HUMAN, SIAH1_HUMAN, ZN286_HUMAN, ZNF22_HUMAN, FKBP5_HUMAN, PO5FM_HUMAN, HNRPU_HUMAN, HXA9_HUMAN, PO5FL_HUMAN, TRI32_HUMAN, ZN161_HUMAN, TF2AA_HUMAN, DCP1B_HUMAN, PRS10_HUMAN, RRS1_HUMAN, FANCE_HUMAN, DNL4_HUMAN, T2FB_HUMAN, DET1_HUMAN, EYA1_HUMAN, ZF276_HUMAN, HNRL1_HUMAN, EXOS3_HUMAN, GEMI5_HUMAN, HUCE1_HUMAN, TRI27_HUMAN, DLX2_HUMAN, ELL_HUMAN, STK39_HUMAN, CSTF3_HUMAN

-- 7 of 115--

GOID GO:0005623

TERM cell

P-VALUE 7.839124206139e-14

CORRECTED P-VALUE 1.58350308964008e-11

NUM_ANNOTATIONS 461 (of 16849)

ANNOTATED_GENES TRIM6_HUMAN, TXND5_HUMAN, TNF10_HUMAN, PACE1_HUMAN, IF16_HUMAN, MLP3B_HUMAN, FAF1_HUMAN, APBP2_HUMAN, PPIG_HUMAN, RP9_HUMAN, DYI2_HUMAN, RT18B_HUMAN, IBRD2_HUMAN, AP3M2_HUMAN, BIRC3_HUMAN, CCNT2_HUMAN, WDR33_HUMAN, HA25_HUMAN, AP4E1_HUMAN, PKD1_HUMAN, APC10_HUMAN, BNIP2_HUMAN, PRND_HUMAN, B3GN1_HUMAN, LIPB2_HUMAN, TBA6_HUMAN, DDEF1_HUMAN, KPVM_HUMAN, TERF1_HUMAN, SYR_HUMAN, HOP_HUMAN, TPM3_HUMAN, ACHB_HUMAN, SATT_HUMAN, ZN646_HUMAN, SMDF_HUMAN, FANCA_HUMAN, ZN264_HUMAN, RUNX3_HUMAN, TDG_HUMAN, ZN174_HUMAN, BCLX_HUMAN, UGPA1_HUMAN, BLM_HUMAN, ZN143_HUMAN, IF4G3_HUMAN, CSKI2_HUMAN, RFXAP_HUMAN, BRCA1_HUMAN, HCA66_HUMAN, ATF2_HUMAN, STX6_HUMAN, STK35_HUMAN, SOCS6_HUMAN, TMM24_HUMAN, PCDG3_HUMAN, ZN222_HUMAN, RGR_HUMAN, CCR2_HUMAN, ATF4_HUMAN, FOXO1_HUMAN, MYPT1_HUMAN, ATRX_HUMAN, HCN1_HUMAN, HSP47_HUMAN, CV106_HUMAN, LIPB_HUMAN, PCDG2_HUMAN, KLF10_HUMAN, PDRN4_HUMAN, LBR_HUMAN, EMD_HUMAN, EZRI_HUMAN, ST1A3_HUMAN, TRPS1_HUMAN, ZFHX2_HUMAN, ZN350_HUMAN, RNF6_HUMAN, NARGL_HUMAN, NUPL1_HUMAN, PHTF1_HUMAN, JERKL_HUMAN, NISM_HUMAN, TRIM4_HUMAN, SODM_HUMAN, FIBA_HUMAN, RANB9_HUMAN, PIM1_HUMAN, IF5_HUMAN, NECP2_HUMAN, NR1H2_HUMAN, SUFU_HUMAN, RBM12_HUMAN, CDC42_HUMAN, CERK1_HUMAN, AP4S1_HUMAN, PP1RA_HUMAN, ATRN_HUMAN, YPEL2_HUMAN, MTO1_HUMAN, RECK_HUMAN, T103_HUMAN, CA022_HUMAN, PA24A_HUMAN, PLSB_HUMAN, MAF_HUMAN, TF3C4_HUMAN, K2C8_HUMAN, PDE4A_HUMAN, SMRA3_HUMAN, MFN1_HUMAN, ZBTB3_HUMAN, SK2L2_HUMAN, KLF11_HUMAN, FPGT_HUMAN, NIPBL_HUMAN, G6B_HUMAN, CDN1C_HUMAN, TF2H2_HUMAN, ANM6_HUMAN, NMI_HUMAN, DRAP1_HUMAN, ZNF7_HUMAN, NINJ1_HUMAN, KLF7_HUMAN, MUTA_HUMAN, PTAFR_HUMAN, RPA2_HUMAN, ZBTB1_HUMAN, ZFP95_HUMAN, SETX_HUMAN, GIMA1_HUMAN, RB_HUMAN, ZNF12_HUMAN, GLYC_HUMAN, SPOP_HUMAN, AT2B2_HUMAN, CYC_HUMAN, DDX31_HUMAN, TREM1_HUMAN, NCBP2_HUMAN, UBP1_HUMAN, ETS2_HUMAN, SYNE2_HUMAN, POLH_HUMAN, RT18C_HUMAN, HEN2_HUMAN, TRI34_HUMAN, HA22_HUMAN, S23IP_HUMAN, EMP3_HUMAN, SETB1_HUMAN, SMCA5_HUMAN, RREB1_HUMAN, TNPO1_HUMAN, ETV5_HUMAN, CLPX_HUMAN, PTH2_HUMAN, ZFY_HUMAN, SUV91_HUMAN, SPEB_HUMAN, M4K5_HUMAN, RS10_HUMAN, SALL3_HUMAN, FZD1_HUMAN, FBX38_HUMAN, SIP1_HUMAN, EGFL8_HUMAN, ZN200_HUMAN, TCF7_HUMAN, DUS11_HUMAN, SEP10_HUMAN, FN14_HUMAN, ZN397_HUMAN, VPS4B_HUMAN, SIRT1_HUMAN, ARD1_HUMAN, LERL1_HUMAN, AP3S2_HUMAN, C5AR_HUMAN, T2EA_HUMAN, VAPB_HUMAN, CBLN1_HUMAN, RT27_HUMAN, RAB9A_HUMAN, NALDL_HUMAN, S23IP_HUMAN, REN3B_HUMAN, RM46_HUMAN, EEA1_HUMAN, SPH2_HUMAN, AA2AR_HUMAN, ZNF79_HUMAN, ZN217_HUMAN,

Cellular Component.txt

UT14C_HUMAN, FUT8_HUMAN, IRF2_HUMAN, SIAH1_HUMAN, CAD22_HUMAN, ZN286_HUMAN, PO5FM_HUMAN, TPPC2_HUMAN, LYST_HUMAN, PO5FL_HUMAN, EMP1_HUMAN, MOB3_HUMAN, IDD_HUMAN, GPR86_HUMAN, TRI32_HUMAN, KELL_HUMAN, AFAD_HUMAN, ADML_HUMAN, IBRD3_HUMAN, TBB6_HUMAN, TF2AA_HUMAN, GIMA2_HUMAN, DCP1B_HUMAN, PRS10_HUMAN, ANGL7_HUMAN, FANCE_HUMAN, DHRS3_HUMAN, T2FB_HUMAN, LRFN5_HUMAN, SIA10_HUMAN, RN146_HUMAN, ZF276_HUMAN, OST3B_HUMAN, PCDGB_HUMAN, GPR18_HUMAN, EXOS3_HUMAN, HUCE1_HUMAN, DLX2_HUMAN, RM35_HUMAN, S22A3_HUMAN, TRIPB_HUMAN, TBA2_HUMAN, CSTF3_HUMAN, MK14_HUMAN, APG5_HUMAN, PARP4_HUMAN, TACD2_HUMAN, AF17_HUMAN, ACADM_HUMAN, TRPM3_HUMAN, CHIC2_HUMAN, STRN3_HUMAN, PFTA_HUMAN, EGFL5_HUMAN, THA_HUMAN, GIMA5_HUMAN, ARFP1_HUMAN, SMRCD_HUMAN, ZN408_HUMAN, ZN223_HUMAN, LAT_HUMAN, DYL2_HUMAN, P2Y14_HUMAN, DYI3_HUMAN, PP14C_HUMAN, PAPOG_HUMAN, CDR2_HUMAN, ZN492_HUMAN, NR1D1_HUMAN, SFTA2_HUMAN, NU160_HUMAN, BET1_HUMAN, NUP50_HUMAN, TNR8_HUMAN, SLAP2_HUMAN, G6PE_HUMAN, MYADM_HUMAN, RM19_HUMAN, BAZ1A_HUMAN, MPP8_HUMAN, MOL1A_HUMAN, KYNU_HUMAN, EAA2_HUMAN, ARF6_HUMAN, PPBI_HUMAN, BORG1_HUMAN, CADH4_HUMAN, GATA5_HUMAN, RPC2_HUMAN, BCL3_HUMAN, HMG2_HUMAN, AMFR1_HUMAN, LIS1_HUMAN, FTMT_HUMAN, DCMC_HUMAN, AK1C1_HUMAN, STX7_HUMAN, DAPP1_HUMAN, K0690_HUMAN, GPR83_HUMAN, KLC8_HUMAN, CAR12_HUMAN, TBB4_HUMAN, PE2R2_HUMAN, ZNF10_HUMAN, PDPK1_HUMAN, INSI1_HUMAN, SON_HUMAN, AMFR2_HUMAN, NOP56_HUMAN, GLI4_HUMAN, SEN2_HUMAN, SPNXB_HUMAN, MKL2_HUMAN, BCL9_HUMAN, UT14A_HUMAN, GTR3_HUMAN, LDLR_HUMAN, MEF2C_HUMAN, PRP17_HUMAN, SNN_HUMAN, HS105_HUMAN, AGGF1_HUMAN, 5NT1B_HUMAN, PPBT_HUMAN, CRSP6_HUMAN, ANR12_HUMAN, KCNQ2_HUMAN, ZEP2_HUMAN, BCDO2_HUMAN, NF2L1_HUMAN, NEUL_HUMAN, PARVG_HUMAN, FLNA_HUMAN, KCMA1_HUMAN, ICAM1_HUMAN, WDR3_HUMAN, PCDGA_HUMAN, CCG1_HUMAN, NRG1_HUMAN, PFTK1_HUMAN, VNN3_HUMAN, P2RY5_HUMAN, PEPP1_HUMAN, MUC15_HUMAN, TRI12_HUMAN, PO6F2_HUMAN, CD97_HUMAN, UBP33_HUMAN, RTP4_HUMAN, PCDG8_HUMAN, BAZ1B_HUMAN, EPC1_HUMAN, FLI1_HUMAN, MK67I_HUMAN, CSTF1_HUMAN, ZCHC6_HUMAN, ICOS_HUMAN, CREB1_HUMAN, DDX52_HUMAN, CDN2D_HUMAN, MTERF_HUMAN, SCRT2_HUMAN, CN108_HUMAN, MPRB_HUMAN, ZN516_HUMAN, TTRAP_HUMAN, ZN189_HUMAN, ACHA_HUMAN, PHF20_HUMAN, ID3_HUMAN, PLRG1_HUMAN, PUS3_HUMAN, UB2J1_HUMAN, ZN430_HUMAN, B4GT4_HUMAN, INGR1_HUMAN, VKORL_HUMAN, MSH2_HUMAN, CO9A3_HUMAN, TLR7_HUMAN, GEMI6_HUMAN, TOB2_HUMAN, MIZF_HUMAN, FCAR_HUMAN, SPHK1_HUMAN, BRD1_HUMAN, NCK1_HUMAN, RUNX1_HUMAN, STAG2_HUMAN, POGZ_HUMAN, SPI1_HUMAN, ZN202_HUMAN, SNX18_HUMAN, RAD18_HUMAN, APG7L_HUMAN, CB80_HUMAN, MDM4_HUMAN, MSH6_HUMAN, IDS_HUMAN, SF3B3_HUMAN, HDAC4_HUMAN, ID2_HUMAN, ID1_HUMAN, MGAT2_HUMAN, RHG07_HUMAN, IRK2_HUMAN, MYO9B_HUMAN, CTNL1_HUMAN, CARD6_HUMAN, KCNG4_HUMAN, SMS2_HUMAN, ZN133_HUMAN, GRAN_HUMAN, TADBP_HUMAN, TRIP4_HUMAN, PSN1_HUMAN, S12A4_HUMAN, ARP6_HUMAN, SPFH1_HUMAN, GRAP2_HUMAN, SP3_HUMAN, AXUD1_HUMAN, BRD8_HUMAN, ZNF25_HUMAN, BIM_HUMAN, TOM1_HUMAN, MGR7_HUMAN, DYLX_HUMAN, MFAP3_HUMAN, NCKX1_HUMAN, FBX25_HUMAN, CSE1_HUMAN, TDF1_HUMAN, CSR2B_HUMAN, ZN363_HUMAN, PLAK_HUMAN, ZNF22_HUMAN, TBBX_HUMAN, FKBP5_HUMAN, HNRPU_HUMAN, ADDB_HUMAN, IRK3_HUMAN, TBA1_HUMAN, HXA9_HUMAN, RT31_HUMAN, RABE1_HUMAN, DYL1_HUMAN, ZN161_HUMAN, GALT3_HUMAN, ZNT1_HUMAN, PPT2_HUMAN, MSPD2_HUMAN, RRS1_HUMAN, DNL4_HUMAN, DET1_HUMAN, EYA1_HUMAN, HNRL1_HUMAN, GEMI5_HUMAN, TRI27_HUMAN, FZD2_HUMAN, TMM33_HUMAN, RGP2_HUMAN, CD1D_HUMAN, ELL_HUMAN, STK39_HUMAN, CETN3_HUMAN

-- 8 of 115--

GOID GO:0005737

TERM cytoplasm

P-VALUE 1.65894662217879e-07

CORRECTED P-VALUE 3.35107217680116e-05

NUM_ANNOTATIONS 145 (of 4347)

ANNOTATED_GENES MK14_HUMAN, APG5_HUMAN, TXND5_HUMAN, TACD2_HUMAN, PACE1_HUMAN, MLP3B_HUMAN, FAF1_HUMAN, APBP2_HUMAN, ACADM_HUMAN, DYI2_HUMAN, RT18B_HUMAN, STRN3_HUMAN, AP3M2_HUMAN, PFTA_HUMAN, GIMA5_HUMAN, WDR33_HUMAN, ARFP1_HUMAN, AP4E1_HUMAN, BNIP2_HUMAN, B3GN1_HUMAN, KPVM_HUMAN, SFTA2_HUMAN, SYR_HUMAN, TPM3_HUMAN, BET1_HUMAN, FANCA_HUMAN, SLAP2_HUMAN, G6PE_HUMAN, RM19_HUMAN, MPP8_HUMAN, BCLX_HUMAN, KYNU_HUMAN, UGPA1_HUMAN, ARF6_HUMAN, BORG1_HUMAN, IF4G3_HUMAN, CSKI2_HUMAN, BRCA1_HUMAN, STX6_HUMAN, HMG2_HUMAN, SOCS6_HUMAN, LIS1_HUMAN, FTMT_HUMAN, DCMC_HUMAN, AK1C1_HUMAN, STX7_HUMAN, DAPP1_HUMAN, ATF4_HUMAN, HSP47_HUMAN, LIPB_HUMAN, TBB4_HUMAN, PDPK1_HUMAN, EZRI_HUMAN, ST1A3_HUMAN, AMFR2_HUMAN, NARGL_HUMAN, NISM_HUMAN, SODM_HUMAN, PIM1_HUMAN, IF5_HUMAN, NECP2_HUMAN, SUFU_HUMAN, CDC42_HUMAN, AP4S1_HUMAN, HS105_HUMAN, MTO1_HUMAN, 5NT1B_HUMAN, CA022_HUMAN, NEUL_HUMAN, PA24A_HUMAN, PLSB_HUMAN,

Cellular Component.txt

PFTK1_HUMAN, TRI12_HUMAN, MFN1_HUMAN, UBP33_HUMAN, FPGT_HUMAN, G6B_HUMAN, MK67I_HUMAN, NMI_HUMAN, CDN2D_HUMAN, MTERF_HUMAN, MUTA_HUMAN, CN108_HUMAN, GIMA1_HUMAN, GLYC_HUMAN, CYC_HUMAN, UB2J1_HUMAN, B4GT4_HUMAN, RT18C_HUMAN, S23IP_HUMAN, CO9A3_HUMAN, GEMI6_HUMAN, NCK1_HUMAN, TNPO1_HUMAN, SPHK1_HUMAN, CLPX_HUMAN, SNX18_HUMAN, APG7L_HUMAN, IDS_HUMAN, PTH2_HUMAN, HDAC4_HUMAN, SPEB_HUMAN, M4K5_HUMAN, RS10_HUMAN, MGAT2_HUMAN, RHG07_HUMAN, SMS2_HUMAN, GRAN_HUMAN, TRIP4_HUMAN, VPS4B_HUMAN, PSN1_HUMAN, ARD1_HUMAN, GRAP2_HUMAN, AP3S2_HUMAN, TOM1_HUMAN, RT27_HUMAN, RAB9A_HUMAN, REN3B_HUMAN, EEA1_HUMAN, RM46_HUMAN, SPH2_HUMAN, CSE1_HUMAN, FUT8_HUMAN, ZN363_HUMAN, SIAH1_HUMAN, PLAK_HUMAN, TBBX_HUMAN, TPPC2_HUMAN, LYST_HUMAN, RABE1_HUMAN, RT31_HUMAN, MOB3_HUMAN, GALT3_HUMAN, PPT2_HUMAN, TBB6_HUMAN, PRS10_HUMAN, ANGL7_HUMAN, SIA10_HUMAN, OST3B_HUMAN, GEMI5_HUMAN, EXOS3_HUMAN, RM35_HUMAN, STK39_HUMAN, TRIPB_HUMAN, CETN3_HUMAN

-- 9 of 115--

GOID GO:0005768

TERM endosome

P-VALUE 3.66941478648353e-06

CORRECTED P-VALUE 0.000741221786869672

NUM_ANNOTATIONS 10 (of 71)

ANNOTATED_GENES STX7_HUMAN, ARF6_HUMAN, RAB9A_HUMAN, LYST_HUMAN, EEA1_HUMAN, VPS4B_HUMAN, RABE1_HUMAN, SLAP2_HUMAN, STX6_HUMAN, TOM1_HUMAN

-- 10 of 115--

GOID GO:0005795

TERM Golgi stack

P-VALUE 1.19769208669463e-05

CORRECTED P-VALUE 0.00241933801512316

NUM_ANNOTATIONS 23 (of 373)

ANNOTATED_GENES B4GT4_HUMAN, TPPC2_HUMAN, BET1_HUMAN, S23IP_HUMAN, PACE1_HUMAN, PSN1_HUMAN, MOB3_HUMAN, AP3M2_HUMAN, GALT3_HUMAN, AP3S2_HUMAN, SNX18_HUMAN, ARF6_HUMAN, RAB9A_HUMAN, AP4E1_HUMAN, SIA10_HUMAN, OST3B_HUMAN, STX6_HUMAN, MGAT2_HUMAN, FUT8_HUMAN, B3GN1_HUMAN, TRIPB_HUMAN, G6B_HUMAN, SMS2_HUMAN

Molecular Function.txt

Terms from the function ontology exceeding a pvalue cutoff of 0.01.

The total number of genes used to calculate the background distribution of GO terms is 28042.

-- 1 of 270--

GOID GO:0005515

TERM protein binding

P-VALUE 3.81466194827487e-17

CORRECTED P-VALUE 2.18961595830977e-14

NUM_ANNOTATIONS 196 (of 4994)

ANNOTATED_GENES MK14_HUMAN, PARP4_HUMAN, TNF10_HUMAN, PACE1_HUMAN, IF16_HUMAN, MLP3B_HUMAN, MUTED_HUMAN, FAF1_HUMAN, SNX27_HUMAN, AF17_HUMAN, TDRD7_HUMAN, RP9_HUMAN, IBRD2_HUMAN, STRN3_HUMAN, BIRC3_HUMAN, CCNT2_HUMAN, MELPH_HUMAN, ANGP2_HUMAN, THA_HUMAN, LCMT2_HUMAN, APC10_HUMAN, SMRCD_HUMAN, ZN408_HUMAN, LAT_HUMAN, BMP10_HUMAN, DYL2_HUMAN, DDEF1_HUMAN, KPYM_HUMAN, TERF1_HUMAN, NR1D1_HUMAN, NUI60_HUMAN, TPM3_HUMAN, TNR8_HUMAN, SMDF_HUMAN, FANCA_HUMAN, SLAP2_HUMAN, TDG_HUMAN, BAZ1A_HUMAN, ZN174_HUMAN, BCLX_HUMAN, ARF6_HUMAN, STAM1_HUMAN, ANGL1_HUMAN, APBA2_HUMAN, BORG1_HUMAN, IF4G3_HUMAN, RFXAP_HUMAN, BRCA1_HUMAN, CADH4_HUMAN, ATF2_HUMAN, STX6_HUMAN, ING5_HUMAN, TSG6_HUMAN, LIS1_HUMAN, PPID_HUMAN, PCDG3_HUMAN, CCR2_HUMAN, ATF4_HUMAN, HSP47_HUMAN, CAR12_HUMAN, PCDG2_HUMAN, PDRN4_HUMAN, LBR_HUMAN, EMD_HUMAN, EZRI_HUMAN, AMFR2_HUMAN, BAG4_HUMAN, NARGL_HUMAN, IL16_HUMAN, FIBA_HUMAN, RANB9_HUMAN, IF5_HUMAN, BCL9_HUMAN, MKL2_HUMAN, NECP2_HUMAN, UGRP2_HUMAN, SUFU_HUMAN, UT14A_HUMAN, LDLR_HUMAN, CDC42_HUMAN, MEF2C_HUMAN, WBS18_HUMAN, CRSP6_HUMAN, KLHL9_HUMAN, NF2L1_HUMAN, PARVG_HUMAN, FLNA_HUMAN, KCMA1_HUMAN, ICAM1_HUMAN, CASPA_HUMAN, PCDGA_HUMAN, NRG1_HUMAN, TRI12_HUMAN, ZBTB3_HUMAN, CD97_HUMAN, UBP33_HUMAN, SK2L2_HUMAN, PCDG8_HUMAN, BAZ1B_HUMAN, CDN1C_HUMAN, MK67I_HUMAN, CSTF1_HUMAN, NMI_HUMAN, CREB1_HUMAN, DRAP1_HUMAN, NINJ1_HUMAN, KLF7_HUMAN, OSTP_HUMAN, ZBTB1_HUMAN, LAMC1_HUMAN, RB_HUMAN, TTRAP_HUMAN, WHRN_HUMAN, SPOP_HUMAN, AT2B2_HUMAN, CYC_HUMAN, PHF20_HUMAN, ID3_HUMAN, DOK1_HUMAN, STXB2_HUMAN, PLRG1_HUMAN, TR11B_HUMAN, SYNE2_HUMAN, EHD1_HUMAN, PLK3_HUMAN, INGR1_HUMAN, S23IP_HUMAN, SETB1_HUMAN, GEMI6_HUMAN, SMCA5_HUMAN, FCAR_HUMAN, BRD1_HUMAN, NCK1_HUMAN, RUNX1_HUMAN, SPHK1_HUMAN, SPI1_HUMAN, SNX18_HUMAN, DISC1_HUMAN, CLPX_HUMAN, CB80_HUMAN, MDM4_HUMAN, SF3B3_HUMAN, HDAC4_HUMAN, SUV91_HUMAN, M4K5_HUMAN, RHG07_HUMAN, MYO9B_HUMAN, IRK2_HUMAN, CTNL1_HUMAN, CARD6_HUMAN, SIP1_HUMAN, TADBP_HUMAN, TRIP4_HUMAN, CASP3_HUMAN, FN14_HUMAN, CUL5_HUMAN, VPS4B_HUMAN, PSN1_HUMAN, FKB1A_HUMAN, ARP6_HUMAN, GRAP2_HUMAN, SP3_HUMAN, BRD8_HUMAN, BIM_HUMAN, TOM1_HUMAN, ANGL2_HUMAN, ZCSL3_HUMAN, REN3B_HUMAN, FGF18_HUMAN, EEA1_HUMAN, SPH2_HUMAN, CSE1_HUMAN, NAMPT_HUMAN, ZN363_HUMAN, CSR2B_HUMAN, PLAK_HUMAN, CAD22_HUMAN, TBBX_HUMAN, FKBP5_HUMAN, TPPC2_HUMAN, ADDB_HUMAN, TBA1_HUMAN, RAB1_HUMAN, IDD_HUMAN, TRI32_HUMAN, AFAD_HUMAN, ADML_HUMAN, TF2AA_HUMAN, FANCE_HUMAN, M3K5_HUMAN, PCDGB_HUMAN, GEMI5_HUMAN, EXOS3_HUMAN, CD1D_HUMAN, TRIPB_HUMAN, DNJA1_HUMAN

-- 2 of 270--

GOID GO:0008134

TERM transcription factor binding

P-VALUE 4.60279499613778e-09

CORRECTED P-VALUE 2.64200432778309e-06

NUM_ANNOTATIONS 27 (of 323)

ANNOTATED_GENES SUFU_HUMAN, TPPC2_HUMAN, MEF2C_HUMAN, TRIP4_HUMAN, FAF1_HUMAN, NMI_HUMAN, TRI32_HUMAN, CREB1_HUMAN, DRAP1_HUMAN, CRSP6_HUMAN, KLF7_HUMAN, BRD8_HUMAN, NF2L1_HUMAN, TF2AA_HUMAN, RB_HUMAN, HDAC4_HUMAN, TTRAP_HUMAN, RFXAP_HUMAN, BRCA1_HUMAN, ATF2_HUMAN, NRG1_HUMAN, ID3_HUMAN, PLRG1_HUMAN, TRI12_HUMAN, TRIPB_HUMAN, MKL2_HUMAN, NR1D1_HUMAN

-- 3 of 270--

GOID GO:0008270

TERM zinc ion binding

P-VALUE 1.03228871974018e-08

CORRECTED P-VALUE 5.92533725130862e-06

NUM_ANNOTATIONS 116 (of 3098)

ANNOTATED_GENES TRIM6_HUMAN, TF2H2_HUMAN, TNF10_HUMAN, GIT2_HUMAN, AF17_HUMAN,

Molecular Function.txt

RP9_HUMAN, ZCHC6_HUMAN, ZNF7_HUMAN, IBRD2_HUMAN, KLF7_HUMAN, BIRC3_HUMAN, SCRT2_HUMAN, MELPH_HUMAN, RPA2_HUMAN, ZBTB1_HUMAN, ZFP95_HUMAN, THA_HUMAN, ZN516_HUMAN, ZNF12_HUMAN, ZN189_HUMAN, CBPA1_HUMAN, K0853_HUMAN, ZN408_HUMAN, ZN223_HUMAN, PHF20_HUMAN, DDEF1_HUMAN, ZN492_HUMAN, NR1D1_HUMAN, ZN430_HUMAN, TRI34_HUMAN, SETB1_HUMAN, ZN646_HUMAN, MIZF_HUMAN, RREB1_HUMAN, ZN264_HUMAN, BRD1_HUMAN, POGZ_HUMAN, BAZ1A_HUMAN, ZN202_HUMAN, ZN174_HUMAN, CLPX_HUMAN, RAD18_HUMAN, MOL1A_HUMAN, MDM4_HUMAN, PPBI_HUMAN, ZN143_HUMAN, ZFY_HUMAN, DHSO_HUMAN, SUV91_HUMAN, BRCA1_HUMAN, GATA5_HUMAN, ATF2_HUMAN, RPC2_HUMAN, CENB5_HUMAN, SALL3_HUMAN, ING5_HUMAN, MYO9B_HUMAN, SIP1_HUMAN, MORC2_HUMAN, CAH8_HUMAN, ZN133_HUMAN, ZN200_HUMAN, ZN222_HUMAN, TRIP4_HUMAN, ZN397_HUMAN, QORL_HUMAN, SIRT1_HUMAN, ARD1_HUMAN, ATRX_HUMAN, SP3_HUMAN, ZNF25_HUMAN, T2EA_HUMAN, KLF10_HUMAN, ZNF10_HUMAN, ZCSL3_HUMAN, PDRN4_HUMAN, NALDL_HUMAN, RN5A_HUMAN, AMFR2_HUMAN, TRPS1_HUMAN, EEA1_HUMAN, ZFH2_HUMAN, ZNF79_HUMAN, ZN350_HUMAN, ZN217_HUMAN, THAP6_HUMAN, RNF6_HUMAN, GLI4_HUMAN, TRIM4_HUMAN, ZN363_HUMAN, SIAH1_HUMAN, ZN286_HUMAN, NR1H2_HUMAN, ZNF22_HUMAN, ZCHC4_HUMAN, PP1RA_HUMAN, MOB3_HUMAN, TRI32_HUMAN, PPBT_HUMAN, LC7L2_HUMAN, ZC3H6_HUMAN, KELL_HUMAN, ZN161_HUMAN, ZEP2_HUMAN, ZNT1_HUMAN, IBRD3_HUMAN, NEUL_HUMAN, RN146_HUMAN, ZF276_HUMAN, SMRA3_HUMAN, TRI27_HUMAN, ZBTB3_HUMAN, KLF11_HUMAN, UBP33_HUMAN, DNJA1_HUMAN, BAZ1B_HUMAN

-- 4 of 270--

GOID GO:0046914

TERM transition metal ion binding

P-VALUE 1.06862082279868e-08

CORRECTED P-VALUE 6.13388352286441e-06

NUM_ANNOTATIONS 131 (of 3643)

ANNOTATED_GENES TRIM6_HUMAN, TF2H2_HUMAN, TNF10_HUMAN, GIT2_HUMAN, AF17_HUMAN, RP9_HUMAN, ZCHC6_HUMAN, ZNF7_HUMAN, IBRD2_HUMAN, KLF7_HUMAN, BIRC3_HUMAN, SCRT2_HUMAN, MUTA_HUMAN, MELPH_HUMAN, RPA2_HUMAN, ZBTB1_HUMAN, ZFP95_HUMAN, THA_HUMAN, ZN516_HUMAN, ZNF12_HUMAN, ZN189_HUMAN, CBPA1_HUMAN, K0853_HUMAN, CYC_HUMAN, ZN408_HUMAN, ZN223_HUMAN, PHF20_HUMAN, B3GN1_HUMAN, DDEF1_HUMAN, ZN492_HUMAN, NR1D1_HUMAN, ZN430_HUMAN, B4GT4_HUMAN, TRI34_HUMAN, HGD_HUMAN, SETB1_HUMAN, ZN646_HUMAN, MIZF_HUMAN, RREB1_HUMAN, ZN264_HUMAN, BRD1_HUMAN, POGZ_HUMAN, BAZ1A_HUMAN, ZN202_HUMAN, ZN174_HUMAN, CLPX_HUMAN, RAD18_HUMAN, MOL1A_HUMAN, PP2CB_HUMAN, MDM4_HUMAN, PPBI_HUMAN, ZN143_HUMAN, ZFY_HUMAN, DHSO_HUMAN, SUV91_HUMAN, SPEB_HUMAN, BRCA1_HUMAN, GATA5_HUMAN, ATF2_HUMAN, RPC2_HUMAN, CENB5_HUMAN, SALL3_HUMAN, ING5_HUMAN, MYO9B_HUMAN, FTMT_HUMAN, SIP1_HUMAN, MORC2_HUMAN, CAH8_HUMAN, ZN133_HUMAN, ZN200_HUMAN, ZN222_HUMAN, TRIP4_HUMAN, ZN397_HUMAN, PUR1_HUMAN, QORL_HUMAN, SIRT1_HUMAN, ARD1_HUMAN, ATRX_HUMAN, SP3_HUMAN, ZNF25_HUMAN, T2EA_HUMAN, KLF10_HUMAN, ZNF10_HUMAN, ZCSL3_HUMAN, PDRN4_HUMAN, NALDL_HUMAN, RN5A_HUMAN, AMFR2_HUMAN, TRPS1_HUMAN, EEA1_HUMAN, ZFH2_HUMAN, ZNF79_HUMAN, ZN350_HUMAN, FA8_HUMAN, ZN217_HUMAN, THAP6_HUMAN, RNF6_HUMAN, FETA_HUMAN, GLI4_HUMAN, TRIM4_HUMAN, SODM_HUMAN, ZN363_HUMAN, SIAH1_HUMAN, PIM1_HUMAN, ZN286_HUMAN, NR1H2_HUMAN, ZNF22_HUMAN, ZCHC4_HUMAN, PP1RA_HUMAN, MOB3_HUMAN, TRI32_HUMAN, PPBT_HUMAN, LC7L2_HUMAN, ZC3H6_HUMAN, KELL_HUMAN, ZN161_HUMAN, ZEP2_HUMAN, GALT3_HUMAN, BCDO2_HUMAN, ZNT1_HUMAN, IBRD3_HUMAN, NEUL_HUMAN, RN146_HUMAN, ZF276_HUMAN, SMRA3_HUMAN, TRI27_HUMAN, ZBTB3_HUMAN, KLF11_HUMAN, UBP33_HUMAN, DNJA1_HUMAN, BAZ1B_HUMAN

-- 5 of 270--

GOID GO:0030528

TERM transcription regulator activity

P-VALUE 1.68190079307369e-08

CORRECTED P-VALUE 9.65411055224295e-06

NUM_ANNOTATIONS 78 (of 1816)

ANNOTATED_GENES TF2H2_HUMAN, FLI1_HUMAN, IF16_HUMAN, NMI_HUMAN, CREB1_HUMAN, DRAP1_HUMAN, KLF7_HUMAN, MTERF_HUMAN, ZFP95_HUMAN, THA_HUMAN, RB_HUMAN, TTRAP_HUMAN, ZN189_HUMAN, ID3_HUMAN, PLRG1_HUMAN, ETS2_HUMAN, NR1D1_HUMAN, HEN2_HUMAN, HOP_HUMAN, SMCA5_HUMAN, RUNX1_HUMAN, RUNX3_HUMAN, SPI1_HUMAN, ZN202_HUMAN, ETV5_HUMAN, ZN174_HUMAN, ZN143_HUMAN, HDAC4_HUMAN, ZFY_HUMAN, ID2_HUMAN, RFXAP_HUMAN, BRCA1_HUMAN, GATA5_HUMAN, ATF2_HUMAN, ID1_HUMAN, HMG2_HUMAN, SIP1_HUMAN, ZN133_HUMAN, TADBP_HUMAN, TCF7_HUMAN, TRIP4_HUMAN, ZN397_HUMAN, ATF4_HUMAN, FOXO1_HUMAN, ATRX_HUMAN, SP3_HUMAN, BRD8_HUMAN, T2EA_HUMAN, KLF10_HUMAN,

Molecular Function.txt

TRPS1_HUMAN, ZFH2_HUMAN, ZN217_HUMAN, PHTF1_HUMAN, IRF2_HUMAN, MKL2_HUMAN, NR1H2_HUMAN, SUFU_HUMAN, PO5FM_HUMAN, MEF2C_HUMAN, HXA9_HUMAN, PO5FL_HUMAN, TRI32_HUMAN, CRSP6_HUMAN, ZN161_HUMAN, NF2L1_HUMAN, TF2AA_HUMAN, MAF_HUMAN, TF3C4_HUMAN, T2FB_HUMAN, DLX2_HUMAN, NRG1_HUMAN, PEPPI_HUMAN, ELL_HUMAN, PO6F2_HUMAN, TRIPB_HUMAN, KLF11_HUMAN, BAZ1B_HUMAN, EPC1_HUMAN

-- 6 of 270--

GOID GO:0003712

TERM transcription cofactor activity

P-VALUE 6.32023743065978e-08

CORRECTED P-VALUE 3.62781628519872e-05

NUM_ANNOTATIONS 23 (of 275)

ANNOTATED_GENES SUFU_HUMAN, MEF2C_HUMAN, TRIP4_HUMAN, NMI_HUMAN, TRI32_HUMAN, CREB1_HUMAN, DRAP1_HUMAN, CRSP6_HUMAN, KLF7_HUMAN, BRD8_HUMAN, TF2AA_HUMAN, ZN492_HUMAN, NR1D1_HUMAN, TTRAP_HUMAN, RFXAP_HUMAN, BRCA1_HUMAN, ATF2_HUMAN, NRG1_HUMAN, ID3_HUMAN, PLRG1_HUMAN, TRIPB_HUMAN, MKL2_HUMAN, NR1D1_HUMAN

-- 7 of 270--

GOID GO:0043167

TERM ion binding

P-VALUE 1.09020421713325e-07

CORRECTED P-VALUE 6.25777220634485e-05

NUM_ANNOTATIONS 170 (of 5283)

ANNOTATED_GENES TRIM6_HUMAN, TNF10_HUMAN, GIT2_HUMAN, AF17_HUMAN, RP9_HUMAN, TRPM3_HUMAN, IBRD2_HUMAN, BIRC3_HUMAN, MELPH_HUMAN, EGFL5_HUMAN, THA_HUMAN, K0853_HUMAN, ZN408_HUMAN, ZN223_HUMAN, B3GN1_HUMAN, DDEF1_HUMAN, KPYM_HUMAN, ZN492_HUMAN, NR1D1_HUMAN, SFTA2_HUMAN, HGD_HUMAN, ZN646_HUMAN, ZN264_HUMAN, BAZ1A_HUMAN, ZN174_HUMAN, MOL1A_HUMAN, PPBI_HUMAN, ZN143_HUMAN, DHSO_HUMAN, PURA2_HUMAN, BRCA1_HUMAN, CADH4_HUMAN, GATA5_HUMAN, RPC2_HUMAN, ATF2_HUMAN, ING5_HUMAN, FTMT_HUMAN, PCDG3_HUMAN, ZN222_HUMAN, PUR1_HUMAN, ATRX_HUMAN, HCN1_HUMAN, PCDG2_HUMAN, KLF10_HUMAN, ZNF10_HUMAN, PDRN4_HUMAN, AMFR2_HUMAN, TRPS1_HUMAN, ZFH2_HUMAN, ZN350_HUMAN, FA8_HUMAN, RNF6_HUMAN, FETA_HUMAN, GLI4_HUMAN, TRIM4_HUMAN, SODM_HUMAN, PIM1_HUMAN, NR1H2_HUMAN, LDLR_HUMAN, CERK1_HUMAN, ZCHC4_HUMAN, PP1RA_HUMAN, PPBT_HUMAN, 5NT1B_HUMAN, KCNQ2_HUMAN, ZEP2_HUMAN, BCDO2_HUMAN, CA022_HUMAN, NEUL_HUMAN, PA24A_HUMAN, KCMA1_HUMAN, PCDGA_HUMAN, CCG1_HUMAN, SMRA3_HUMAN, ZBTB3_HUMAN, KLF11_HUMAN, UBP33_HUMAN, CD97_HUMAN, PCDG8_HUMAN, BAZ1B_HUMAN, TF2H2_HUMAN, ZCHC6_HUMAN, ZNF7_HUMAN, KLF7_HUMAN, RFIP4_HUMAN, SCRT2_HUMAN, MUTA_HUMAN, ZBTB1_HUMAN, RPA2_HUMAN, ZFP95_HUMAN, ZN516_HUMAN, ZNF12_HUMAN, ZN189_HUMAN, CBPA1_HUMAN, AT2B2_HUMAN, CYC_HUMAN, PHF20_HUMAN, EHD1_HUMAN, ZN430_HUMAN, POLH_HUMAN, B4GT4_HUMAN, TRI34_HUMAN, AGM1_HUMAN, S23IP_HUMAN, SETB1_HUMAN, MIZF_HUMAN, BRD1_HUMAN, SPHK1_HUMAN, RREB1_HUMAN, POGZ_HUMAN, ZN202_HUMAN, CLPX_HUMAN, RAD18_HUMAN, PP2CB_HUMAN, MDM4_HUMAN, ZFY_HUMAN, SUV91_HUMAN, SPEB_HUMAN, CENB5_HUMAN, SALL3_HUMAN, MYO9B_HUMAN, IRK2_HUMAN, KCNG4_HUMAN, SIP1_HUMAN, MORC2_HUMAN, EGFL8_HUMAN, CAH8_HUMAN, ZN133_HUMAN, GRAN_HUMAN, ZN200_HUMAN, TRIP4_HUMAN, ZN397_HUMAN, QORL_HUMAN, SIRT1_HUMAN, S12A4_HUMAN, ARD1_HUMAN, SP3_HUMAN, ZNF25_HUMAN, T2EA_HUMAN, ZCSL3_HUMAN, NALDL_HUMAN, EEA1_HUMAN, RN5A_HUMAN, ZNF79_HUMAN, THAP6_HUMAN, ZN217_HUMAN, NCKX1_HUMAN, ZN363_HUMAN, SIAH1_HUMAN, CAD22_HUMAN, ZN286_HUMAN, ZNF22_HUMAN, IRK3_HUMAN, MOB3_HUMAN, TRI32_HUMAN, KELL_HUMAN, ZC3H6_HUMAN, LC7L2_HUMAN, ZN161_HUMAN, GALT3_HUMAN, ZNT1_HUMAN, IBRD3_HUMAN, M3K5_HUMAN, RN146_HUMAN, EYA1_HUMAN, ZF276_HUMAN, PCDGB_HUMAN, TRI27_HUMAN, DNJA1_HUMAN, CETN3_HUMAN

-- 8 of 270--

GOID GO:0046872

TERM metal ion binding

P-VALUE 1.09020421713325e-07

CORRECTED P-VALUE 6.25777220634485e-05

NUM_ANNOTATIONS 170 (of 5283)

ANNOTATED_GENES TRIM6_HUMAN, TNF10_HUMAN, GIT2_HUMAN, AF17_HUMAN, RP9_HUMAN, TRPM3_HUMAN, IBRD2_HUMAN, BIRC3_HUMAN, MELPH_HUMAN, EGFL5_HUMAN, THA_HUMAN, K0853_HUMAN, ZN408_HUMAN, ZN223_HUMAN, B3GN1_HUMAN, DDEF1_HUMAN, KPYM_HUMAN, ZN492_HUMAN, NR1D1_HUMAN, SFTA2_HUMAN, HGD_HUMAN, ZN646_HUMAN, ZN264_HUMAN,

Molecular Function.txt

BAZ1A_HUMAN, ZN174_HUMAN, MOL1A_HUMAN, PPBI_HUMAN, ZN143_HUMAN, DHSO_HUMAN, PURA2_HUMAN, BRCA1_HUMAN, CADH4_HUMAN, GATA5_HUMAN, RPC2_HUMAN, ATF2_HUMAN, ING5_HUMAN, FTMT_HUMAN, PCDG3_HUMAN, ZN222_HUMAN, PUR1_HUMAN, ATRX_HUMAN, HCN1_HUMAN, PCDG2_HUMAN, KLF10_HUMAN, ZNF10_HUMAN, PDRN4_HUMAN, AMFR2_HUMAN, TRPS1_HUMAN, ZFH2_HUMAN, ZN350_HUMAN, FA8_HUMAN, RNF6_HUMAN, FETA_HUMAN, GLI4_HUMAN, TRIM4_HUMAN, SODM_HUMAN, PIM1_HUMAN, NR1H2_HUMAN, LDLR_HUMAN, CERK1_HUMAN, ZCHC4_HUMAN, PP1RA_HUMAN, PPBT_HUMAN, 5NT1B_HUMAN, KCNQ2_HUMAN, ZEP2_HUMAN, BCDO2_HUMAN, CA022_HUMAN, NEUL_HUMAN, PA24A_HUMAN, KCMA1_HUMAN, PCDGA_HUMAN, CCG1_HUMAN, SMRA3_HUMAN, ZBTB3_HUMAN, KLF11_HUMAN, UBP33_HUMAN, CD97_HUMAN, PCDG8_HUMAN, BAZ1B_HUMAN, TF2H2_HUMAN, ZCHC6_HUMAN, ZNF7_HUMAN, KLF7_HUMAN, RFIP4_HUMAN, SCRT2_HUMAN, MUTA_HUMAN, ZBTB1_HUMAN, RPA2_HUMAN, ZFP95_HUMAN, ZN516_HUMAN, ZNF12_HUMAN, ZN189_HUMAN, CBPA1_HUMAN, AT2B2_HUMAN, CYC_HUMAN, PHF20_HUMAN, EHD1_HUMAN, ZN430_HUMAN, POLH_HUMAN, B4GT4_HUMAN, TRI34_HUMAN, AGM1_HUMAN, S23IP_HUMAN, SETB1_HUMAN, MIZF_HUMAN, BRD1_HUMAN, SPHK1_HUMAN, RREB1_HUMAN, POGZ_HUMAN, ZN202_HUMAN, CLPX_HUMAN, RAD18_HUMAN, PP2CB_HUMAN, MDM4_HUMAN, ZFY_HUMAN, SUV91_HUMAN, SPEB_HUMAN, CENB5_HUMAN, SALL3_HUMAN, MYO9B_HUMAN, IRK2_HUMAN, KCNG4_HUMAN, SIP1_HUMAN, MORC2_HUMAN, EGFL8_HUMAN, CAH8_HUMAN, ZN133_HUMAN, GRAN_HUMAN, ZN200_HUMAN, TRIP4_HUMAN, ZN397_HUMAN, QORL_HUMAN, SIRT1_HUMAN, S12A4_HUMAN, ARD1_HUMAN, SP3_HUMAN, ZNF25_HUMAN, T2EA_HUMAN, ZCSL3_HUMAN, NALDL_HUMAN, EEA1_HUMAN, RN5A_HUMAN, ZNF79_HUMAN, THAP6_HUMAN, ZN217_HUMAN, NCKX1_HUMAN, ZN363_HUMAN, SIAH1_HUMAN, CAD22_HUMAN, ZN286_HUMAN, ZNF22_HUMAN, IRK3_HUMAN, MOB3_HUMAN, TRI32_HUMAN, KELL_HUMAN, ZC3H6_HUMAN, LC7L2_HUMAN, ZN161_HUMAN, GALT3_HUMAN, ZNT1_HUMAN, IBRD3_HUMAN, M3K5_HUMAN, RN146_HUMAN, EYA1_HUMAN, ZF276_HUMAN, PCDGB_HUMAN, TRI27_HUMAN, DNJA1_HUMAN, CETN3_HUMAN

-- 9 of 270--

GOID GO:0003677

TERM DNA binding

P-VALUE 1.14085647987635e-07

CORRECTED P-VALUE 6.54851619449025e-05

NUM_ANNOTATIONS 110 (of 3020)

ANNOTATED_GENES PARP4_HUMAN, TF2H2_HUMAN, FLI1_HUMAN, IF16_HUMAN, CREB1_HUMAN, DRAP1_HUMAN, ZNF7_HUMAN, KLF7_HUMAN, MTERF_HUMAN, SCRT2_HUMAN, RPA2_HUMAN, ZBTB1_HUMAN, ZFP95_HUMAN, THA_HUMAN, RB_HUMAN, ZN516_HUMAN, ZNF12_HUMAN, ZN189_HUMAN, SMRCD_HUMAN, ZN408_HUMAN, ZN223_HUMAN, PHF20_HUMAN, ETS2_HUMAN, ZN492_HUMAN, TERF1_HUMAN, NR1D1_HUMAN, ZN430_HUMAN, POLH_HUMAN, HEN2_HUMAN, HOP_HUMAN, SETB1_HUMAN, MSH2_HUMAN, ZN646_HUMAN, MIZF_HUMAN, SMCA5_HUMAN, RREB1_HUMAN, SPHK1_HUMAN, RUNX1_HUMAN, ZN264_HUMAN, RUNX3_HUMAN, TDG_HUMAN, SPI1_HUMAN, ZN202_HUMAN, ETV5_HUMAN, ZN174_HUMAN, RAD18_HUMAN, MSH6_HUMAN, BLM_HUMAN, ZN143_HUMAN, ZFY_HUMAN, RFXAP_HUMAN, BRCA1_HUMAN, GATA5_HUMAN, RPC2_HUMAN, ATF2_HUMAN, HMG2_HUMAN, SALL3_HUMAN, SIP1_HUMAN, ZN133_HUMAN, ZN222_HUMAN, TADBP_HUMAN, TCF7_HUMAN, ZN397_HUMAN, ATF4_HUMAN, FOXO1_HUMAN, SIRT1_HUMAN, ATRX_HUMAN, SP3_HUMAN, CV106_HUMAN, BRD8_HUMAN, ZNF25_HUMAN, KLF10_HUMAN, ZNF10_HUMAN, SON_HUMAN, LBR_HUMAN, TRPS1_HUMAN, ZFH2_HUMAN, ZNF79_HUMAN, ZN350_HUMAN, ZN217_HUMAN, THAP6_HUMAN, PHTF1_HUMAN, GLI4_HUMAN, IRF2_HUMAN, ZN286_HUMAN, MKL2_HUMAN, NR1H2_HUMAN, ZNF22_HUMAN, PO5FM_HUMAN, HNRPU_HUMAN, MEF2C_HUMAN, HXA9_HUMAN, PP1RA_HUMAN, PO5FL_HUMAN, ZN161_HUMAN, ZEP2_HUMAN, NF2L1_HUMAN, MAF_HUMAN, TF3C4_HUMAN, DNL4_HUMAN, T2FB_HUMAN, ZF276_HUMAN, SMRA3_HUMAN, TRI27_HUMAN, DLX2_HUMAN, PEPP1_HUMAN, ZBTB3_HUMAN, PO6F2_HUMAN, KLF11_HUMAN, BAZ1B_HUMAN

-- 10 of 270--

GOID GO:0043169

TERM cation binding

P-VALUE 1.84781748434755e-07

CORRECTED P-VALUE 0.000106064723601549

NUM_ANNOTATIONS 161 (of 4972)

ANNOTATED_GENES TRIM6_HUMAN, TNF10_HUMAN, GIT2_HUMAN, AF17_HUMAN, RP9_HUMAN, TRPM3_HUMAN, IBRD2_HUMAN, BIRC3_HUMAN, MELPH_HUMAN, EGFL5_HUMAN, THA_HUMAN, K0853_HUMAN, ZN408_HUMAN, ZN223_HUMAN, B3GN1_HUMAN, DDEF1_HUMAN, ZN492_HUMAN, NR1D1_HUMAN, SFTA2_HUMAN, HGD_HUMAN, ZN646_HUMAN, ZN264_HUMAN, BAZ1A_HUMAN, ZN174_HUMAN, MOL1A_HUMAN, PPBI_HUMAN, ZN143_HUMAN, DHSO_HUMAN, BRCA1_HUMAN,

Molecular Function.txt

CADH4_HUMAN, GATA5_HUMAN, RPC2_HUMAN, ATF2_HUMAN, ING5_HUMAN, FTMT_HUMAN, PCDG3_HUMAN, ZN222_HUMAN, PUR1_HUMAN, ATRX_HUMAN, HCN1_HUMAN, PCDG2_HUMAN, KLF10_HUMAN, ZNF10_HUMAN, PDRN4_HUMAN, AMFR2_HUMAN, TRPS1_HUMAN, ZFH2_HUMAN, ZN350_HUMAN, FA8_HUMAN, RNF6_HUMAN, FETA_HUMAN, GLI4_HUMAN, TRIM4_HUMAN, SODM_HUMAN, PIM1_HUMAN, NR1H2_HUMAN, LDLR_HUMAN, CERK1_HUMAN, ZCHC4_HUMAN, PP1RA_HUMAN, PPBT_HUMAN, KCNQ2_HUMAN, ZEP2_HUMAN, BCDO2_HUMAN, CA022_HUMAN, NEUL_HUMAN, PA24A_HUMAN, KCMA1_HUMAN, PCDGA_HUMAN, CCG1_HUMAN, SMRA3_HUMAN, ZBTB3_HUMAN, KLF11_HUMAN, UBP33_HUMAN, CD97_HUMAN, PCDG8_HUMAN, BAZ1B_HUMAN, TF2H2_HUMAN, ZCHC6_HUMAN, ZNF7_HUMAN, KLF7_HUMAN, RFIP4_HUMAN, SCRT2_HUMAN, MUTA_HUMAN, ZBTB1_HUMAN, RPA2_HUMAN, ZFP95_HUMAN, ZN516_HUMAN, ZNF12_HUMAN, ZN189_HUMAN, AT2B2_HUMAN, CBPA1_HUMAN, CYC_HUMAN, PHF20_HUMAN, EHD1_HUMAN, ZN430_HUMAN, B4GT4_HUMAN, TRI34_HUMAN, SETB1_HUMAN, MIZF_HUMAN, BRD1_HUMAN, RREB1_HUMAN, POGZ_HUMAN, ZN202_HUMAN, CLPX_HUMAN, RAD18_HUMAN, PP2CB_HUMAN, MDM4_HUMAN, ZFY_HUMAN, SUV91_HUMAN, SPEB_HUMAN, CENB5_HUMAN, SALL3_HUMAN, MYO9B_HUMAN, IRK2_HUMAN, KCNG4_HUMAN, SIP1_HUMAN, MORC2_HUMAN, EGFL8_HUMAN, CAH8_HUMAN, ZN133_HUMAN, GRAN_HUMAN, ZN200_HUMAN, TRIP4_HUMAN, ZN397_HUMAN, QORL_HUMAN, SIRT1_HUMAN, S12A4_HUMAN, ARD1_HUMAN, SP3_HUMAN, ZNF25_HUMAN, T2EA_HUMAN, ZCSL3_HUMAN, NALDL_HUMAN, EEA1_HUMAN, RN5A_HUMAN, ZNF79_HUMAN, THAP6_HUMAN, ZN217_HUMAN, NCKX1_HUMAN, ZN363_HUMAN, SIAH1_HUMAN, CAD22_HUMAN, ZN286_HUMAN, ZNF22_HUMAN, IRK3_HUMAN, MOB3_HUMAN, TRI32_HUMAN, KELL_HUMAN, ZC3H6_HUMAN, LC7L2_HUMAN, GALT3_HUMAN, ZN161_HUMAN, ZNT1_HUMAN, IBD3_HUMAN, RN146_HUMAN, ZF276_HUMAN, PCDGB_HUMAN, TRI27_HUMAN, DNJA1_HUMAN, CETN3_HUMAN

-- 11 of 270--

GOID GO:0005488

TERM binding

P-VALUE 5.59271096870498e-07

CORRECTED P-VALUE 0.000321021609603666

NUM_ANNOTATIONS 413 (of 15946)

ANNOTATED_GENES TRIM6_HUMAN, TNF10_HUMAN, PACE1_HUMAN, IF16_HUMAN, MLP3B_HUMAN, FAF1_HUMAN, APBP2_HUMAN, PPIG_HUMAN, RP9_HUMAN, IBD2_HUMAN, AIM1_HUMAN, BIRC3_HUMAN, CCNT2_HUMAN, ANGP2_HUMAN, IFIT2_HUMAN, K0562_HUMAN, AP4E1_HUMAN, PKD1_HUMAN, APC10_HUMAN, B3GN1_HUMAN, TBA6_HUMAN, DDEF1_HUMAN, KPYM_HUMAN, TERF1_HUMAN, SYR_HUMAN, HOP_HUMAN, TPM3_HUMAN, ACHB_HUMAN, HGD_HUMAN, ZN646_HUMAN, SMDF_HUMAN, FANCA_HUMAN, ZN264_HUMAN, RUNX3_HUMAN, TDG_HUMAN, ZN174_HUMAN, BCLX_HUMAN, ANGL1_HUMAN, APBA2_HUMAN, BLM_HUMAN, ZN143_HUMAN, IF4G3_HUMAN, DHSO_HUMAN, RFXAP_HUMAN, BRCA1_HUMAN, HCA66_HUMAN, ATF2_HUMAN, STX6_HUMAN, STK35_HUMAN, ING5_HUMAN, PCDG3_HUMAN, ZN222_HUMAN, CCR2_HUMAN, ATF4_HUMAN, FOXO1_HUMAN, ATRX_HUMAN, HCN1_HUMAN, HSP47_HUMAN, CV106_HUMAN, ZG16_HUMAN, PCDG2_HUMAN, KLF10_HUMAN, PDRN4_HUMAN, LBR_HUMAN, EMD_HUMAN, EZRI_HUMAN, TRPS1_HUMAN, ZFH2_HUMAN, ZN350_HUMAN, FA8_HUMAN, RNF6_HUMAN, NARGL_HUMAN, FETA_HUMAN, PHTF1_HUMAN, JERKL_HUMAN, TRIM4_HUMAN, SODM_HUMAN, FIBA_HUMAN, DDX10_HUMAN, RANB9_HUMAN, PIM1_HUMAN, IF5_HUMAN, NECP2_HUMAN, NR1H2_HUMAN, SUFU_HUMAN, RBM12_HUMAN, CDC42_HUMAN, CERK1_HUMAN, PP1RA_HUMAN, WBS18_HUMAN, ATRN_HUMAN, T103_HUMAN, CA022_HUMAN, PA24A_HUMAN, MAF_HUMAN, TF3C4_HUMAN, MK06_HUMAN, SMRA3_HUMAN, MFN1_HUMAN, ZBTB3_HUMAN, SK2L2_HUMAN, KLF11_HUMAN, NIPBL_HUMAN, CDN1C_HUMAN, TF2H2_HUMAN, NMI_HUMAN, DRAP1_HUMAN, ZNF7_HUMAN, NINJ1_HUMAN, KLF7_HUMAN, MUTA_HUMAN, PTAFR_HUMAN, RPA2_HUMAN, ZBTB1_HUMAN, ZFP95_HUMAN, SETX_HUMAN, GIMA1_HUMAN, RB_HUMAN, ZNF12_HUMAN, WHRN_HUMAN, SPOP_HUMAN, CBPA1_HUMAN, AT2B2_HUMAN, CYC_HUMAN, STXB2_HUMAN, DOK1_HUMAN, DDX31_HUMAN, TR11B_HUMAN, NCBP2_HUMAN, ETS2_HUMAN, EHD1_HUMAN, SYNE2_HUMAN, POLH_HUMAN, HEN2_HUMAN, TRI34_HUMAN, RAB10_HUMAN, AGM1_HUMAN, S23IP_HUMAN, SETB1_HUMAN, SMCA5_HUMAN, RREB1_HUMAN, TNPO1_HUMAN, ETV5_HUMAN, DISC1_HUMAN, CLPX_HUMAN, ZFY_HUMAN, SUV91_HUMAN, SPEB_HUMAN, PUM2_HUMAN, M4K5_HUMAN, RS10_HUMAN, CENB5_HUMAN, SALL3_HUMAN, SIP1_HUMAN, MORC2_HUMAN, EGFL8_HUMAN, ZN200_HUMAN, TCF7_HUMAN, DUS11_HUMAN, PANK2_HUMAN, SEP10_HUMAN, CASP3_HUMAN, FN14_HUMAN, ZN397_HUMAN, VPS4B_HUMAN, SIRT1_HUMAN, ARD1_HUMAN, C5AR_HUMAN, T2EA_HUMAN, ANGL2_HUMAN, ZCSL3_HUMAN, NALDL_HUMAN, RAB9A_HUMAN, REN3B_HUMAN, RN5A_HUMAN, EEA1_HUMAN, FGF18_HUMAN, SPH2_HUMAN, ZNF79_HUMAN, ZN217_HUMAN, IRF2_HUMAN, SIAH1_HUMAN, CAD22_HUMAN, ZN286_HUMAN, PO5FM_HUMAN, TPPC2_HUMAN, PO5FL_HUMAN, MOB3_HUMAN, IDD_HUMAN, TRI32_HUMAN, LC7L2_HUMAN, KELL_HUMAN, AFAD_HUMAN, ADML_HUMAN, IBD3_HUMAN, TF2AA_HUMAN, TBB6_HUMAN, OBP2B_HUMAN, GIMA2_HUMAN, PRS10_HUMAN, IF2P_HUMAN, FANCE_HUMAN, DHRS3_HUMAN, ICT1_HUMAN, T2FB_HUMAN, RN146_HUMAN,

Molecular Function.txt

ZF276_HUMAN, PCDGB_HUMAN, EXOS3_HUMAN, LARP4_HUMAN, DLX2_HUMAN, TRIPB_HUMAN, DNJA1_HUMAN, TBA2_HUMAN, PIM3_HUMAN, CSTF3_HUMAN, MK14_HUMAN, PARP4_HUMAN, GIT2_HUMAN, MUTED_HUMAN, SNX27_HUMAN, AF17_HUMAN, TDRD7_HUMAN, TRPM3_HUMAN, STRN3_HUMAN, MELPH_HUMAN, EGFL5_HUMAN, THA_HUMAN, LCMT2_HUMAN, GIMA5_HUMAN, SMRCD_HUMAN, K0853_HUMAN, ZN408_HUMAN, ZN223_HUMAN, LAT_HUMAN, BMP10_HUMAN, DYL2_HUMAN, PAPOG_HUMAN, ZN492_HUMAN, NR1D1_HUMAN, SFTA2_HUMAN, NU160_HUMAN, CT006_HUMAN, TNR8_HUMAN, SLAP2_HUMAN, BAZ1A_HUMAN, MPP8_HUMAN, MOL1A_HUMAN, KYNU_HUMAN, ARF6_HUMAN, STAM1_HUMAN, PPBI_HUMAN, BORG1_HUMAN, PURA2_HUMAN, CADH4_HUMAN, GATA5_HUMAN, RPC2_HUMAN, RIOK3_HUMAN, HMG2_HUMAN, TSG6_HUMAN, LIS1_HUMAN, FTMT_HUMAN, AK1C1_HUMAN, PPID_HUMAN, DAPP1_HUMAN, PUR1_HUMAN, GPR83_HUMAN, KLC8_HUMAN, CAR12_HUMAN, TBB4_HUMAN, ZNF10_HUMAN, PDPK1_HUMAN, SON_HUMAN, AMFR2_HUMAN, BAG4_HUMAN, NOP56_HUMAN, GLI4_HUMAN, IL16_HUMAN, MKL2_HUMAN, BCL9_HUMAN, UGRP2_HUMAN, UT14A_HUMAN, LDLR_HUMAN, MEF2C_HUMAN, ZCHC4_HUMAN, HS105_HUMAN, AGGF1_HUMAN, 5NT1B_HUMAN, PPBT_HUMAN, CRSP6_HUMAN, KCNQ2_HUMAN, KLHL9_HUMAN, ZEP2_HUMAN, BCDO2_HUMAN, NF2L1_HUMAN, NEUL_HUMAN, PARVG_HUMAN, FLNA_HUMAN, KCMA1_HUMAN, ICAM1_HUMAN, CASPA_HUMAN, PCDGA_HUMAN, CCG1_HUMAN, NRG1_HUMAN, PFTK1_HUMAN, PEPP1_HUMAN, TRI12_HUMAN, PO6F2_HUMAN, CD97_HUMAN, UBP33_HUMAN, PCDG8_HUMAN, BAZ1B_HUMAN, FLI1_HUMAN, MK67I_HUMAN, GIMA4_HUMAN, CSTF1_HUMAN, RIOK2_HUMAN, ZCHC6_HUMAN, DDX52_HUMAN, CREB1_HUMAN, TGDS_HUMAN, RFIP4_HUMAN, MTERF_HUMAN, SCRT2_HUMAN, OSTP_HUMAN, LAMC1_HUMAN, MPRB_HUMAN, ZN516_HUMAN, TTRAP_HUMAN, ZN189_HUMAN, ACHA_HUMAN, PHF20_HUMAN, ID3_HUMAN, PLRG1_HUMAN, ZN430_HUMAN, B4GT4_HUMAN, PLK3_HUMAN, INGR1_HUMAN, CPNE1_HUMAN, MSH2_HUMAN, GEMI6_HUMAN, MIZF_HUMAN, FCAR_HUMAN, SPHK1_HUMAN, BRD1_HUMAN, NCK1_HUMAN, RUNX1_HUMAN, STAG2_HUMAN, POGZ_HUMAN, SPI1_HUMAN, ZN202_HUMAN, SNX18_HUMAN, RAD18_HUMAN, PP2CB_HUMAN, RAP2B_HUMAN, CB80_HUMAN, MDM4_HUMAN, MSH6_HUMAN, SF3B3_HUMAN, HDAC4_HUMAN, RHG07_HUMAN, MYO9B_HUMAN, IRK2_HUMAN, CTNL1_HUMAN, CARD6_HUMAN, KCNG4_HUMAN, CAH8_HUMAN, ZN133_HUMAN, GRAN_HUMAN, TADBP_HUMAN, TRIP4_HUMAN, CUL5_HUMAN, PSN1_HUMAN, QORL_HUMAN, FKB1A_HUMAN, S12A4_HUMAN, ARP6_HUMAN, GRAP2_HUMAN, SP3_HUMAN, BRD8_HUMAN, ZNF25_HUMAN, BIM_HUMAN, TOM1_HUMAN, THAP6_HUMAN, NCKX1_HUMAN, CSE1_HUMAN, NAMPT_HUMAN, CSR2B_HUMAN, ZN363_HUMAN, PLAK_HUMAN, GIMA7_HUMAN, ZNF22_HUMAN, TBBX_HUMAN, FKBP5_HUMAN, HNRPU_HUMAN, ADDB_HUMAN, IRK3_HUMAN, TBA1_HUMAN, HXA9_HUMAN, RAB1_HUMAN, ZC3H6_HUMAN, ZN161_HUMAN, GALT3_HUMAN, ZNT1_HUMAN, DNL4_HUMAN, M3K5_HUMAN, EYA1_HUMAN, HNRL1_HUMAN, GEMI5_HUMAN, TRI27_HUMAN, CD1D_HUMAN, STK39_HUMAN, CETN3_HUMAN

-- 12 of 270--

GOID GO:0016563

TERM transcriptional activator activity

P-VALUE 3.05244056638247e-06

CORRECTED P-VALUE 0.00175210088510354

NUM_ANNOTATIONS 19 (of 247)

ANNOTATED_GENES MEF2C_HUMAN, TRIP4_HUMAN, HXA9_HUMAN, ATF4_HUMAN, TRI32_HUMAN, RUNX1_HUMAN, CRSP6_HUMAN, SP3_HUMAN, KLF7_HUMAN, BRD8_HUMAN, TF2AA_HUMAN, RB_HUMAN, RFXAP_HUMAN, BRCA1_HUMAN, GATA5_HUMAN, ATF2_HUMAN, TRIPB_HUMAN, MKL2_HUMAN, EPC1_HUMAN