

# Pancreatic cancer differential methylation atlas in blood, peri-carcinomatous and diseased tissue

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**Background:** Pancreatic cancer is common in elderly persons, and less than 20% of patients present with localized, potentially curable tumors.

**Methods:** We compared the methylated sites and genes in pericarcinous tissues compared to cancer tissue, and blood compared to pericarcinous tissues in order to harvest methylation markers for putative diagnostic and therapy monitoring purposes.

**Results:** Of 15,397 CpG sites detected in 7,440 genes, 5,605 (36.4%, 5,605 of 15,397) CpG sites were hypomethylated and 5,870 (38.12%, 5,870 of 15,397) CpG sites were hypermethylated. We then performed Gene Ontology (GO) and KEGG analysis to systematically characterize the ten significantly differentially methylated genes: *PTPRN2*, *MAD1L1*, *TNXB*, *PRDM16*, *GNAS*, *KCNQ1*, *TSNARE1*, *HDAC4*, *TBCD*, and *DIP2C*. Meanwhile, function analysis of genes with differentially methylated sites located in promoter regions of overlap group was also performed. According to previous studies, we further screened 22 pancreatic cancer related key genes. The results suggested that these key genes can influence methylation. GO and KEGG analysis indicated that these genes are involved in a wide range of functions.

**Conclusions:** The identification of differentially methylated genes in this study provides valuable information for liquid biopsy methylation markers in pancreatic cancer.

Keywords: Pancreatic cancer; blood; DNA methylation; CpG sites; KEGG

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#### Introduction

Pancreatic cancer is more common in elderly persons than in younger persons, and less than 20% of patients present with localized, potentially curable tumors (1). The estimated incidence of pancreatic cancer in the United States was 37,700 cases, and an estimated 34,300 patients died from the disease in 2008. The overall 5-year survival rate among patients with pancreatic cancer is <5% (2). Several environmental factors have been implicated, but evidence of a causative role exists only for tobacco use. The risk of pancreatic cancer in smokers is 2.5 to 3.6 times that in nonsmokers (3) Some studies have shown an increased incidence of pancreatic cancer among patients with a history of diabetes or chronic pancreatitis, and there is also evidence that chronic cirrhosis, a high-fat, high-cholesterol diet, and previous cholecystectomy are associated with an increased incidence (4,5).

Presently, there is no valid diagnostic marker for pancreatic cancer. Carbohydrate antigen 19-9 (CA 19-9) levels are elevated in pancreatic cancer but frequently only

mean age:  $58.83 \pm 14.95$  y), without radiation, chemotherapy and immunotherapy treatment, were recruited from the

in advanced disease. It can also be elevated in other cancers, chronic pancreatitis, and autoimmune diseases such as rheumatoid arthritis. Approximately 10% of the population lacks expression of Lewis antigen, which is required to produce CA 19-9. Furthermore, CA 19-9 is used in a clinical setting based on response to treatment (6,7). Up to now, a combination of complex and advanced imaging modalities, such as positron emission tomography scanning, 3-phase computed tomography scanning, endoscopic ultrasound, laparoscopic ultrasound, endoscopic retrograde cholangiopancreatography, and trans-abdominal ultrasound, are necessary for the diagnosis of pancreatic cancer. However, several of these methods are invasive and thus risk complications. Consequently, a minimally or noninvasive marker for pancreatic cancer is urgently needed.

Epigenetics is defined as the study of mitotically or meiotically heritable variations in gene function that cannot be explained by changes in DNA sequence (8). Epigenetic modifications, such as DNA promoter hypermethylation, are known to be aspects of early carcinogenesis and have shown significant potential in the development of a useful diagnostic marker (9,10). Recently, attention to its role in pancreatic cancer has recently increased. DNA methylation has gained much recent interest for its role in cancer biology. Aberrant patterns of DNA methylation can be associated with carcinogenesis and affect the regulation of genome stability and gene transcription (11). Genome wide studies of CpG islands have uncovered thousands of loci where differential methylation can segregate pancreatic tumor tissue from normal tissue (12).

Cancer-linked global genomic hypomethylation in tumor tissue is a common characteristic in a wide variety of malignancies, ranging from solid tumors, such as breast, colon, oral, and lung cancers, to cancers of the blood (13,14). In this study, in order to identify candidate liquid biopsy methylation markers in pancreatic cancer, we have employed a global methylation profiling platform to comprehensively survey a large scale of CpG sites between blood and cancer tissues versus pericarcinous tissues. We compared pericarcinous tissues vs. cancer tissue and blood vs. pericarcinous tissues in order to harvest methylation markers for diagnostic purposes. These genes could be the most likely candidate methylation markers for future liquid biopsies in pancreatic cancer.

#### **Methods**

#### Subjects

Six patients with pancreatic cancer (2 males and 4 females,

Chinese General Hospital of PLA in China (Table S1). The diagnosis of pancreatic cancer was made by at least two experienced oncologists. Sample collection was carried out accorded to the following criteria: (I) the minimum diameter of tumor was greater than 2 cm. Meanwhile, pancreatic cancer was identified by Hematoxylin and Eosin (H&E) staining and the ratio of cancer cells in the whole cells section was over 80%. (II) Tissue adjacent to cancer was collected as far as possible from the cancer tissue in order to avoid the mistake sampling. (III) Blood samples were collected before surgery. Pancreatic cancer tissue and tissue adjacent to cancer of each patient were collected and stored in liquid nitrogen immediately for DNA extraction. All specimens were subjected to autolysis for 4 to 8 h and then snap-frozen at -80 °C until use in analysis. DNA was extracted from 25 mg samples of the tissue specimens using the QIAamp DNA Mini Kit (Qiagen) according to the manufacturer's instructions. gDNA of Blood samples were extracted by FitAmp™ Plasma/ Serum DNA Isolation Kit (Epigentek, USA) according to the manufacturer's instructions. The DNA yield and purity were determined spectrophotometrically (NanoDrop® ND1000; Thermo Fisher Scientific Inc., Waltham, MA, USA) and by gel electrophoresis, respectively. DNA of sample was stored at -20 °C for further study. This study was approved by the Ethics Committee of Chinese General Hospital of PLA (No. S2018-013-02). All patients provided signed informed consent.

## DNA methylation methods

Bisulfite conversion of 500 ng genomic DNA was performed using the EZ DNA methylation kit (Zymo Research). DNA methylation level was assessed according to the manufacturer's instructions using Infinium-HumanMethylation450 Beadchips (Illumina Inc.). The technical schemes, the accuracy, and the high reproducibility of this array have been described previously (15). Quantitative measurements of DNA methylation were determined for 485,577 CpG dinucleotides, which covered 99% of the RefSeq genes and were distributed across the whole gene regions, including promoter, gene body, and 30-untranslated regions (UTRs). They also covered 96% of CGIs from the UCSC database with additional coverage in CGI shores (0-2 kb from CGI) and CGI shelves (2-4 kb from CGI). Detailed information on the contents of the array is available in the Infinium HumanMethylation450 User Guide and Human-Methylation 450 manifest (www.

TADIC I Dasic informa	tion of six patients in	uns study		
Patient	Age	A (blood)	B (pericarcinous tissue)	C (pancreatic cancer tissue)
Patient 1 (F)	74	A1 <sup>&amp;</sup>	B1 <sup>&amp;</sup>	C1 <sup>&amp;</sup>
Patient 2 (M)	36	A2 <sup>&amp;</sup>	B2*	C2 <sup>&amp;</sup>
Patient 3 (M)	66	A3 <sup>&amp;</sup>	B3 <sup>&amp;</sup>	C3 <sup>&amp;</sup>
Patient 4 (F)	60	A4 <sup>&amp;</sup>	B4*	C4 <sup>&amp;</sup>
Patient 5 (F)	46	A5 <sup>&amp;</sup>	B5 <sup>&amp;</sup>	C5 <sup>&amp;</sup>
Patient 6 (F)	71	A6 <sup>&amp;</sup>	B6 <sup>&amp;</sup>	C6 <sup>&amp;</sup>

Table 1 Basic information of six patients in this study

<sup>&</sup>, represents qualified sample; \*, represents unqualified samples. F, female; M, male.

illumina.com) and in recent papers (16). DNA methylation data were analyzed with the methylation analysis module within the BeadStudio software (Illumina Inc.). DNA methylation status of the CpG sites was calculated as the ratio of the signal from a methylated probe relative to the sum of both methylated and unmethylated probes. This value, known as b, ranges from 0 (completely unmethylated) to 1 (fully methylated). Given the batch effects normally associated with this platform and especially for small sample sizes as in the current study, we performed batch effect correction as described previously (17). For intra-chip normalization of probe intensities, colored balance and background corrections in every set of ten samples from the same chip were performed using internal control probes. X chromosome CpG sites in the CGIs in the AR gene in this array as well as the internal control probes were checked to validate the DNA methylation measurements.

#### **Bioinformatics**

GO enrichment analysis was performed using GOEAST (http://omicslab.genetics.ac.cn/GOEAST/index.php). Hypergeometric distribution was used to calculate the P value of GOID enrichment, and P<1E-4 cut-off value was applied (18). The graph size was reduced by condensing non-significant nodes to points. The smaller the P value is, the more significant the GO term is enriched in the dataset. And the graph size was reduced by condensing non-significant nodes to points. KEGG is a database resource for understanding high-level functions and utilities of the biological system, such as the cell, the organism and the ecosystem, from molecular-level information, especially large-scale molecular datasets generated by genome sequencing and other high-through put experimental technologies (http://www.genome.jp/kegg/). We used

KOBAS software to test the statistical enrichment of differentially methylated genes in KEGG pathways.

## **Results**

# Overlap of differential DNA methylation sites between pericarcinous tissues vs. cancer tissue and blood vs. pericarcinous tissues

DNA methylation levels were compared between four pericarcinous tissues (B) vs. six pancreatic cancer tissues (C) and six blood samples (A) vs. four pericarcinous tissues (B) using Infinium HumanMethylation450 Bead Chips (Table 1). Sites simultaneously present in B versus C and A versus B group comparisons were group defined as hypermethylation sites. Same was done to define hypomethylation sites. Meanwhile, hypomethylation sits simultaneously existed in B vs. C group and A vs. B group was defined as hypomethylation sits. Of 485,577 CpG sites, significant diagnostic differences in DNA methylation were observed at 15,397 CpG sites representing 7,440 genes at FDR 5 % correction (Figure 1 and http://fp.amegroups.cn/cms/961 4487675fcbfcb574c6af25b586775/tcr.2019.11.26-1.pdf). Of these sites, 5,605 (36.4%, 5,605 of 15,397) CpG sites were hypomethylated and 5,870 (38.12%, 5,870 of 15,397) CpG sites were hypermethylated. Functional distribution of 5,870 hypermethylated CpG sites suggested that 47.4% of these sites were located in promoter regions, 38.86% of these sites were located in gene bodies, 12.42% of these sites were located in intergenic regions and 6.01% of these sites were located in the 3'-untranslated regions (UTRs). Furthermore, sublocation analysis of 2,659 CpG sites in promoter region with hypermethylated indicated that 31.74% of these sites were located in regions from -200 to -1,500 nt upstream of the transcription start site (TSS1500),

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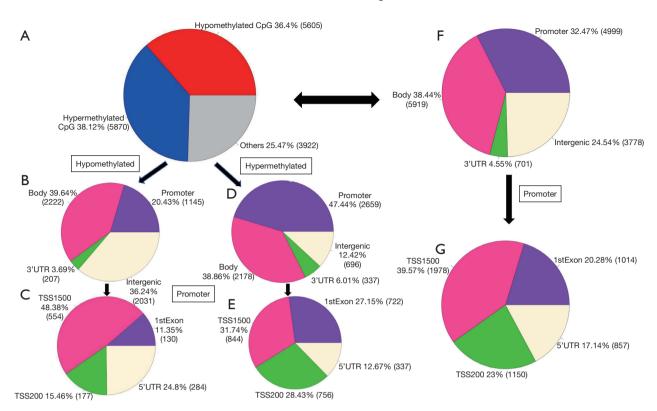


Figure 1 Graphic illustration of functional distribution and differentially methylated CpG sites identified in this study.

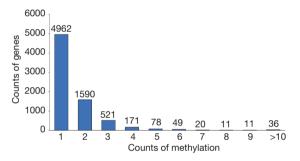
28.43% of these sites were located in regions from -200 nt upstream to the TSS itself (TSS200), 27.15% of these sites were located in 1st Exon regions and 12.67% of these sites were located in the 5'-untranslated regions (UTRs). These hypermethylated CpG sites were mostly located in gene bodies and promoter regions. Meanwhile, Functional distribution of 5,605 hypomethylated CpG sites suggested that 20.43% of these sites were located in promoter regions, 39.64% of these sites were located in gene bodies, 36.24% of these sites were located in intergenic regions and 3.69% of these sites were located in 3'UTR regions. Furthermore, sublocation analysis of 5,605 hypomethylated CpG sites in promoter regions indicated that 48.38% of these sites were located in TSS1500 regions, 15.46% of these sites were located in TSS200 regions, 11.35% of these sites were located in 1st Exon regions and 24.8% of these sites were located in 5'UTR regions. These hypomethylated CpG sites were mostly located in gene bodies, promoter regions and intergenic regions. The results above seem to be in apparent contradiction to widely held belief that promoter hypomethylation is correlated to increased transcription and vice versa. This also indicates the possibility that transcription factors are modified which dictate their regulation of anomalous transcription in the cancer cells.

Because the 15,397 methylated CpG sites corresponded to 7,440 genes, some of the methylated genes must contain more than one methylated site. Further analysis showed that among the 7,440 methylated genes, 4,962 (67%) possessed only one methylated site, 1,590 (21%) contained two methylated sites, and 888 (12%) contained three or more methylated sites (Figure 2 and http://fp.amegroups.cn/cms/3adcaa480666f581 911c4ab936783571/tcr.2019.11.26-2.pdf). In particular, one methylated gene (PTPRN2) possessed 40 methylated sites in overlap. Meanwhile, the MAD1 mitotic arrest deficient-like 1 (yeast) (MAD1L1, ENSG0000002822) possessed over 25 methylated sites (Figure 3). Of note, number of methylation sites can be correlated to gene length and mere presence of more methylation sites does not mean increased methylationbased regulation. Instead, methylation sites normalized over gene length is a better indicator of propensity to regulation by methylation.

# Gene Ontology (GO) and KEGG pathway analysis of differentially methylated genes in overlap group

In order to improve the credibility of this research, the

genes with counts of methylation sites were equal or greater than 15 were selected to perform intensive study. After such screening, 10 genes with more than three counts of differentially methylated CpG sites were harvested. GO terms were further assigned to Homo sapiens differentially methylated genes based on their sequence similarities to known proteins in the UniProt database annotated with GO terms as well as InterPro and Pfam domains they contain. GO annotation and enrichment analysis of ten significantly differentially methylated genes was implemented by GOEAST software (http://omicslab. genetics.ac.cn/GOEAST/index.php), in which gene length bias was corrected. GO terms with corrected P value less than  $10^{-4}$  were considered significantly enriched (*Figure 4*). Biological processes, cellular components, and molecular functions are shown in Figure 4 and Table S2. From the perspective of biological processes, there are 75 GO terms were assigned under this catalogues. Among these terms,



**Figure 2** Analysis of the identified methylated CpG sites. Distribution of the methylated CpG sites in the methylated genes.

spindle checkpoint (GO: 0031577, P value: 8.98E-21), mitotic spindle assembly checkpoint (GO: 0007094, P value: 3.5E-21) and negative regulation of mitotic sister chromatid segregation (GO: 0033048, P value: 3.5E-21) were the top three significantly enriched terms. From the cellular component perspective, there are 3 GO terms were assigned under this catalogues. Among these terms, A band (GO: 0031672, P value: 1.1E-05) was the top significantly enriched terms. From the molecular function perspective, there are 4 GO terms were assigned under this catalogues. Among these terms, G-protein beta/gamma-subunit complex binding (GO: 0031683, P value: 2.4E-11) was the top significantly over-represented terms.

In vivo, various biological functions were implemented by cooperation of different genes. Pathways enrichment analysis can give some clues to the biochemical and signal transduction pathways that differentially expressed genes may participate in. KEGG is a database resource for understanding high-level functions and utilities of the biological system, such as the cell, the organism and the ecosystem, from molecular-level information, especially large-scale molecular datasets generated by genome sequencing and other high-through put experimental technologies (http://www.genome.jp/kegg/). We used KOBAS software to test the statistical enrichment of differentially methylated genes in KEGG pathways (19). In this study, ten significantly differentially methylated genes involve 52 pathways (Table S3). It was worthy noticed that 43 pathways owned the same corrected P value (0.31). Table S3 shows the results of pathways enrichment, it clearly displays that vibrio cholerae infection were the top enriched

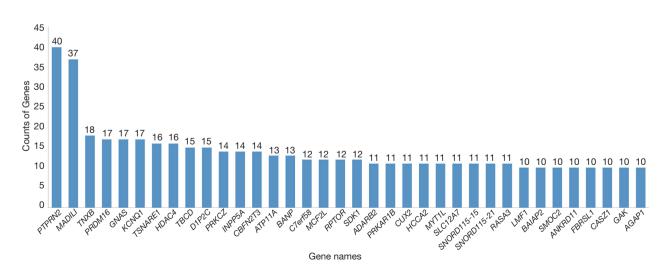
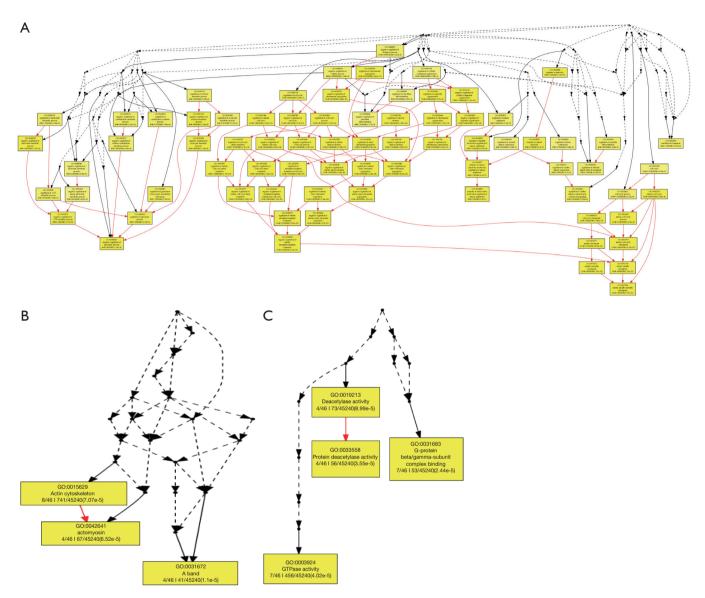


Figure 3 Methylated genes with over ten methylated CpG sites.



**Figure 4** GO enrichment analysis of ten significant differentially methylated genes ( $\geq 15$  methylated CpG sites). The figure is composed of three parts: "biological processes (BP, *Figure 4A*)", "molecular functions (MF, *Figure 4B*)", and "cellular components (CC, *Figure 4C*)". Hypergeometric statistical test methods were used for analysis, and the significance level of enrichment was set at P value <10–4. Black solid lines symbolize the connections between enriched terms. The boxes contain GO functional positioning that is equivalent to the significant GO terms. GO, Gene Ontology.

term. Two differentially methylated genes that identified in our study participate in this pathway. Moreover, it is worth noting that pancreatic secretion, type I diabetes mellitus, Insulin secretion and Adrenergic signaling in cardiomyocytes were also significant enriched in this study. The pathways mentioned above were adopted with the function that pancreas played.

# GO and KEGG pathway analysis of differentially methylated sites located in promoter regions of genes in overlap group

The promoter contains specific DNA sequences that are recognized by proteins known as transcription factors. These factors bind to the promoter sequences, recruiting RNA polymerase, the enzyme that synthesizes the RNA

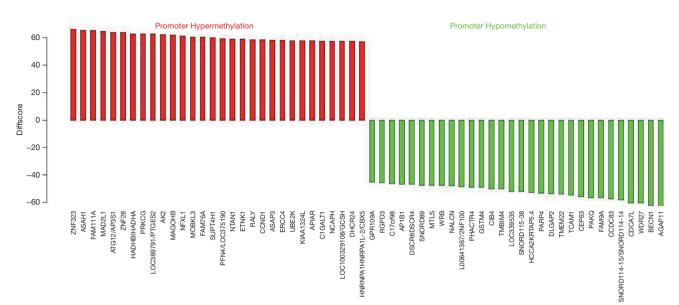


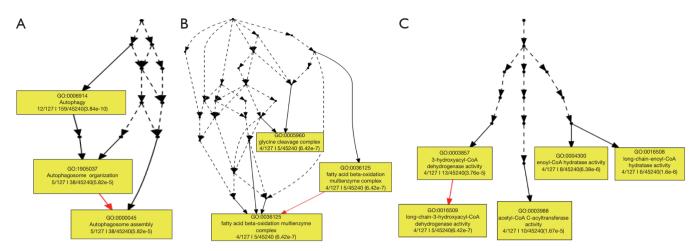
Figure 5 Sixty candidate genes with hypermethylation and hypomethylation status.

from the coding region of the gene. Eukaryotic promoters are extremely diverse and are difficult to characterize. They typically lie upstream of the gene and can have regulatory elements several kilobases away from the transcriptional start site. In eukaryotes, the transcriptional complex can cause the DNA to bend back on itself, which allows for placement of regulatory sequences far from the actual site of transcription. Many eukaryotic promoters, contain a TATA box (sequence TATAAA), which in turn binds a TATA binding protein which assists in the formation of the RNA polymerase transcriptional complex. Of this study, we identified 4,999 differentially methylated sites located in promoter regions in overlap group (http://fp.amegroups.cn/ cms/24bc751fdb7f41b7ce54e74bde803221/tcr.2019.11.26-3.pdf). Moreover, we picked out 30 genes with significantly hypermethylation and 30 genes with significantly hypomethylation in the overlap group (Figure 5 and Table S4). GO and KEGG analysis were performed with these 60 aberrant methylation genes. Of the GO analysis (Figure 6 and Table S5), GO terms with corrected P value less than 10<sup>-4</sup> were considered significantly enriched. From the perspective of biological processes, there are three GO terms were assigned under this catalogues. Among these terms, autophagosome assembly (GO: 0000045, P value: 5.8E-05), autophagy (GO: 0006914, P value: 3.8E-10) and autophagosome organization (GO: 1905037, P value: 5.8E–05) were the top three significantly enriched terms. From the cellular component perspective, there are three

GO terms were assigned under this catalogues. Among these terms, mitochondrial fatty acid beta-oxidation multienzyme complex (GO: 0016507, P value: 6.4E-07), fatty acid betaoxidation multienzyme complex (GO: 0036125, P value: 6.4E-07) and glycine cleavage complex (GO: 0005960, P value: 6.4E-07) were the top three significantly enriched terms. From the molecular function perspective, there are five GO terms were assigned under this catalogues. Among these terms, long-chain-3-hydroxyacyl-CoA dehydrogenase activity (GO: 0016509, P value: 6.4E-07) was the top significantly over-represented terms. Of the KEGG analysis (Table S6), it clearly displays that Regulation of autophagy were the top enriched term. Two differentially methylated genes that identified in our study participate in this pathway. Moreover, it is worth noting that Non-small cell lung cancer, Glioma, ErbB signaling pathway and Fc gamma R-mediated phagocytosis were also significant enriched in this study.

#### Methylation status of key genes related to pancreatic cancer

To pinpoint the methylation status of pancreatic cancer related genes (*Table 2*). We check out 22 pancreatic cancer related genes, including *ERBB2*, *AKT1*, *CDC42*, *KRAS*, *RAC1*, *RALB*, *RALA*, *PIK3R3*, *PIK3R2*, *AKT2*, *PLD1*, *RALBP1*, *SMAD4*, *RAF1*, *SMAD3*, *SMAD2*, *RB1*, *MAPK10*, *BAD*, *CDK4*, *STAT3* and *CCND1*, which has been reported before. The results indicated that *ERBB2*, *KRAS*, *PIK3R3*, *PLD1*, *RALBP1*, *RB1* and *MAPK10* all



**Figure 6** GO enrichment analysis of 60 candidate genes with hypermethylation and hypomethylation status. The figure is composed of three parts: "biological processes (BP, *Figure 6A*)", "molecular functions (MF, *Figure 6B*)", and "cellular components (CC, *Figure 6C*)". Hypergeometric statistical test methods were used for analysis, and the significance level of enrichment was set at P value <10–4. Black solid lines symbolize the connections between enriched terms. The boxes contain GO functional positioning that is equivalent to the significant GO terms. GO, Gene Ontology.

showed hypomethylation status. On the contrary, the other genes all showed hypermethylation status. Of note, effect size estimation was not calculated in this case.

#### Discussion

It is now evident that epigenetic abnormalities are extremely common in cancers, and these abnormalities provide an alternative mechanism of transcriptional silencing. Epigenetic abnormalities in cancer predominantly encompass methylation of CG dinucleotides (CpG islands) in the 5' regulatory region of tumor suppressor genes, which abrogates RNA polymerase from binding and initiating transcription. In cancers, there is preferential methylation of the gene promoter, but not in the corresponding normal cells within the tissue of origin. Methylome sequencing, without a priori bias to known CpG islands, yielded novel highly discriminant methylation markers for pancreatic cancer. Importantly, these findings were confirmed using an independent sample set of tumor and control tissues, showing that the method used in this study successfully identify pancreatic cancer markers with low background levels. Many of the markers with the strongest association to pancreatic cancer also showed greater than 10-fold increases in the median copies per sample compared with controls; this observation is critical to the application of these markers in diagnostic test development where assays must detect tumor signal against the

background biologic milieu. Novel candidates identified by this method were clinically piloted by assay from pancreatic juice, demonstrating utility for the detection of pancreatic cancer in blinded comparisons, even to diseased controls with chronic pancreatitis.

In this study, genome-wide DNA methylation profiling was conducted between four pericarcinous tissues vs. six pancreatic cancer tissues and six blood samples vs. four pericarcinous tissues using Infinium HumanMethylation450 Beadchips. Sampling from pancreatic cancer tissues, pericarcinous tissues and blood of one patient is a useful method for investigating DNA methylation biomarkers without the influence of genetic discordance. Actually, the approach used in this study has identified vagarious epigenetic differences, including non-small cell lung cancer (20), colorectal carcinoma (21) and hepatocellular carcinoma (22), etc. Of this study, a total of 15,397 differentially methylated CpG sites (3.2%, of 485,577 CpG sites,) corresponding 7,440 genes that were identified in overlap. Of these 15,397 CpG sites with significant diagnostic differences in DNA methylation, 5,605 (36.4%, 5,605 of 15,397) CpG sites were hypomethylated and 5,870 (38.12%, 5,870 of 15,397) CpG sites were hypermethylated. Functional distribution of 5,870 hypermethylated CpG sites suggested that 47.4% of these sites were located in promoter regions, 38.86% of these sites were located in gene bodies, 12.42% of these

Table 2 Methyl	ation status	of key	genes re	lated to	pancreatic	cancer

Series number	Gene	Methylat	ion status
Series number	Gene	Hypermethylation	Hypomethylation
1	ERBB2	N/A	Yes
2	AKT1	Yes	N/A
3	CDC42	Yes	N/A
4	KRAS	N/A	Yes
5	RAC1	Yes	N/A
6	RALB	Yes	N/A
7	RALA	Yes	N/A
8	PIK3R3	N/A	Yes
9	AKT2	Yes	N/A
10	PIK3R2	Yes	N/A
11	PLD1	N/A	Yes
12	RALBP1	N/A	Yes
13	SMAD4	Yes	N/A
14	RAF1	Yes	N/A
15	SMAD3	Yes	N/A
16	SMAD2	Yes	N/A
17	RB1	N/A	Yes
18	MAPK10	N/A	Yes
19	BAD	Yes	N/A
20	CDK4	Yes	N/A
21	STAT3	Yes	N/A
22	CCND1	Yes	N/A

sites were located in intergenic regions and 6.01% of these sites were located in the 3'-untranslated regions (UTRs). Furthermore, sublocation analysis of 2,659 CpG sites in promoter region with hypermethylated indicated that 31.74% of these sites were located in regions from -200 to -1,500 nt upstream of the transcription start site (TSS1500), 28.43% of these sites were located in regions from -200 nt upstream to the TSS itself (TSS200), 27.15% of these sites were located in 1st Exon regions and 12.67% of these sites were located in the 5'-untranslated regions (UTRs). These hypermethylated CpG sites were mostly located in gene bodies and promoter regions. Meanwhile, Functional distribution of 5,605 hypomethylated CpG sites suggested that 20.43% of these sites were located in gene bodies, 39.64% of these sites were located in gene bodies,

36.24% of these sites were located in intergenic regions and 3.69% of these sites were located in 3'UTR regions. Furthermore, sublocation analysis of 5,605 hypomethylated CpG sites in promoter regions indicated that 48.38% of these sites were located in TSS1500 regions, 15.46% of these sites were located in TSS200 regions, 11.35% of these sites were located in 1st Exon regions and 24.8% of these sites were located in 5'UTR regions. This seems to be consistent with previous findings that methylation of these regions inhibits transcription. For example, Irizarry et al. demonstrated that altered DNA methylation in cancer occurred in CGI shores rather than in the CGIs, and DNA methylation changes in CGI shores were strongly related to gene expression (23). In addition, we had noticed that numerous differential CpG sites were located in gene bodies. Recently, it became apparent that CGIs in gene bodies act as alternative promoters (24,25) and that tissuespecific or cell type-specific CGI methylation is prevalent in gene bodies (26). GO analysis of these significantly differentially methylated genes revealed that spindle checkpoint, mitotic spindle assembly checkpoint and negative regulation of mitotic sister chromatid segregation were the top three significantly enriched terms from perspective of biological processes. Meanwhile, from the cellular component perspective, there are 3 GO terms were assigned under this catalogues. Among these terms, A band was the top significantly enriched terms. In addition, from the molecular function perspective, there are 4 GO terms were assigned under this catalogues. Among these terms, G-protein beta/gamma-subunit complex binding was the top significantly over-represented terms. KEGG analysis showed that vibrio cholerae infection was the top enriched term. Moreover, pancreatic secretion, Type I diabetes mellitus, Insulin secretion and Adrenergic signaling in cardiomyocytes were also significant enriched in this study. Furthermore, GO analysis of differentially methylated sites located in promoter regions of genes showed that autophagosome assembly, autophagy and autophagosome organization were the top three significantly enriched terms from the perspective of biological processes. From the cellular component perspective, there are three GO terms were assigned under this catalogues. Among these terms, mitochondrial fatty acid beta-oxidation multienzyme complex, fatty acid beta-oxidation multienzyme complex and glycine cleavage complex were the top three significantly enriched terms. From the molecular function perspective, long-chain-3-hydroxyacyl-CoA dehydrogenase activity was the top significantly over-represented terms. Of the KEGG analysis, it clearly displays that Regulation of autophagy were the top enriched term. It is worth noting that Non-small cell lung cancer, Glioma, ErbB signaling pathway and Fc gamma R-mediated phagocytosis were also significant enriched in this study. Meanwhile, we have invested methylation status of 22 pancreatic cancer related key genes, and revealed the aberrant methylation status. For example, Cyclin D1 (CCND1) has been showed to be overexpressed in human pancreatic cancer (27). Here, CCND1 was identified as hypermethylated candidate gene that is inconsistent with a previous study (28), which suggested that over-expression of cyclin D1 in pancreatic cancer is associated with the loss of methylation.

There are several limitations to the present study. First, the sample size was not large. Further validation in studies encompassing more samples is warranted in the future. Second, the analyzed CpG sites were limited in number, although the 450 K microarray is one of the most powerful and cost-effective tools currently available for assessing methylation changes. Third, it is not possible to differentiate methylation from 5-hydroxymethylation of cytosine, which also plays a critical role in gene regulation (29). In summary, aberrant DNA methylation in pancreatic cancer tissues was identified at numerous CpG sites across the whole genome in using two independent sets of samples. Of the differently methylated CpG sites in the CGIs, most of them were located in the promoter regions. These findings support the hypothesis that altered DNA methylation could be involved in the pathophysiology of pancreatic cancer. Although the number of analyzed individuals was limited, the analysis was sufficient to provide DNA methylation distribution patterns across different genomic regions that were largely in agreement with patterns previously observed. The methylome data alone was sufficient for correctly distinguishing between all the ten tissues studied, collectively demonstrating that tissues are characterized by distinctive methylation patterns that reflect their tissue-specific functions. Our study provoked the question, of how differentially methylated CpG sites mechanistically contribute to the gene functions, especially for the numerous methylation regions that were found in gene body areas. In addition, it remains unclear, however, how the gene body differentially methylated CpG sites may function as regulators of gene expression, and this question should be addressed in the future epigenetic studies.

In conclusion, previous studies have demonstrated that DNA methylation play important roles in the regulation of developmental processes of several cancers. The identification of differentially methylated genes in this Wang et al. Pancreatic cancer differentiation atlas in blood

study provides information valuable to the in-depth study of pancreatic cancer. Moreover, the results of this study will not only improve our understanding of the differentially methylated genes but will also help to enhance methylome studies of pancreatic cancer.

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#### Footnote

*Conflicts of Interest:* The authors have completed the ICMJE uniform disclosure form (available at http://dx.doi. org/10.21037/tcr.2019.11.26). The authors have no conflicts of interest to declare.

*Ethical Statement:* The authors are accountable for all aspects of the work in ensuring that questions related to the accuracy or integrity of any part of the work are appropriately investigated and resolved. The study was conducted in accordance with the Declaration of Helsinki (as revised in 2013). This study was approved by the Ethics Committee of Chinese General Hospital of PLA. All patients provided signed informed consent.

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# Supplementary

# Table S1 Clinicopathological details of patients

Patient No.	Age	Gender	Histology
1	F	74	Highly differentiated ductal adenocarcinoma
2	Μ	36	Poorly differentiated adenocarcinoma
3	Μ	66	Moderately differentiated adenocarcinoma
4	F	60	Moderately differentiated ductal adenocarcinoma
5	F	46	Moderately differentiated ductal adenocarcinoma
6	F	71	Moderately-poorly differentiated adenocarcinoma

F, female; M, male.

<b>Table S2</b> Gene ontology annotation of the 10 genes with significant methylation frequency of the overlaps group ( $\geq$ 15 count	Table S2 Gene ontology annotation of the	e 10 genes with significant methylation f	requency of the overlaps group ( $\geq 15$ counts
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GOID GO: 0048519											
	Ontology Biological	Term Negative regulation of biological process	Level 2	q 19	m 4,961	t 45,240	k 46	Gene IDs Q92932, B3KR41, C9J9H5, C9JIR0, C9JJ38, C9JKI7,	PTPRN2, MAD1L1, MAD1L1, MAD1L1, MAD1L1, MAD1L1,	Log odds ratio	P 1.42711E-05
	process							C9JP81, C9JPS1, C9JTA2, C9JX80, C9K086, Q9Y6D9, Q9HAZ2, P51787, C9J0X4, F5GX36, F5H0B1, P56524, Q9BTW9	MAD1L1, MAD1L1, MAD1L1, MAD1L1, MAD1L1, MAD1L1, PRDM16, KCNQ1, HDAC4, HDAC4, HDAC4, HDAC4, TBCD		
GO: 0000075	Biological process	Cell cycle checkpoint	3	11	264	45,240	46	B3KR41, C9J9H5, C9JIR0, C9JJ38, C9JKI7, C9JP81, C9JPS1, C9JTA2, C9JX80, C9K086, Q9Y6D9	MAD1L1, MAD1L1	5.356787	5.86265E-13
GO: 0000278	Biological process	Mitotic cell cycle	2	11	810	45,240	46	B3KR41, C9J9H5, C9JIR0, C9JJ38, C9JKI7, C9JP81, C9JPS1, C9JTA2, C9JX80, C9K086, Q9Y6D9	MAD1L1, MAD1L1	3.739403	6.84714E-08
GO: 0007049	Biological process	Cell cycle	2	11	1,636	45,240	46	B3KR41, C9J9H5, C9JIR0, C9JJ38, C9JKI7, C9JP81, C9JPS1, C9JTA2, C9JX80, C9K086, Q9Y6D9	MAD1L1, MAD1L1	2.725224	5.43394E-05
GO: 0007088	Biological process	Regulation of mitotic nuclear division	4	11	154	45,240	46	B3KR41, C9J9H5, C9JIR0, C9JJ38, C9JKI7, C9JP81, C9JPS1, C9JTA2, C9JX80, C9K086, Q9Y6D9	MAD1L1, MAD1L1	6.134394	2.24109E-15
GO: 0007093	Biological	Mitotic cell cycle checkpoint	7	11	166	45,240	46	B3KR41, C9J9H5, C9JIR0, C9JJ38, C9JKI7, C9JP81, C9JPS1, C9JTA2, C9JX80, C9K086, Q9Y6D9	MAD1L1, MAD1L1	6.026142	4.53154E-15
GO: 0007094	Biological	Mitotic spindle assembly checkpoint	13	11	42	45,240	46	B3KR41, C9J9H5, C9JIR0, C9JJ38, C9JKI7, C9JP81, C9JPS1, C9JTA2, C9JX80, C9K086, Q9Y6D9	MAD1L1, MAD1L1	8.008864	3.49706E-21
GO: 0007346	process Biological	Regulation of mitotic cell cycle	2	11	388	45,240	46	B3KR41, C9J9H5, C9JIR0, C9JJ38, C9JKI7, C9JP81,	MAD1L1, MAD1L1, MAD1L1, MAD1L1, MAD1L1, MAD1L1,	4.801268	3.6196E-11
GO: 0010564	process Biological	Regulation of cell cycle process	2	11	462	45,240	46	C9JPS1, C9JTA2, C9JX80, C9K086, Q9Y6D9 B3KR41, C9J9H5, C9JIR0, C9JJ38, C9JKI7, C9JP81,	MAD1L1, MAD1L1, MAD1L1, MAD1L1, MAD1L1 MAD1L1, MAD1L1, MAD1L1, MAD1L1, MAD1L1, MAD1L1,	4.549432	2.32842E-10
GO: 0010639	process Biological	Negative regulation of organelle organization	5	12	264	45,240	46	C9JPS1, C9JTA2, C9JX80, C9K086, Q9Y6D9 B3KR41, C9J9H5, C9JIR0, C9JJ38, C9JKI7, C9JP81,	MAD1L1, MAD1L1, MAD1L1, MAD1L1, MAD1L1 MAD1L1, MAD1L1, MAD1L1, MAD1L1, MAD1L1, MAD1L1,	5.482318	1.24116E-14
GO: 0010948	process Biological	Negative regulation of cell cycle process	3	11	226	45,240	46	C9JPS1, C9JTA2, C9JX80, C9K086, Q9Y6D9, Q9BTW9 B3KR41, C9J9H5, C9JIR0, C9JJ38, C9JKI7, C9JP81,	MAD1L1, MAD1L1, MAD1L1, MAD1L1, MAD1L1, TBCD MAD1L1, MAD1L1, MAD1L1, MAD1L1, MAD1L1, MAD1L1,	5.581002	1.20706E-13
GO: 0010965	process Biological	Regulation of mitotic sister chromatid separation	5	11	80	45,240	46	C9JPS1, C9JTA2, C9JX80, C9K086, Q9Y6D9 B3KR41, C9J9H5, C9JIR0, C9JJ38, C9JKI7, C9JP81,	MAD1L1, MAD1L1, MAD1L1, MAD1L1, MAD1L1 MAD1L1, MAD1L1, MAD1L1, MAD1L1, MAD1L1, MAD1L1,	7.079253	1.5405E–18
GO: 0022402	process Biological	Cell cycle process	3	11	1,278	45,240	46	C9JPS1, C9JTA2, C9JX80, C9K086, Q9Y6D9 B3KR41, C9J9H5, C9JIR0, C9JJ38, C9JKI7, C9JP81,	MAD1L1, MAD1L1, MAD1L1, MAD1L1, MAD1L1 MAD1L1, MAD1L1, MAD1L1, MAD1L1, MAD1L1, MAD1L1,	3.081509	6.23166E-06
GO: 0030071	process Biological	Regulation of mitotic metaphase/anaphase	7	11	76	45,240	46	C9JPS1, C9JTA2, C9JX80, C9K086, Q9Y6D9 B3KR41, C9J9H5, C9JIR0, C9JJ38, C9JKI7, C9JP81,	MAD1L1, MAD1L1	7.153253	9.65074E-19
	process	transition	7					C9JPS1, C9JTA2, C9JX80, C9K086, Q9Y6D9	MAD1L1, MAD1L1, MAD1L1, MAD1L1, MAD1L1		
GO: 0031577	Biological process	Spindle checkpoint	3	11	50	45,240	46	B3KR41, C9J9H5, C9JIR0, C9JJ38, C9JKI7, C9JP81, C9JPS1, C9JTA2, C9JX80, C9K086, Q9Y6D9	MAD1L1, MAD1L1, MAD1L1, MAD1L1, MAD1L1	7.757325	8.97641E-21
GO: 0033043	Biological process	Regulation of organelle organization	2	12	854	45,240	46	B3KR41, C9J9H5, C9JIR0, C9JJ38, C9JKI7, C9JP81, C9JPS1, C9JTA2, C9JX80, C9K086, Q9Y6D9, Q9BTW9	MAD1L1, TBCD	3.78862	7.71321E-09
GO: 0033044	Biological process	Regulation of chromosome organization	2	11	239	45,240	46	B3KR41, C9J9H5, C9JIR0, C9JJ38, C9JKI7, C9JP81, C9JPS1, C9JTA2, C9JX80, C9K086, Q9Y6D9	MAD1L1, MAD1L1	5.500314	2.01867E-13
GO: 0033045	Biological process	Regulation of sister chromatid segregation	4	11	91	45,240	46	B3KR41, C9J9H5, C9JIR0, C9JJ38, C9JKI7, C9JP81, C9JPS1, C9JTA2, C9JX80, C9K086, Q9Y6D9	MAD1L1, MAD1L1	6.893386	6.4978E-18
GO: 0033046	Biological process	Negative regulation of sister chromatid segregation	7	11	47	45,240	46	B3KR41, C9J9H5, C9JIR0, C9JJ38, C9JKI7, C9JP81, C9JPS1, C9JTA2, C9JX80, C9K086, Q9Y6D9	MAD1L1, MAD1L1	7.846592	4.66045E-21
GO: 0033047	Biological process	Regulation of mitotic sister chromatid segregation	5	11	80	45,240	46	B3KR41, C9J9H5, C9JIR0, C9JJ38, C9JKI7, C9JP81, C9JPS1, C9JTA2, C9JX80, C9K086, Q9Y6D9	MAD1L1, MAD1L1	7.079253	1.5405E-18
GO: 0033048	Biological	Negative regulation of mitotic sister chromatid segregation	8	11	45	45,240	46	B3KR41, C9J9H5, C9JIR0, C9JJ38, C9JKI7, C9JP81, C9JPS1, C9JTA2, C9JX80, C9K086, Q9Y6D9	MAD1L1, MAD1L1	7.909328	3.49706E-21
GO: 0045786	Biological	Negative regulation of cell cycle	3	11	481	45,240	46	C9JPS1, C9J1A2, C9JX80, C9X086, Q9Y6D9 B3KR41, C9J9H5, C9JIR0, C9JJ38, C9JKI7, C9JP81, C9JPS1, C9JTA2, C9JX80, C9K086, Q9Y6D9	MADILI, MADILI, MADILI, MADILI, MADILI, MADILI, MADILI, MADILI, MADILI, MADILI, MADILI, MADILI, MADILI, MADILI, MADILI, MADILI, MADILI	4.491288	3.49572E-10
GO: 0045839	process Biological	Negative regulation of mitotic nuclear division	7	11	53	45,240	46	B3KR41, C9J9H5, C9JIR0, C9JJ38, C9JKI7, C9JP81,	MAD1L1, MAD1L1, MAD1L1, MAD1L1, MAD1L1, MAD1L1,	7.673261	1.66166E-20
GO: 0045841	process Biological	Negative regulation of mitotic metaphase/anaphase	9	11	45	45,240	46	C9JPS1, C9JTA2, C9JX80, C9K086, Q9Y6D9 B3KR41, C9J9H5, C9JIR0, C9JJ38, C9JKI7, C9JP81,	MAD1L1, MAD1L1, MAD1L1, MAD1L1, MAD1L1 MAD1L1, MAD1L1, MAD1L1, MAD1L1, MAD1L1, MAD1L1, MAD1L1,	7.909328	3.49706E-21
GO: 0045930	process Biological	transition Negative regulation of mitotic cell cycle	3	11	204	45,240	46	C9JPS1, C9JTA2, C9JX80, C9K086, Q9Y6D9 B3KR41, C9J9H5, C9JIR0, C9JJ38, C9JKI7, C9JP81,	MAD1L1, MAD1L1, MAD1L1, MAD1L1, MAD1L1 MAD1L1, MAD1L1, MAD1L1, MAD1L1, MAD1L1, MAD1L1,	5.728756	4.01676E-14
GO: 0048523	process Biological	Negative regulation of cellular process	3	18	4,555	45,240	46	C9JPS1, C9JTA2, C9JX80, C9K086, Q9Y6D9 B3KR41, C9J9H5, C9JIR0, C9JJ38, C9JKI7, C9JP81,	MAD1L1, MAD1L1, MAD1L1, MAD1L1, MAD1L1 MAD1L1, MAD1L1, MAD1L1, MAD1L1, MAD1L1, MAD1L1,	1.958439	2.17828E-05
-	process							C9JPS1, C9JTA2, C9JX80, C9K086, Q9Y6D9, Q9HAZ2, P51787, C9J0X4, F5GX36, F5H0B1, P56524, Q9BTW9	MAD1L1, MAD1L1, MAD1L1, MAD1L1, MAD1L1, PRDM16, KCNQ1, HDAC4, HDAC4, HDAC4, HDAC4, TBCD		
GO: 0051128	Biological process	Regulation of cellular component organization	2	12	2,006	45,240	46	B3KR41, C9J9H5, C9JIR0, C9JJ38, C9JKI7, C9JP81, C9JPS1, C9JTA2, C9JX80, C9K086, Q9Y6D9, Q9BTW9	MAD1L1, TBCD	2.556606	5.28453E-05
GO: 0051129	Biological process	Negative regulation of cellular component organization	4	12	524	45,240	46	B3KR41, C9J9H5, C9JIR0, C9JJ38, C9JKI7, C9JP81, C9JPS1, C9JTA2, C9JX80, C9K086, Q9Y6D9, Q9BTW9	MAD1L1, MAD1L1	4.493289	3.19493E-11
GO: 0051726	Biological process	Regulation of cell cycle	2	11	966	45,240	46	B3KR41, C9J9H5, C9JIR0, C9JJ38, C9K1609, Q9T6D9, Q9B1W9 C9JPS1, C9J9H5, C9JIR0, C9JJ38, C9JK17, C9JP81, C9JPS1, C9JTA2, C9JX80, C9K086, Q9Y6D9	MAD1L1, MAD1L1	3.485302	4.03765E-07
GO: 0051783	Biological	Regulation of nuclear division	2	11	186	45,240	46	B3KR41, C9J9H5, C9JIR0, C9JJ38, C9JKI7, C9JP81,	MAD1L1, MAD1L1, MAD1L1, MAD1L1, MAD1L1, MAD1L1,	5.862022	1.49082E-14
GO: 0051784	process Biological	Negative regulation of nuclear division	5	11	71	45,240	46	C9JPS1, C9JTA2, C9JX80, C9K086, Q9Y6D9 B3KR41, C9J9H5, C9JIR0, C9JJ38, C9JKI7, C9JP81,	MAD1L1, MAD1L1, MAD1L1, MAD1L1, MAD1L1 MAD1L1, MAD1L1, MAD1L1, MAD1L1, MAD1L1, MAD1L1, MAD1L1,	7.251434	5.05177E-19
GO: 0051983	process Biological	Regulation of chromosome segregation	2	11	103	45,240	46	C9JPS1, C9JTA2, C9JX80, C9K086, Q9Y6D9 B3KR41, C9J9H5, C9JIR0, C9JJ38, C9JKI7, C9JP81,	MAD1L1, MAD1L1, MAD1L1, MAD1L1, MAD1L1 MAD1L1, MAD1L1, MAD1L1, MAD1L1, MAD1L1, MAD1L1,	6.71468	2.42944E-17
GO: 0051985	process Biological	Negative regulation of chromosome segregation	4	11	47	45,240	46	C9JPS1, C9JTA2, C9JX80, C9K086, Q9Y6D9 B3KR41, C9J9H5, C9JIR0, C9JJ38, C9JKI7, C9JP81,	MAD1L1, MAD1L1, MAD1L1, MAD1L1, MAD1L1 MAD1L1, MAD1L1, MAD1L1, MAD1L1, MAD1L1, MAD1L1,	7.846592	4.66045E-21
GO: 0071173	process Biological	Spindle assembly checkpoint	3	11	45	45,240	46	C9JPS1, C9JTA2, C9JX80, C9K086, Q9Y6D9 B3KR41, C9J9H5, C9JIR0, C9JJ38, C9JKI7, C9JP81,	MAD1L1, MAD1L1	7.909328	3.49706E-21
GO: 0071174	process Biological	Mitotic spindle checkpoint	11	11	45	45,240	46	C9JPS1, C9JTA2, C9JX80, C9K086, Q9Y6D9 B3KR41, C9J9H5, C9JIR0, C9JJ38, C9JKI7, C9JP81,	MAD1L1, MAD1L1	7.909328	3.49706E-21
	process					ŗ		C9JPS1, C9JTA2, C9JX80, C9K086, Q9Y6D9	MAD1L1, MAD1L1, MAD1L1, MAD1L1, MAD1L1		
O:1901987	Biological process	Regulation of cell cycle phase transition	2	11	237	45,240	46	B3KR41, C9J9H5, C9JIR0, C9JJ38, C9JKI7, C9JP81, C9JPS1, C9JTA2, C9JX80, C9K086, Q9Y6D9	MAD1L1, MAD1L1	5.512438	1.9028E-13
O:1901988	Biological process	Negative regulation of cell cycle phase transition	3	11	160	45,240	46	B3KR41, C9J9H5, C9JIR0, C9JJ38, C9JKI7, C9JP81, C9JPS1, C9JTA2, C9JX80, C9K086, Q9Y6D9	MAD1L1, MAD1L1	6.079253	3.13253E-15
GO:1901990	Biological process	Regulation of mitotic cell cycle phase transition	3	11	234	45,240	46	B3KR41, C9J9H5, C9JIR0, C9JJ38, C9JKI7, C9JP81, C9JPS1, C9JTA2, C9JX80, C9K086, Q9Y6D9	MAD1L1, MAD1L1	5.530816	1.71147E–13
GO:1901991	Biological process	Negative regulation of mitotic cell cycle phase transition	5	11	157	45,240	46	B3KR41, C9J9H5, C9JIR0, C9JJ38, C9JKI7, C9JP81, C9JPS1, C9JTA2, C9JX80, C9K086, Q9Y6D9	MAD1L1, MAD1L1	6.10656	2.65226E-15
GO:1902099	Biological process	Regulation of metaphase/anaphase transition of cell cycle	4	11	76	45,240	46	B3KR41, C9J9H5, C9JIR0, C9JJ38, C9JKI7, C9JP81, C9JPS1, C9JTA2, C9JX80, C9K086, Q9Y6D9	MAD1L1, MAD1L1	7.153253	9.65074E-19
GO:1902100	Biological process	Negative regulation of metaphase/anaphase transition of cell cycle	4	11	45	45,240	46	B3KR41, C9J9H5, C9JIR0, C9JJ38, C9JKI7, C9JP81, C9JPS1, C9JTA2, C9JX80, C9K086, Q9Y6D9	MAD1L1, MAD1L1	7.909328	3.49706E-21
GO:1903047	Biological	Mitotic cell cycle process	4	11	726	45,240	46	B3KR41, C9J9H5, C9JIR0, C9JJ38, C9JKI7, C9JP81, C9JPS1, C9JTA2, C9JX80, C9K086, Q9Y6D9	MAD1L1, MAD1L1	3.897355	2.31135E-08
GO:2000816	Biological	Negative regulation of mitotic sister chromatid separation	8	11	45	45,240	46	B3KR41, C9J9H5, C9JIR0, C9JJ38, C9JKI7, C9JP81, C9JPS1, C9JTA2, C9JX80, C9K086, Q9Y6D9	MAD1L1, MAD1L1	7.909328	3.49706E-21
GO:2001251	process Biological	Negative regulation of chromosome organization	5	11	99	45,240	46	B3KR41, C9J9H5, C9JIR0, C9JJ38, C9JKI7, C9JP81,	MAD1L1, MAD1L1, MAD1L1, MAD1L1, MAD1L1, MAD1L1,	6.771824	1.62527E-17
GO: 0015629	process Cellular	Actin cytoskeleton	4	8	741	45,240	46	C9JPS1, C9JTA2, C9JX80, C9K086, Q9Y6D9 B3KR41, C9JKI7, C9JP81, Q9Y6D9, C9J0X4, F5GX36,	MAD1L1, MAD1L1, MAD1L1, MAD1L1, MAD1L1 MAD1L1, MAD1L1, MAD1L1, MAD1L1, HDAC4, HDAC4,	3.40842	7.07259E-05
GO: 0043467	component Biological	Regulation of generation of precursor metabolites	3	5	71	45,240	46	F5H0B1, P56524 Q9HAZ2, C9J0X4, F5GX36, F5H0B1, P56524	HDAC4, HDAC4 PRDM16, HDAC4, HDAC4, HDAC4, HDAC4	6.11393	1.58738E-06
GO: 0003924	process Molecular	and energy Gtpase activity	1				40				
GO: 0031683	function			7	456	45,240	46	A2A2R6, H0Y7E8, H0Y7F4, P63092, Q5JWD1, Q5JWE9,	GNAS, GNAS, GNAS, GNAS, GNAS, GNAS, GNAS	3.916214	4.02427E-05
GO: 0045667	Molecular	G-protein beta/gamma-subunit complex binding	2	7		45,240 45,240		A2A2R6, H0Y7E8, H0Y7F4, P63092, Q5JWD1, Q5JWE9, Q5JWF2 A2A2R6, H0Y7E8, H0Y7E4, P63092, Q5JWD1, Q5JWE9,			
JU: 0045667	Molecular function	G-protein beta/gamma-subunit complex binding	2	7 7	53	45,240	46	Q5JWF2 A2A2R6, H0Y7E8, H0Y7F4, P63092, Q5JWD1, Q5JWE9, Q5JWF2	GNAS, GNAS, GNAS, GNAS, GNAS, GNAS, GNAS	7.021184	2.43723E-11
	function Biological process	Regulation of osteoblast differentiation	3	7 7 5	53 157	45,240 45,240	46 46	Q5JWF2 A2A2R6, H0Y7E8, H0Y7F4, P63092, Q5JWD1, Q5JWE9, Q5JWF2 Q5JWF2, C9J0X4, F5GX36, F5H0B1, P56524	GNAS, GNAS, GNAS, GNAS, GNAS, GNAS, GNAS, GNAS GNAS, HDAC4, HDAC4, HDAC4, HDAC4	7.021184 4.969057	2.43723E-11 5.56829E-05
GO: 0008016	function Biological process Biological process	Regulation of osteoblast differentiation Regulation of heart contraction	3 2	7 7 5 5	53 157 178	45,240	46	Q5JWF2 A2A2R6, H0Y7E8, H0Y7F4, P63092, Q5JWD1, Q5JWE9, Q5JWF2 Q5JWF2, C9J0X4, F5GX36, F5H0B1, P56524 P51787, C9J0X4, F5GX36, F5H0B1, P56524	GNAS, GNAS, GNAS, GNAS, GNAS, GNAS, GNAS	7.021184 4.969057 4.787944	2.43723E-11 5.56829E-05 9.84102E-05
GO: 0008016	function Biological process Biological	Regulation of osteoblast differentiation	3	Ū	53 157	45,240 45,240	46 46	Q5JWF2 A2A2R6, H0Y7E8, H0Y7F4, P63092, Q5JWD1, Q5JWE9, Q5JWF2 Q5JWF2, C9J0X4, F5GX36, F5H0B1, P56524	GNAS, GNAS, GNAS, GNAS, GNAS, GNAS, GNAS, GNAS GNAS, HDAC4, HDAC4, HDAC4, HDAC4	7.021184 4.969057	2.43723E-11 5.56829E-05
GO: 0008016 GO: 0002076	function Biological process Biological process Biological	Regulation of osteoblast differentiation Regulation of heart contraction	3 2	Ū	53 157 178	45,240 45,240 45,240	46 46 46	Q5JWF2 A2A2R6, H0Y7E8, H0Y7F4, P63092, Q5JWD1, Q5JWE9, Q5JWF2 Q5JWF2, C9J0X4, F5GX36, F5H0B1, P56524 P51787, C9J0X4, F5GX36, F5H0B1, P56524	GNAS, GNAS, GNAS, GNAS, GNAS, GNAS, GNAS, GNAS GNAS, HDAC4, HDAC4, HDAC4, HDAC4 KCNQ1, HDAC4, HDAC4, HDAC4, HDAC4	7.021184 4.969057 4.787944	2.43723E-11 5.56829E-05 9.84102E-05
GO: 0008016 GO: 0002076 GO: 0006942	function Biological process Biological process Biological process Biological	Regulation of osteoblast differentiation Regulation of heart contraction Osteoblast development	3 2 6	Ū	53 157 178 33	45,240 45,240 45,240 45,240	46 46 46	Q5JWF2 A2A2R6, H0Y7E8, H0Y7F4, P63092, Q5JWD1, Q5JWE9, Q5JWF2 Q5JWF2, C9J0X4, F5GX36, F5H0B1, P56524 P51787, C9J0X4, F5GX36, F5H0B1, P56524 C9J0X4, F5GX36, F5H0B1, P56524	GNAS, GNAS, GNAS, GNAS, GNAS, GNAS, GNAS, GNAS GNAS, HDAC4, HDAC4, HDAC4, HDAC4 KCNQ1, HDAC4, HDAC4, HDAC4, HDAC4 HDAC4, HDAC4, HDAC4, HDAC4	<ol> <li>7.021184</li> <li>4.969057</li> <li>4.787944</li> <li>6.897355</li> </ol>	2.43723E-11 5.56829E-05 9.84102E-05 5.03412E-06
GO: 0008016 GO: 0002076 GO: 0006942 GO: 0010882	function Biological process Biological process Biological process Biological process	Regulation of osteoblast differentiation Regulation of heart contraction Osteoblast development Regulation of striated muscle contraction Regulation of cardiac muscle contraction by	3 2 6 2	Ū	53 157 178 33 63	45,240 45,240 45,240 45,240 45,240	46 46 46 46	Q5JWF2 A2A2R6, H0Y7E8, H0Y7F4, P63092, Q5JWD1, Q5JWE9, Q5JWF2 Q5JWF2, C9J0X4, F5GX36, F5H0B1, P56524 P51787, C9J0X4, F5GX36, F5H0B1, P56524 C9J0X4, F5GX36, F5H0B1, P56524 C9J0X4, F5GX36, F5H0B1, P56524	GNAS, GNAS, GNAS, GNAS, GNAS, GNAS, GNAS, GNAS GNAS, HDAC4, HDAC4, HDAC4, HDAC4 KCNQ1, HDAC4, HDAC4, HDAC4, HDAC4 HDAC4, HDAC4, HDAC4, HDAC4 HDAC4, HDAC4, HDAC4, HDAC4	<ul> <li>7.021184</li> <li>4.969057</li> <li>4.787944</li> <li>6.897355</li> <li>5.964469</li> </ul>	2.43723E-11 5.56829E-05 9.84102E-05 5.03412E-06 5.28453E-05
GO: 0008016 GO: 0002076 GO: 0006942 GO: 0010882 GO: 0055117	function Biological process Biological process Biological process Biological process Biological process Biological process	Regulation of osteoblast differentiation Regulation of heart contraction Osteoblast development Regulation of striated muscle contraction Regulation of cardiac muscle contraction by calcium ion signaling	3 2 6 2 5	Ū	53 157 178 33 63 25	45,240 45,240 45,240 45,240 45,240 45,240	46 46 46 46 46	Q5JWF2 A2A2R6, H0Y7E8, H0Y7F4, P63092, Q5JWD1, Q5JWE9, Q5JWF2 Q5JWF2, C9J0X4, F5GX36, F5H0B1, P56524 P51787, C9J0X4, F5GX36, F5H0B1, P56524 C9J0X4, F5GX36, F5H0B1, P56524 C9J0X4, F5GX36, F5H0B1, P56524	GNAS, GNAS, GNAS, GNAS, GNAS, GNAS, GNAS GNAS, HDAC4, HDAC4, HDAC4, HDAC4 KCNQ1, HDAC4, HDAC4, HDAC4, HDAC4 HDAC4, HDAC4, HDAC4, HDAC4 HDAC4, HDAC4, HDAC4, HDAC4 HDAC4, HDAC4, HDAC4, HDAC4	<ul> <li>7.021184</li> <li>4.969057</li> <li>4.787944</li> <li>6.897355</li> <li>5.964469</li> <li>7.297893</li> </ul>	2.43723E-11 5.56829E-05 9.84102E-05 5.03412E-06 5.28453E-05 1.65414E-06
GO: 0008016 GO: 0002076 GO: 0006942 GO: 0010882 GO: 0055117 GO: 0014854	function Biological process Biological process Biological process Biological process Biological process Biological process Biological process	Regulation of osteoblast differentiation Regulation of heart contraction Osteoblast development Regulation of striated muscle contraction Regulation of cardiac muscle contraction by calcium ion signaling Regulation of cardiac muscle contraction	3 2 6 2 5	Ū	53 157 178 33 63 25 52	45,240 45,240 45,240 45,240 45,240 45,240	46 46 46 46 46 46	Q5JWF2 A2A2R6, H0Y7E8, H0Y7F4, P63092, Q5JWD1, Q5JWE9, Q5JWF2, C9J0X4, F5GX36, F5H0B1, P56524 P51787, C9J0X4, F5GX36, F5H0B1, P56524 C9J0X4, F5GX36, F5H0B1, P56524 C9J0X4, F5GX36, F5H0B1, P56524 C9J0X4, F5GX36, F5H0B1, P56524	GNAS, GNAS, GNAS, GNAS, GNAS, GNAS, GNAS GNAS, HDAC4, HDAC4, HDAC4, HDAC4 KCNQ1, HDAC4, HDAC4, HDAC4, HDAC4 HDAC4, HDAC4, HDAC4, HDAC4 HDAC4, HDAC4, HDAC4, HDAC4 HDAC4, HDAC4, HDAC4, HDAC4 HDAC4, HDAC4, HDAC4, HDAC4	<ul> <li>7.021184</li> <li>4.969057</li> <li>4.787944</li> <li>6.897355</li> <li>5.964469</li> <li>7.297893</li> <li>6.24131</li> </ul>	2.43723E-11 5.56829E-05 9.84102E-05 5.03412E-06 5.28453E-05 1.65414E-06 2.70438E-05
AC: 0008016 AC: 0002076 AC: 0006942 AC: 0010882 AC: 0055117 AC: 0014854 AC: 0014870	function Biological process Biological process Biological process Biological process Biological process Biological process Biological process Biological process Biological	Regulation of osteoblast differentiation         Regulation of heart contraction         Osteoblast development         Regulation of striated muscle contraction         Regulation of cardiac muscle contraction by calcium ion signaling         Regulation of cardiac muscle contraction         Response to inactivity         Response to muscle inactivity         Response to stimulus involved in regulation of	3 2 6 2 5	Ū	53 157 178 33 63 25 52	45,240 45,240 45,240 45,240 45,240 45,240 45,240	46 46 46 46 46 46 46	Q5JWF2 A2A2R6, H0Y7E8, H0Y7F4, P63092, Q5JWD1, Q5JWE9, Q5JWF2 Q5JWF2, C9J0X4, F5GX36, F5H0B1, P56524 P51787, C9J0X4, F5GX36, F5H0B1, P56524 C9J0X4, F5GX36, F5H0B1, P56524 C9J0X4, F5GX36, F5H0B1, P56524 C9J0X4, F5GX36, F5H0B1, P56524 C9J0X4, F5GX36, F5H0B1, P56524	GNAS, GNAS, GNAS, GNAS, GNAS, GNAS, GNAS GNAS, HDAC4, HDAC4, HDAC4, HDAC4 KCNQ1, HDAC4, HDAC4, HDAC4, HDAC4 HDAC4, HDAC4, HDAC4, HDAC4	<ul> <li>7.021184</li> <li>4.969057</li> <li>4.787944</li> <li>6.897355</li> <li>5.964469</li> <li>7.297893</li> <li>6.24131</li> <li>8.619821</li> </ul>	2.43723E-11 5.56829E-05 9.84102E-05 5.03412E-06 5.28453E-05 1.65414E-06 2.70438E-05 3.27042E-08
aO: 0008016 aO: 0002076 aO: 0006942 aO: 0010882 aO: 0055117 aO: 0014854 aO: 0014870 aO: 0014874	function Biological process Biological process Biological process Biological process Biological process Biological process Biological process Biological process Biological process	Regulation of osteoblast differentiationRegulation of heart contractionOsteoblast developmentRegulation of striated muscle contractionRegulation of cardiac muscle contraction by calcium ion signalingRegulation of cardiac muscle contractionResponse to inactivityResponse to muscle inactivityResponse to stimulus involved in regulation of muscle adaptationResponse to muscle inactivity involved in regulation	3 2 6 2 5 3 1 1	Ū	53 157 178 33 63 25 52 10 7	45,240 45,240 45,240 45,240 45,240 45,240 45,240 45,240	46 46 46 46 46 46 46	Q5JWF2 A2A2R6, H0Y7E8, H0Y7F4, P63092, Q5JWD1, Q5JWE9, Q5JWF2, C9J0X4, F5GX36, F5H0B1, P56524 P51787, C9J0X4, F5GX36, F5H0B1, P56524 C9J0X4, F5GX36, F5H0B1, P56524	GNAS, GNAS, GNAS, GNAS, GNAS, GNAS, GNAS GNAS, HDAC4, HDAC4, HDAC4, HDAC4 KCNQ1, HDAC4, HDAC4, HDAC4, HDAC4 HDAC4, HDAC4, HDAC4, HDAC4	<ul> <li>7.021184</li> <li>4.969057</li> <li>4.787944</li> <li>6.897355</li> <li>5.964469</li> <li>7.297893</li> <li>6.24131</li> <li>8.619821</li> <li>9.134394</li> </ul>	2.43723E-11 5.56829E-05 9.84102E-05 5.03412E-06 5.28453E-05 1.65414E-06 2.70438E-05 3.27042E-08 6.30331E-09
aO: 0008016 aO: 0002076 aO: 0006942 aO: 0010882 aO: 0055117 aO: 0014854 aO: 0014870 aO: 0014874 aO: 0014874	function Biological process Biological process Biological process Biological process Biological process Biological process Biological process Biological process	Regulation of osteoblast differentiationRegulation of heart contractionOsteoblast developmentRegulation of striated muscle contractionRegulation of cardiac muscle contraction by calcium ion signalingRegulation of cardiac muscle contractionResponse to inactivityResponse to inactivityResponse to stimulus involved in regulation of muscle adaptationResponse to denervation involved in regulation of muscle adaptationResponse to denervation involved in regulation of	3 2 6 2 5 3 1 1 3	5 4 4 4 4 4 4 4 4	53 157 178 33 63 25 52 10 7	45,240 45,240 45,240 45,240 45,240 45,240 45,240 45,240	46 46 46 46 46 46 46 46	Q5JWF2 A2A2R6, H0Y7E8, H0Y7F4, P63092, Q5JWD1, Q5JWE9, Q5JWF2, C9J0X4, F5GX36, F5H0B1, P56524 P51787, C9J0X4, F5GX36, F5H0B1, P56524 C9J0X4, F5GX36, F5H0B1, P56524	GNAS, GNAS, GNAS, GNAS, GNAS, GNAS, GNAS GNAS, HDAC4, HDAC4, HDAC4, HDAC4 KCNQ1, HDAC4, HDAC4, HDAC4, HDAC4 HDAC4, HDAC4, HDAC4, HDAC4	<ul> <li>7.021184</li> <li>4.969057</li> <li>4.787944</li> <li>6.897355</li> <li>5.964469</li> <li>7.297893</li> <li>6.24131</li> <li>8.619821</li> <li>9.134394</li> <li>8.482318</li> </ul>	2.43723E-11 5.56829E-05 9.84102E-05 5.03412E-06 5.28453E-05 1.65414E-06 2.70438E-05 3.27042E-08 6.30331E-09 5.02378E-08
aO: 0008016 aO: 0002076 aO: 0006942 aO: 0010882 aO: 0010882 aO: 0014854 aO: 0014874 aO: 0014874 aO: 0014877 aO: 0014877 aO: 0014894	function Biological process Biological process Biological process Biological process Biological process Biological process Biological process Biological process Biological process	Regulation of osteoblast differentiationRegulation of heart contractionOsteoblast developmentRegulation of striated muscle contractionRegulation of cardiac muscle contraction by calcium ion signalingRegulation of cardiac muscle contractionResponse to inactivityResponse to muscle inactivityResponse to stimulus involved in regulation of muscle adaptationResponse to muscle inactivity involved in regulation	3 2 6 2 5 3 1 1 3 5	5 4 4 4 4 4 4 4 4	53 157 178 33 63 25 52 10 7	45,240 45,240 45,240 45,240 45,240 45,240 45,240 45,240 45,240	46 46 46 46 46 46 46 46 46	Q5JWF2 A2A2R6, H0Y7E8, H0Y7F4, P63092, Q5JWD1, Q5JWE9, Q5JWF2, C9J0X4, F5GX36, F5H0B1, P56524 P51787, C9J0X4, F5GX36, F5H0B1, P56524 C9J0X4, F5GX36, F5H0B1, P56524	GNAS, GNAS, GNAS, GNAS, GNAS, GNAS, GNAS, GNAS GNAS, HDAC4, HDAC4, HDAC4, HDAC4 KCNQ1, HDAC4, HDAC4, HDAC4, HDAC4 HDAC4, HDAC4, HDAC4, HDAC4	7.021184 4.969057 4.787944 6.897355 5.964469 7.297893 6.24131 8.619821 9.134394 8.482318 9.134394	2.43723E-11 5.56829E-05 9.84102E-05 5.03412E-06 5.28453E-05 1.65414E-06 2.70438E-05 3.27042E-08 6.30331E-09 5.02378E-08 6.30331E-09
GO: 0008016 GO: 0002076 GO: 0006942 GO: 0010882 GO: 0055117 GO: 0014854 GO: 0014874 GO: 0014874 GO: 0014877 GO: 0014894 GO: 0043502	function Biological process Biological process Biological process Biological process Biological process Biological process Biological process Biological process Biological process Biological process	Regulation of osteoblast differentiationRegulation of heart contractionOsteoblast developmentRegulation of striated muscle contractionRegulation of cardiac muscle contraction by calcium ion signalingRegulation of cardiac muscle contractionResponse to inactivityResponse to inactivityResponse to stimulus involved in regulation of muscle adaptationResponse to denervation involved in regulation of muscle adaptationResponse to denervation involved in regulation of muscle adaptation	3 2 6 2 5 3 1 1 3 5 5	5 4 4 4 4 4 4 4 4	<ol> <li>53</li> <li>157</li> <li>178</li> <li>33</li> <li>63</li> <li>25</li> <li>52</li> <li>10</li> <li>7</li> <li>11</li> <li>7</li> <li>7</li> <li>7</li> </ol>	45,240 45,240 45,240 45,240 45,240 45,240 45,240 45,240 45,240	46 46 46 46 46 46 46 46 46 46	Q5JWF2 A2A2R6, H0Y7E8, H0Y7F4, P63092, Q5JWD1, Q5JWE9, Q5JWF2, C9J0X4, F5GX36, F5H0B1, P56524 P51787, C9J0X4, F5GX36, F5H0B1, P56524 C9J0X4, F5GX36, F5H0B1, P56524	GNAS, GNAS, GNAS, GNAS, GNAS, GNAS, GNAS, GNAS GNAS, HDAC4, HDAC4, HDAC4, HDAC4 KCNQ1, HDAC4, HDAC4, HDAC4, HDAC4 HDAC4, HDAC4, HDAC4, HDAC4	7.021184 4.969057 4.787944 6.897355 5.964469 7.297893 6.24131 8.619821 9.134394 8.482318 9.134394 9.134394	2.43723E-11 5.56829E-05 9.84102E-05 5.03412E-06 5.28453E-05 1.65414E-06 2.70438E-05 3.27042E-08 6.30331E-09 5.02378E-08 6.30331E-09 6.30331E-09
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AO: 0008016 AO: 0002076 AO: 0006942 AO: 0010882 AO: 0014854 AO: 0014874 AO: 0014874 AO: 0014877 AO: 0014877 AO: 0014877 AO: 0014877 AO: 0014877 AO: 0014877 AO: 0014877 AO: 0014874 AO: 0014877 AO: 0014874 AO: 0014873	function Biological process Biological process Biological process Biological process Biological process Biological process Biological process Biological process Biological process Biological process Biological process Cellular component	Regulation of osteoblast differentiation Regulation of heart contraction Osteoblast development Regulation of striated muscle contraction by calcium ion signaling Regulation of cardiac muscle contraction by calcium ion signaling Regulation of cardiac muscle contraction Response to inactivity Response to inactivity Response to muscle inactivity Response to stimulus involved in regulation of muscle adaptation Response to denervation involved in regulation of muscle adaptation Response to denervation involved in regulation of muscle adaptation A band Deacetylase activity	3 2 6 2 5 3 1 1 3 5 5	5 4 4 4 4 4 4 4 4	<ol> <li>53</li> <li>157</li> <li>178</li> <li>33</li> <li>63</li> <li>25</li> <li>52</li> <li>10</li> <li>7</li> <li>11</li> <li>7</li> <li>7</li> <li>44</li> <li>41</li> <li>73</li> </ol>	45,240 45,240 45,240 45,240 45,240 45,240 45,240 45,240 45,240 45,240 45,240 45,240	46 46 46 46 46 46 46 46 46 46 46 46	Q5JWF2 A2A2R6, H0Y7E8, H0Y7F4, P63092, Q5JWD1, Q5JWE9, Q5JWF2 Q5JWF2, C9J0X4, F5GX36, F5H0B1, P56524 P51787, C9J0X4, F5GX36, F5H0B1, P56524 C9J0X4, F5GX36, F5H0B1, P56524	GNAS, GNAS, GNAS, GNAS, GNAS, GNAS, GNAS GNAS, HDAC4, HDAC4, HDAC4, HDAC4 KCNQ1, HDAC4, HDAC4, HDAC4, HDAC4 HDAC4, HDAC4, HDAC4, HDAC4	7.021184 4.969057 4.787944 6.897355 5.964469 7.297893 6.24131 8.619821 9.134394 8.482318 9.134394 9.134394 9.134394 6.482318 6.584197 5.751925	2.43723E–11 5.56829E–05 9.84102E–05 5.03412E–06 5.28453E–05 1.65414E–06 2.70438E–05 3.27042E–08 6.30331E–09 6.30331E–09 6.30331E–09 1.42711E–05 1.10087E–05 8.98652E–05
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AC: 0008016         AC: 0002076         AC: 0006942         AC: 0010882         AC: 00114854         AC: 0014870         AC: 0014874         AC: 0033558	function Biological process Biological process Biological process Biological process Biological process Biological process Biological process Biological process Biological process Biological process Cellular component Molecular function	Regulation of osteoblast differentiation Regulation of heart contraction Osteoblast development Regulation of striated muscle contraction by calcium ion signaling Regulation of cardiac muscle contraction by calcium ion signaling Regulation of cardiac muscle contraction Response to inactivity Response to inactivity Response to muscle inactivity Response to stimulus involved in regulation of muscle adaptation Response to denervation involved in regulation of muscle adaptation Response to denervation involved in regulation of muscle adaptation A band Deacetylase activity	3 2 6 2 5 3 1 1 3 5 5	5 4 4 4 4 4 4 4 4	<ol> <li>53</li> <li>157</li> <li>178</li> <li>33</li> <li>63</li> <li>25</li> <li>52</li> <li>10</li> <li>7</li> <li>11</li> <li>7</li> <li>7</li> <li>44</li> <li>41</li> <li>73</li> </ol>	45,240 45,240 45,240 45,240 45,240 45,240 45,240 45,240 45,240 45,240 45,240 45,240	46 46 46 46 46 46 46 46 46 46 46 46	Q5JWF2 A2A2R6, H0Y7E8, H0Y7F4, P63092, Q5JWD1, Q5JWE9, Q5JWF2 Q5JWF2, C9J0X4, F5GX36, F5H0B1, P56524 P51787, C9J0X4, F5GX36, F5H0B1, P56524 C9J0X4, F5GX36, F5H0B1, P56524	GNAS, GNAS, GNAS, GNAS, GNAS, GNAS, GNAS GNAS, HDAC4, HDAC4, HDAC4, HDAC4 KCNQ1, HDAC4, HDAC4, HDAC4, HDAC4 HDAC4, HDAC4, HDAC4, HDAC4	7.021184 4.969057 4.787944 6.897355 5.964469 7.297893 6.24131 8.619821 9.134394 8.482318 9.134394 9.134394 6.482318 6.584197 5.751925 6.134394 5.87566	2.43723E-11 5.56829E-05 9.84102E-05 5.03412E-06 5.28453E-05 1.65414E-06 2.70438E-05 3.27042E-08 6.30331E-09 6.30331E-09 6.30331E-09 1.42711E-05 1.10087E-05 8.98652E-05 3.5536E-05 6.51755E-05
AC: 0008016         AC: 0002076         AC: 0006942         AC: 0010882         AC: 00114854         AC: 0014870         AC: 0014874         AC: 0043502         AC: 00331672         AC: 0033558         AC: 0042641	function Biological process Biological process Biological process Biological process Biological process Biological process Biological process Biological process Biological process Biological process Biological process Cellular component Molecular function	Regulation of osteoblast differentiation Regulation of heart contraction Osteoblast development Regulation of striated muscle contraction Regulation of cardiac muscle contraction by calcium ion signaling Regulation of cardiac muscle contraction by calcium ion signaling Response to inactivity Response to inactivity Response to muscle inactivity Response to stimulus involved in regulation of muscle adaptation Response to muscle inactivity involved in regulation of muscle adaptation Response to denervation involved in regulation of muscle adaptation A band Deacetylase activity Protein deacetylase activity	3 2 6 2 5 3 1 1 3 5 5	5 4 4 4 4 4 4 4 4	<ul> <li>53</li> <li>157</li> <li>178</li> <li>33</li> <li>63</li> <li>25</li> <li>52</li> <li>10</li> <li>7</li> <li>11</li> <li>7</li> <li>7</li> <li>44</li> <li>41</li> <li>73</li> <li>56</li> </ul>	45,240 45,240 45,240 45,240 45,240 45,240 45,240 45,240 45,240 45,240 45,240 45,240	46 46 46 46 46 46 46 46 46 46 46 46 46	Q5JWF2 A2A2R6, H0Y7E8, H0Y7F4, P63092, Q5JWD1, Q5JWE9, Q5JWF2 Q5JWF2, C9J0X4, F5GX36, F5H0B1, P56524 P51787, C9J0X4, F5GX36, F5H0B1, P56524 C9J0X4, F5GX36, F5H0B1, P56524	GNAS, GNAS, GNAS, GNAS, GNAS, GNAS, GNAS GNAS, HDAC4, HDAC4, HDAC4, HDAC4 KCNQ1, HDAC4, HDAC4, HDAC4, HDAC4 HDAC4, HDAC4, HDAC4, HDAC4	7.021184 4.969057 4.787944 6.897355 5.964469 7.297893 6.24131 8.619821 9.134394 8.482318 9.134394 9.134394 9.134394 6.482318 6.584197 5.751925 6.134394	2.43723E-11 5.56829E-05 9.84102E-05 5.03412E-06 5.28453E-05 1.65414E-06 2.70438E-05 3.27042E-08 6.30331E-09 6.30331E-09 6.30331E-09 1.42711E-05 1.10087E-05 8.98652E-05
<ul> <li>O: 0008016</li> <li>O: 0002076</li> <li>O: 0006942</li> <li>O: 0010882</li> <li>O: 00155117</li> <li>O: 0014874</li> <li>O: 0014870</li> <li>O: 0014877</li> <li>O: 0014877</li> <li>O: 0014894</li> <li>O: 0014894</li> <li>O: 00143502</li> <li>O: 0031672</li> <li>O: 0033558</li> <li>O: 0042641</li> <li>O: 0045668</li> </ul>	function Biological process Biological process Biological process Biological process Biological process Biological process Biological process Biological process Biological process Biological process Biological process Cellular component Molecular function Cellular component Biological	Regulation of osteoblast differentiation Regulation of heart contraction Osteoblast development Regulation of striated muscle contraction by calcium ion signaling Regulation of cardiac muscle contraction by calcium ion signaling Regulation of cardiac muscle contraction by calcium ion signaling Regulation of cardiac muscle contraction Response to inactivity Response to muscle inactivity Response to muscle inactivity Response to stimulus involved in regulation of muscle adaptation Response to denervation involved in regulation of muscle adaptation Response to denervation involved in regulation of muscle adaptation Regulation of muscle adaptation A band Deacetylase activity Protein deacetylase activity	3 2 6 2 5 3 1 1 3 5 5 3 7 1 1 1 6	5 4 4 4 4 4 4 4 4	<ol> <li>53</li> <li>157</li> <li>178</li> <li>33</li> <li>63</li> <li>25</li> <li>52</li> <li>10</li> <li>7</li> <li>11</li> <li>7</li> <li>44</li> <li>41</li> <li>73</li> <li>56</li> <li>67</li> </ol>	45,240 45,240 45,240 45,240 45,240 45,240 45,240 45,240 45,240 45,240 45,240 45,240 45,240	46 46 46 46 46 46 46 46 46 46 46 46 46	Q5JWF2 A2A2R6, H0Y7E8, H0Y7F4, P63092, Q5JWD1, Q5JWE9, Q5JWF2 Q5JWF2, C9J0X4, F5GX36, F5H0B1, P56524 P51787, C9J0X4, F5GX36, F5H0B1, P56524 C9J0X4, F5GX36, F5H0B1, P56524	GNAS, GNAS, GNAS, GNAS, GNAS, GNAS, GNAS GNAS, HDAC4, HDAC4, HDAC4, HDAC4 KCNQ1, HDAC4, HDAC4, HDAC4, HDAC4 HDAC4, HDAC4, HDAC4, HDAC4	7.021184 4.969057 4.787944 6.897355 5.964469 7.297893 6.24131 8.619821 9.134394 8.482318 9.134394 9.134394 6.482318 6.584197 5.751925 6.134394 5.87566	2.43723E-11 5.56829E-05 9.84102E-05 5.03412E-06 5.28453E-05 1.65414E-06 2.70438E-05 3.27042E-08 6.30331E-09 6.30331E-09 6.30331E-09 1.42711E-05 1.10087E-05 8.98652E-05 3.5536E-05 6.51755E-05
<ul> <li>O: 0008016</li> <li>O: 0002076</li> <li>O: 0006942</li> <li>O: 0010882</li> <li>O: 00155117</li> <li>O: 0014874</li> <li>O: 0014870</li> <li>O: 0014874</li> <li>O: 0014874</li> <li>O: 0014894</li> <li>O: 0014894</li> <li>O: 00143502</li> <li>O: 0031672</li> <li>O: 0019213</li> <li>O: 0033558</li> <li>O: 0042641</li> <li>O: 0045668</li> <li>O: 0006110</li> </ul>	function Biological process Biological process Biological process Biological process Biological process Biological process Biological process Biological process Biological process Biological process Cellular component Molecular function Cellular component Biological	Regulation of osteoblast differentiation Regulation of heart contraction Osteoblast development Regulation of striated muscle contraction by calcium ion signaling Regulation of cardiac muscle contraction by calcium ion signaling Regulation of cardiac muscle contraction Response to inactivity Response to inactivity Response to muscle inactivity Response to muscle inactivity Response to muscle inactivity involved in regulation of muscle adaptation Response to denervation involved in regulation of muscle adaptation Response to denervation involved in regulation of muscle adaptation Regulation of muscle adaptation A band Deacetylase activity Protein deacetylase activity Negative regulation of osteoblast differentiation	3 2 6 2 5 3 1 1 3 5 5 3 7 1 1 1 6	5 4 4 4 4 4 4 4 4	<ol> <li>53</li> <li>157</li> <li>178</li> <li>33</li> <li>63</li> <li>25</li> <li>52</li> <li>10</li> <li>7</li> <li>11</li> <li>7</li> <li>44</li> <li>41</li> <li>73</li> <li>56</li> <li>67</li> <li>57</li> </ol>	45,240 45,240 45,240 45,240 45,240 45,240 45,240 45,240 45,240 45,240 45,240 45,240 45,240 45,240	46 46 46 46 46 46 46 46 46 46 46 46 46 4	Q5JWF2         A2A2R6, H0Y7E8, H0Y7F4, P63092, Q5JWD1, Q5JWE9, Q5JWF2         Q5JWF2, C9J0X4, F5GX36, F5H0B1, P56524         P51787, C9J0X4, F5GX36, F5H0B1, P56524	GNAS, GNAS, GNAS, GNAS, GNAS, GNAS, GNAS GNAS, HDAC4, HDAC4, HDAC4, HDAC4 KCNQ1, HDAC4, HDAC4, HDAC4, HDAC4 HDAC4, HDAC4, HDAC4, HDAC4	7.021184 4.969057 4.787944 6.897355 5.964469 7.297893 6.24131 8.619821 9.134394 8.482318 9.134394 9.134394 9.134394 6.482318 6.584197 5.751925 6.134394 5.87566 6.108859	2.43723E-11 5.56829E-05 9.84102E-05 5.03412E-06 5.28453E-05 1.65414E-06 2.70438E-05 3.27042E-08 6.30331E-09 6.30331E-09 6.30331E-09 1.42711E-05 1.42711E-05 1.42711E-05 3.5536E-05 3.5536E-05 6.51755E-05 3.76518E-05
<ul> <li>O: 0008016</li> <li>O: 0002076</li> <li>O: 0006942</li> <li>O: 0010882</li> <li>O: 00114854</li> <li>O: 0014874</li> <li>O: 0014874</li> <li>O: 0014874</li> <li>O: 0014877</li> <li>O: 0014874</li> <li>O: 0006110</li> <li>O: 0009118</li> </ul>	function Biological process Biological	Regulation of osteoblast differentiation Regulation of heart contraction Osteoblast development Regulation of striated muscle contraction by calcium ion signaling Regulation of cardiac muscle contraction by calcium ion signaling Response to inactivity Response to inactivity Response to muscle inactivity Response to stimulus involved in regulation of muscle adaptation Response to stimulus involved in regulation of muscle adaptation Response to denervation involved in regulation of muscle adaptation Response to denervation involved in regulation of muscle adaptation Regulation of muscle adaptation A band Deacetylase activity Protein deacetylase activity Negative regulation of osteoblast differentiation	3 2 6 2 5 3 1 1 3 5 5 3 7 1 1 1 6 5 7	5 4 4 4 4 4 4 4 4	<ol> <li>53</li> <li>157</li> <li>178</li> <li>33</li> <li>63</li> <li>25</li> <li>52</li> <li>10</li> <li>7</li> <li>11</li> <li>7</li> <li>44</li> <li>41</li> <li>73</li> <li>56</li> <li>67</li> <li>57</li> <li>25</li> </ol>	45,240 45,240 45,240 45,240 45,240 45,240 45,240 45,240 45,240 45,240 45,240 45,240 45,240 45,240 45,240	46 46 46 46 46 46 46 46 46 46 46 46 46 4	Q5JWF2         A2A2R6, H0Y7E8, H0Y7F4, P63092, Q5JWD1, Q5JWE9, Q5JWF2         Q5JWF2, C9J0X4, F5GX36, F5H0B1, P56524         P51787, C9J0X4, F5GX36, F5H0B1, P56524	GNAS, GNAS, GNAS, GNAS, GNAS, GNAS, GNAS GNAS, HDAC4, HDAC4, HDAC4, HDAC4 KCNQ1, HDAC4, HDAC4, HDAC4, HDAC4 HDAC4, HDAC4, HDAC4, HDAC4	<ul> <li>7.021184</li> <li>4.969057</li> <li>4.787944</li> <li>6.897355</li> <li>5.964469</li> <li>7.297893</li> <li>6.24131</li> <li>8.619821</li> <li>9.134394</li> <li>9.134394</li> <li>9.134394</li> <li>9.134394</li> <li>6.482318</li> <li>9.134394</li> <li>6.584197</li> <li>5.751925</li> <li>6.134394</li> <li>5.87566</li> <li>6.108859</li> <li>7.297893</li> </ul>	2.43723E-11 5.56829E-05 9.84102E-05 5.03412E-06 5.28453E-05 1.65414E-06 2.70438E-05 3.27042E-08 6.30331E-09 6.30331E-09 6.30331E-09 1.42711E-05 1.42711E-05 1.42711E-05 8.98652E-05 8.98652E-05 3.5536E-05 3.5536E-05 3.76518E-05
<ul> <li>O: 0008016</li> <li>O: 0002076</li> <li>O: 0006942</li> <li>O: 0010882</li> <li>O: 00135117</li> <li>O: 0014874</li> <li>O: 0014874</li> <li>O: 0014877</li> <li>O: 0014874</li> <li>O: 0019213</li> <li>O: 0019213</li> <li>O: 0033558</li> <li>O: 0042641</li> <li>O: 0045668</li> <li>O: 0006110</li> <li>O: 0009118</li> <li>O: 0010677</li> </ul>	functionBiological process	Regulation of osteoblast differentiation         Regulation of heart contraction         Osteoblast development         Regulation of striated muscle contraction         Regulation of cardiac muscle contraction by calcium ion signaling         Regulation of cardiac muscle contraction         Response to inactivity         Response to muscle inactivity         Response to muscle inactivity involved in regulation of muscle adaptation         Response to denervation involved in regulation of muscle adaptation         Response to denervation involved in regulation of muscle adaptation         A band         Deacetylase activity         Protein deacetylase activity         Negative regulation of osteoblast differentiation         Regulation of glycolytic process         Regulation of nucleoside metabolic process	3 2 6 2 5 3 1 1 3 5 5 3 7 1 1 6 5 7 1 1 6 5 7 4	5 4 4 4 4 4 4 4 4	<ol> <li>53</li> <li>157</li> <li>178</li> <li>33</li> <li>63</li> <li>25</li> <li>52</li> <li>10</li> <li>7</li> <li>11</li> <li>7</li> <li>44</li> <li>41</li> <li>73</li> <li>56</li> <li>67</li> <li>57</li> <li>25</li> <li>30</li> </ol>	45,240 45,240 45,240 45,240 45,240 45,240 45,240 45,240 45,240 45,240 45,240 45,240 45,240 45,240 45,240 45,240	46 46 46 46 46 46 46 46 46 46 46 46 46 4	Q5JWF2         A2A2R6, H0Y7E8, H0Y7F4, P63092, Q5JWD1, Q5JWE9, Q5JWF2         Q5JWF2, C9J0X4, F5GX36, F5H0B1, P56524         P51787, C9J0X4, F5GX36, F5H0B1, P56524	GNAS, GNAS, GNAS, GNAS, GNAS, GNAS, GNAS GNAS, HDAC4, HDAC4, HDAC4, HDAC4 KCNQ1, HDAC4, HDAC4, HDAC4, HDAC4 HDAC4, HDAC4, HDAC4, HDAC4	<ul> <li>7.021184</li> <li>4.969057</li> <li>4.787944</li> <li>6.897355</li> <li>5.964469</li> <li>7.297893</li> <li>6.24131</li> <li>8.619821</li> <li>9.134394</li> <li>8.482318</li> <li>9.134394</li> <li>6.482318</li> <li>6.584197</li> <li>5.751925</li> <li>6.134394</li> <li>5.87566</li> <li>6.108859</li> <li>7.297893</li> <li>7.034859</li> </ul>	2.43723E-11 5.56829E-05 9.84102E-05 5.03412E-06 5.28453E-05 1.65414E-06 2.70438E-05 3.27042E-08 6.30331E-09 6.30331E-09 6.30331E-09 1.42711E-05 1.42711E-05 1.42711E-05 3.5536E-05 3.5536E-05 3.5536E-05 3.76518E-05 1.65414E-06
<ul> <li>C: 0008016</li> <li>C: 0002076</li> <li>C: 0006942</li> <li>C: 0010882</li> <li>C: 00135117</li> <li>C: 0014874</li> <li>C: 0014874</li> <li>C: 0014874</li> <li>C: 0014874</li> <li>C: 0014874</li> <li>C: 0014874</li> <li>C: 0014894</li> <li>C: 0014894</li> <li>C: 0014894</li> <li>C: 0014894</li> <li>C: 0014894</li> <li>C: 00143502</li> <li>C: 0019213</li> <li>C: 0019213</li> <li>C: 0033558</li> <li>C: 0042641</li> <li>C: 0045668</li> <li>C: 0006110</li> <li>C: 0009118</li> <li>C: 0010677</li> <li>C: 0043470</li> </ul>	functionBiological process	Regulation of osteoblast differentiation Regulation of heart contraction Osteoblast development Regulation of striated muscle contraction by calcium ion signaling Regulation of cardiac muscle contraction by calcium ion signaling Regulation of cardiac muscle contraction Response to inactivity Response to muscle inactivity Response to muscle inactivity Response to muscle inactivity Response to muscle inactivity involved in regulation of muscle adaptation Response to denervation involved in regulation of muscle adaptation Regulation of muscle adaptation A band Deacetylase activity Actomyosin Negative regulation of osteoblast differentiation Regulation of glycolytic process Regulation of nucleoside metabolic process	3 2 6 2 5 3 1 1 3 5 5 3 7 1 1 5 5 3 7 1 1 6 5 7 4 6	5 4 4 4 4 4 4 4 4	<ol> <li>53</li> <li>157</li> <li>178</li> <li>33</li> <li>63</li> <li>25</li> <li>52</li> <li>10</li> <li>7</li> <li>11</li> <li>7</li> <li>44</li> <li>41</li> <li>73</li> <li>56</li> <li>67</li> <li>57</li> <li>25</li> <li>30</li> <li>36</li> </ol>	45,240 45,240 45,240 45,240 45,240 45,240 45,240 45,240 45,240 45,240 45,240 45,240 45,240 45,240 45,240 45,240 45,240	46 46 46 46 46 46 46 46 46 46 46 46 46 4	Q5JWF2         A2A2R6, H0Y7E8, H0Y7F4, P63092, Q5JWD1, Q5JWE9, Q5JWF2         Q5JWF2, C9J0X4, F5GX36, F5H0B1, P56524         P51787, C3J0X4, F5GX36, F5H0B1, P56524         C9J0X4, F5GX36, F5H0B1, P56524	GNAS, GNAS, GNAS, GNAS, GNAS, GNAS, GNAS GNAS, HDAC4, HDAC4, HDAC4, HDAC4 KCNQ1, HDAC4, HDAC4, HDAC4, HDAC4 HDAC4, HDAC4, HDAC4, HDAC4	<ul> <li>7.021184</li> <li>4.969057</li> <li>4.787944</li> <li>6.897355</li> <li>5.964469</li> <li>7.297893</li> <li>6.24131</li> <li>8.619821</li> <li>9.134394</li> <li>9.134394</li> <li>9.134394</li> <li>9.134394</li> <li>6.482318</li> <li>6.584197</li> <li>5.751925</li> <li>6.134394</li> <li>5.87566</li> <li>6.108859</li> <li>7.297893</li> <li>7.034859</li> <li>6.771824</li> </ul>	2.43723E-11 5.56829E-05 9.84102E-05 5.03412E-06 5.28453E-05 1.65414E-06 2.70438E-05 3.27042E-08 6.30331E-09 6.30331E-09 6.30331E-09 1.42711E-05 6.30331E-09 1.42711E-05 1.10087E-05 8.98652E-05 3.5536E-05 3.5536E-05 3.76518E-05 3.76518E-05 3.76518E-05 3.76518E-05
AC: 0008016         AC: 0002076         AC: 0006942         AC: 0010882         AC: 0014874         AC: 0043502         AC: 0043558         AC: 0042641         AC: 0042641         AC: 0042641         AC: 0006110         AC: 0009118         AC: 0009118         AC: 0043470         AC: 0043470         AC: 0043470	functionBiological processBiol	Regulation of osteoblast differentiation         Regulation of heart contraction         Osteoblast development         Regulation of striated muscle contraction by calcium ion signaling         Regulation of cardiac muscle contraction by calcium ion signaling         Regulation of cardiac muscle contraction         Response to inactivity         Response to muscle inactivity involved in regulation of muscle adaptation         Response to stimulus involved in regulation of muscle adaptation         Response to denervation involved in regulation of muscle adaptation         Regulation of muscle adaptation         Regulation of nulceoside metabolic process         Regulation of glycolytic process         Regulation of nucleoside metabolic process         Regulation of carbohydrate catabolic process         Negative regulation of glycolytic process         Regulation of carbohydrate metabolic process	3 2 6 2 5 3 1 1 3 5 5 3 7 1 1 6 5 7 4 6 3	5 4 4 4 4 4 4 4 4	<ol> <li>53</li> <li>157</li> <li>178</li> <li>33</li> <li>63</li> <li>25</li> <li>52</li> <li>10</li> <li>7</li> <li>11</li> <li>7</li> <li>44</li> <li>41</li> <li>73</li> <li>56</li> <li>67</li> <li>57</li> <li>25</li> <li>30</li> <li>36</li> </ol>	45,240 45,240 45,240 45,240 45,240 45,240 45,240 45,240 45,240 45,240 45,240 45,240 45,240 45,240 45,240 45,240 45,240	46 46 46 46 46 46 46 46 46 46 46 46 46 4	Q5JWF2         A2A2R6, H0Y7E8, H0Y7F4, P63092, Q5JWD1, Q5JWE9, Q5JWF2, C9J0X4, F5GX36, F5H0B1, P56524         P51787, C9J0X4, F5GX36, F5H0B1, P56524         C9J0X4, F5GX36, F5H0B1, P	GNAS, GNAS, GNAS, GNAS, GNAS, GNAS, GNAS GNAS, HDAC4, HDAC4, HDAC4, HDAC4 KCNQ1, HDAC4, HDAC4, HDAC4, HDAC4 HDAC4, HDAC4, HDAC4, HDAC4	7.0211844.9690574.7879446.8973555.9644697.2978936.241318.6198219.1343949.1343949.1343946.4823189.1343946.5841975.7519256.1343945.875666.1088597.2978937.0348596.7718246.732296	2.43723E-11 5.56829E-05 9.84102E-05 5.03412E-06 5.28453E-05 1.65414E-06 2.70438E-05 3.27042E-08 6.30331E-09 6.30331E-09 6.30331E-09 1.42711E-05 1.42711E-05 1.42711E-05 8.98652E-05 3.5536E-05 3.5536E-05 3.5536E-05 3.76518E-05 3.76518E-05 3.76518E-05 3.76518E-05
AC: 0008016         AC: 0002076         AC: 0006942         AC: 0010882         AC: 00114874         AC: 0014874         AC: 0043502         AC: 0043502         AC: 0043502         AC: 0043558         AC: 0042641         AC: 0045668         AC: 0009118         AC: 0009118         AC: 0043470         AC: 0045820         AC: 0045820	functionBiologicalprocess <td>Regulation of osteoblast differentiation         Regulation of heart contraction         Osteoblast development         Regulation of striated muscle contraction by calcium ion signaling         Regulation of cardiac muscle contraction by calcium ion signaling         Regulation of cardiac muscle contraction         Response to inactivity         Response to muscle inactivity involved in regulation of muscle adaptation         Response to othervation involved in regulation of muscle adaptation         Response to denervation involved in regulation of muscle adaptation         Aband         Deacetylase activity         Negative regulation of osteoblast differentiation         Regulation of glycolytic process         Regulation of nucleoside metabolic process         Regulation of carbohydrate catabolic process    </td> <td>3 2 6 2 5 3 1 1 3 5 5 3 7 1 1 3 5 5 3 7 1 1 6 5 7 4 6 3 12</td> <td></td> <td><ol> <li>53</li> <li>157</li> <li>178</li> <li>33</li> <li>63</li> <li>25</li> <li>52</li> <li>10</li> <li>7</li> <li>11</li> <li>7</li> <li>44</li> <li>41</li> <li>73</li> <li>56</li> <li>67</li> <li>57</li> <li>44</li> <li>41</li> <li>73</li> <li>56</li> <li>67</li> <li>57</li> <li>30</li> <li>36</li> <li>37</li> <li>8</li> </ol></td> <td>45,240         45,240</td> <td>46 46 46 46 46 46 46 46 46 46 46 46 46 4</td> <td>Q5JWF2         A2A2R6, H0Y7E8, H0Y7F4, P63092, Q5JWD1, Q5JWE9, Q5JWF2         Q5JWF2, C9J0X4, F5GX36, F5H0B1, P56524         P51787, C9J0X4, F5GX36, F5H0B1, P56524         C9J0X4, F5GX36, F5H0B1, P56524</td> <td>GNAS, GNAS, GNAS, GNAS, GNAS, GNAS, GNAS GNAS, HDAC4, HDAC4, HDAC4, HDAC4 KCNQ1, HDAC4, HDAC4, HDAC4, HDAC4 HDAC4, HDAC4, HDAC4, HDAC4</td> <td>7.0211844.9690574.7879446.8973555.9644697.2978936.241318.6198219.1343948.4823189.1343946.4823186.5841975.7519256.1343945.875666.1088597.2978937.0348596.7718246.7322968.941749</td> <td>2.43723E-11 5.56829E-05 9.84102E-05 5.03412E-06 5.28453E-05 1.65414E-06 2.70438E-05 3.27042E-08 6.30331E-09 6.30331E-09 6.30331E-09 1.42711E-05 1.42711E-05 1.42711E-05 3.5536E-05 3.5536E-05 3.5536E-05 3.5536E-05 3.76518E-05 3.76518E-05 1.65414E-06 3.44042E-06 1.698124E-06</td>	Regulation of osteoblast differentiation         Regulation of heart contraction         Osteoblast development         Regulation of striated muscle contraction by calcium ion signaling         Regulation of cardiac muscle contraction by calcium ion signaling         Regulation of cardiac muscle contraction         Response to inactivity         Response to muscle inactivity involved in regulation of muscle adaptation         Response to othervation involved in regulation of muscle adaptation         Response to denervation involved in regulation of muscle adaptation         Aband         Deacetylase activity         Negative regulation of osteoblast differentiation         Regulation of glycolytic process         Regulation of nucleoside metabolic process         Regulation of carbohydrate catabolic process	3 2 6 2 5 3 1 1 3 5 5 3 7 1 1 3 5 5 3 7 1 1 6 5 7 4 6 3 12		<ol> <li>53</li> <li>157</li> <li>178</li> <li>33</li> <li>63</li> <li>25</li> <li>52</li> <li>10</li> <li>7</li> <li>11</li> <li>7</li> <li>44</li> <li>41</li> <li>73</li> <li>56</li> <li>67</li> <li>57</li> <li>44</li> <li>41</li> <li>73</li> <li>56</li> <li>67</li> <li>57</li> <li>30</li> <li>36</li> <li>37</li> <li>8</li> </ol>	45,240         45,240	46 46 46 46 46 46 46 46 46 46 46 46 46 4	Q5JWF2         A2A2R6, H0Y7E8, H0Y7F4, P63092, Q5JWD1, Q5JWE9, Q5JWF2         Q5JWF2, C9J0X4, F5GX36, F5H0B1, P56524         P51787, C9J0X4, F5GX36, F5H0B1, P56524	GNAS, GNAS, GNAS, GNAS, GNAS, GNAS, GNAS GNAS, HDAC4, HDAC4, HDAC4, HDAC4 KCNQ1, HDAC4, HDAC4, HDAC4, HDAC4 HDAC4, HDAC4, HDAC4, HDAC4	7.0211844.9690574.7879446.8973555.9644697.2978936.241318.6198219.1343948.4823189.1343946.4823186.5841975.7519256.1343945.875666.1088597.2978937.0348596.7718246.7322968.941749	2.43723E-11 5.56829E-05 9.84102E-05 5.03412E-06 5.28453E-05 1.65414E-06 2.70438E-05 3.27042E-08 6.30331E-09 6.30331E-09 6.30331E-09 1.42711E-05 1.42711E-05 1.42711E-05 3.5536E-05 3.5536E-05 3.5536E-05 3.5536E-05 3.76518E-05 3.76518E-05 1.65414E-06 3.44042E-06 1.698124E-06
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  Regulation of muscle adaptation         Regulation of osteoblast differentiation         Regulation of muscle adaptation         Negative regulation of osteoblast differentiation         Regulation of glycolytic process         Regulation of carbohydrate catabolic process         Negative regulation of cellular carbohydrate metabolic process         Negative regulation of glycolytic process         Negative regulation of glycolytic process         Negative regulation of carbohydrate metabolic process         Negative regulation of ca</td> <td>3 2 6 2 5 3 1 1 3 5 5 3 7 1 3 5 3 7 1 1 6 5 7 4 6 3 12 4</td> <td></td> <td><ol> <li>53</li> <li>157</li> <li>178</li> <li>33</li> <li>63</li> <li>25</li> <li>52</li> <li>10</li> <li>7</li> <li>11</li> <li>7</li> <li>44</li> <li>41</li> <li>73</li> <li>56</li> <li>67</li> <li>57</li> <li>44</li> <li>41</li> <li>73</li> <li>56</li> <li>67</li> <li>57</li> <li>30</li> <li>36</li> <li>37</li> <li>8</li> <li>40</li> </ol></td> <td>45,240         45,240</td> <td>46 46 46 46 46 46 46 46 46 46 46 46 46 4</td> <td>Q5JWF2         A2A2R6, H0Y7E8, H0Y7F4, P63092, Q5JWD1, Q5JWE9, Q5JWF2         Q5JWF2, C9J0X4, F5GX36, F5H0B1, P56524         P51787, C9J0X4, F5GX36, F5H0B1, P56524         C9J0X4, F5GX36, F5H0B1, P56524</td> <td>GNAS, GNAS, GNAS, GNAS, GNAS, GNAS, GNAS GNAS, HDAC4, HDAC4, HDAC4, HDAC4 KCNQ1, HDAC4, HDAC4, HDAC4, HDAC4 HDAC4, HDAC4, HDAC4, HDAC4</td> <td>7.0211844.9690574.7879446.8973555.9644697.2978936.241318.6198219.1343949.1343949.1343949.1343946.5841975.7519256.1343945.875666.1088597.2978937.0348596.7718246.7322968.9417496.619821</td> <td>2.43723E-11 5.56829E-05 9.84102E-05 5.03412E-06 5.28453E-05 1.65414E-06 2.70438E-05 3.27042E-08 6.30331E-09 6.30331E-09 6.30331E-09 1.42711E-05 1.10087E-05 8.98652E-05 3.5536E-05 3.5536E-05 3.5536E-05 3.76518E-05 3.76518E-05 3.76518E-05 3.76518E-05 1.65414E-06 3.44042E-06 3.44042E-06 1.14254E-08</td>	Regulation of osteoblast differentiation         Regulation of heart contraction         Osteoblast development         Regulation of striated muscle contraction by calcium ion signaling         Regulation of cardiac muscle contraction by calcium ion signaling         Regulation of cardiac muscle contraction         Response to inactivity         Response to muscle inactivity involved in regulation of muscle adaptation         Response to stimulus involved in regulation of muscle adaptation         Response to denervation involved in regulation of muscle adaptation         Regulation of muscle adaptation         Regulation of osteoblast differentiation         Regulation of muscle adaptation         Negative regulation of osteoblast differentiation         Regulation of glycolytic process         Regulation of carbohydrate catabolic process         Negative regulation of cellular carbohydrate metabolic process         Negative regulation of glycolytic process         Negative regulation of glycolytic process         Negative regulation of carbohydrate metabolic process         Negative regulation of ca	3 2 6 2 5 3 1 1 3 5 5 3 7 1 3 5 3 7 1 1 6 5 7 4 6 3 12 4		<ol> <li>53</li> <li>157</li> <li>178</li> <li>33</li> <li>63</li> <li>25</li> <li>52</li> <li>10</li> <li>7</li> <li>11</li> <li>7</li> <li>44</li> <li>41</li> <li>73</li> <li>56</li> <li>67</li> <li>57</li> <li>44</li> <li>41</li> <li>73</li> <li>56</li> <li>67</li> <li>57</li> <li>30</li> <li>36</li> <li>37</li> <li>8</li> <li>40</li> </ol>	45,240         45,240	46 46 46 46 46 46 46 46 46 46 46 46 46 4	Q5JWF2         A2A2R6, H0Y7E8, H0Y7F4, P63092, Q5JWD1, Q5JWE9, Q5JWF2         Q5JWF2, C9J0X4, F5GX36, F5H0B1, P56524         P51787, C9J0X4, F5GX36, F5H0B1, P56524	GNAS, GNAS, GNAS, GNAS, GNAS, GNAS, GNAS GNAS, HDAC4, HDAC4, HDAC4, HDAC4 KCNQ1, HDAC4, HDAC4, HDAC4, HDAC4 HDAC4, HDAC4, HDAC4, HDAC4	7.0211844.9690574.7879446.8973555.9644697.2978936.241318.6198219.1343949.1343949.1343949.1343946.5841975.7519256.1343945.875666.1088597.2978937.0348596.7718246.7322968.9417496.619821	2.43723E-11 5.56829E-05 9.84102E-05 5.03412E-06 5.28453E-05 1.65414E-06 2.70438E-05 3.27042E-08 6.30331E-09 6.30331E-09 6.30331E-09 1.42711E-05 1.10087E-05 8.98652E-05 3.5536E-05 3.5536E-05 3.5536E-05 3.76518E-05 3.76518E-05 3.76518E-05 3.76518E-05 1.65414E-06 3.44042E-06 3.44042E-06 1.14254E-08
<ul> <li>C: 0008016</li> <li>C: 0002076</li> <li>C: 0006942</li> <li>C: 0010882</li> <li>C: 001355117</li> <li>C: 0014874</li> <li>C: 0014874</li> <li>C: 0014877</li> <li>C: 0014877</li> <li>C: 0014874</li> <li>C: 0043502</li> <li>C: 0045978</li> </ul>	functionBiologicalprocess <td>Regulation of osteoblast differentiation         Regulation of heart contraction         Osteoblast development         Regulation of striated muscle contraction         Regulation of cardiac muscle contraction by calcium ion signaling         Regulation of cardiac muscle contraction         Response to inactivity         Response to muscle inactivity involved in regulation of muscle adaptation         Response to stimulus involved in regulation of muscle adaptation         Response to muscle inactivity involved in regulation of muscle adaptation         Response to denervation involved in regulation of muscle adaptation         Response to denervation involved in regulation of muscle adaptation         Regulation of muscle adaptation         A band         Deacetylase activity         Nogative regulation of osteoblast differentiation         Regulation of glycolytic process         Regulation of cellular carbohydrate metabolic process         Regulation of carbohydrate catabolic process         Negative regulation of glycolytic process         Negative regulation of glycolytic process         Negative regulation of carbohydrate metabolic process         Negative regulation of carbohydrate metabolic process         Negative regulation of nucleoside metabolic process         Negative regulation of nucleoside metabolic</td> <td>3 2 6 2 5 3 1 1 3 5 5 3 7 1 1 5 5 3 7 1 1 6 5 7 4 6 3 12 4 7 8</td> <td></td> <td><ol> <li>53</li> <li>157</li> <li>178</li> <li>33</li> <li>63</li> <li>25</li> <li>52</li> <li>10</li> <li>7</li> <li>11</li> <li>7</li> <li>44</li> <li>41</li> <li>73</li> <li>66</li> <li>67</li> <li>57</li> <li>44</li> <li>41</li> <li>73</li> <li>62</li> </ol></td> <td>45,240         45,240</td> <td>46 46 46 46 46 46 46 46 46 46 46 46 46 4</td> <td>Q5JWF2         A2A2R6, H0Y7E8, H0Y7F4, P63092, Q5JWD1, Q5JWE9, Q5JWF2         Q5JWF2, C9J0X4, F5GX36, F5H0B1, P56524         P51787, C9J0X4, F5GX36, F5H0B1, P56524         C9J0X4, F5GX36, F5H0B1, P56524</td> <td>GNAS, GNAS, GNAS, GNAS, GNAS, GNAS, GNAS         GNAS, HDAC4, HDAC4, HDAC4, HDAC4         KCNQ1, HDAC4, HDAC4, HDAC4, HDAC4         HDAC4, HDAC4, HDAC4, HDAC4</td> <td>7.0211844.9690574.7879446.8973555.9644697.2978936.241318.6198219.1343949.1343949.1343946.4823189.1343946.5841975.7519256.1343945.875666.1088597.2978937.0348596.7718246.7322968.9417496.6198218.3567875.987553</td> <td>2.43723E-11 5.56829E-05 9.84102E-05 5.03412E-06 5.28453E-05 1.65414E-06 2.70438E-05 6.30331E-09 6.30331E-09 6.30331E-09 6.30331E-09 1.42711E-05 6.30331E-09 1.42711E-05 6.30331E-09 1.42711E-05 1.3536E-05 3.76518E-05 3.76518E-05 3.76518E-05 1.65414E-06 3.44042E-06 1.65414E-06 1.65414E-06 1.65414E-06 1.65414E-06 1.65414E-06 1.65414E-06</td>	Regulation of osteoblast differentiation         Regulation of heart contraction         Osteoblast development         Regulation of striated muscle contraction         Regulation of cardiac muscle contraction by calcium ion signaling         Regulation of cardiac muscle contraction         Response to inactivity         Response to muscle inactivity involved in regulation of muscle adaptation         Response to stimulus involved in regulation of muscle adaptation         Response to muscle inactivity involved in regulation of muscle adaptation         Response to denervation involved in regulation of muscle adaptation         Response to denervation involved in regulation of muscle adaptation         Regulation of muscle adaptation         A band         Deacetylase activity         Nogative regulation of osteoblast differentiation         Regulation of glycolytic process         Regulation of cellular carbohydrate metabolic process         Regulation of 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HDAC4         KCNQ1, HDAC4, HDAC4, HDAC4, HDAC4	7.0211844.9690574.7879446.8973555.9644697.2978936.241318.6198219.1343949.1343949.1343946.4823189.1343946.5841975.7519256.1343945.875666.1088597.2978937.0348596.7718246.7322968.9417496.6198218.3567875.987553	2.43723E-11 5.56829E-05 9.84102E-05 5.03412E-06 5.28453E-05 1.65414E-06 2.70438E-05 6.30331E-09 6.30331E-09 6.30331E-09 6.30331E-09 1.42711E-05 6.30331E-09 1.42711E-05 6.30331E-09 1.42711E-05 1.3536E-05 3.76518E-05 3.76518E-05 3.76518E-05 1.65414E-06 3.44042E-06 1.65414E-06 1.65414E-06 1.65414E-06 1.65414E-06 1.65414E-06 1.65414E-06
AC: 0008016         AC: 0002076         AC: 0006942         AC: 0010882         AC: 00114874         AC: 0014874         AC: 0043502         AC: 0043502         AC: 0043558         AC: 0045668         AC: 0045668         AC: 0009118         AC: 0045668         AC: 0045820         AC: 0045820         AC: 0045978         AC: 0045980         AC: 0045980         AC: 0051193	functionBiologicalprocess <td>Regulation of osteoblast differentiation         Regulation of heart contraction         Osteoblast development         Regulation of striated muscle contraction by calcium ion signaling         Regulation of cardiac muscle contraction by calcium ion signaling         Regulation of cardiac muscle contraction         Response to inactivity         Response to muscle inactivity involved in regulation of muscle adaptation         Response to stimulus involved in regulation of muscle adaptation         Response to muscle inactivity involved in regulation of muscle adaptation         Response to denervation involved in regulation of muscle adaptation         A band         Deacetylase activity         Protein deacetylase activity         Negative regulation of osteoblast differentiation         Regulation of glycolytic process         Regulation of callular carbohydrate metabolic process         Negative regulation of carbohydrate metabolic process         Negative regulation of carbohydrate metabolic process         Negative regulation of nucleoside metabolic process         Negative regulation of nucleoside metabolic process         Negative regulation of nucleoside metabolic process         Negative regulation of nucleoside metabolic process         Negative regulation of nucleoside metabolic process         Negative regula</td> <td>3 2 6 2 5 3 1 1 3 5 5 3 7 1 3 5 3 7 1 1 6 5 7 4 6 3 12 4 7 8 3</td> <td></td> <td><ol> <li>53</li> <li>157</li> <li>178</li> <li>33</li> <li>63</li> <li>25</li> <li>52</li> <li>10</li> <li>7</li> <li>11</li> <li>7</li> <li>44</li> <li>41</li> <li>73</li> <li>56</li> <li>67</li> <li>57</li> <li>25</li> <li>30</li> <li>36</li> <li>37</li> <li>8</li> <li>40</li> <li>12</li> </ol></td> <td>45,240         45,240</td> <td>46 46 46 46 46 46 46 46 46 46 46 46 46 4</td> <td>GSJWF2           A2A2R6, H0Y7E8, H0Y7F4, P63092, Q5JWD1, Q5JWE9, Q5JWF2           QSJWF2, C9J0X4, F5GX36, F5H0B1, P56524           P51787, C9J0X4, F5GX36, F5H0B1, P56524           &lt;</td> <td>GNAS, GNAS, GNAS, GNAS, GNAS, GNAS, GNAS         GNAS, HDAC4, HDAC4, HDAC4, HDAC4         KGNQ1, HDAC4, HDAC4, HDAC4, HDAC4         HDAC4, HDAC4, HDAC4, HDAC4</td> <td>7.0211844.9690574.7879446.8973555.9644697.2978936.241318.6198219.1343949.1343949.1343949.1343946.5841975.7519256.1343945.875666.1088597.2978937.0348596.7718246.7322968.9417496.6198218.3567875.9875536.656347</td> <td>2.43723E-111 5.56829E-05 9.84102E-05 5.03412E-06 1.65414E-06 2.70438E-05 3.27042E-08 6.30331E-09 6.30331E-09 6.30331E-09 1.42711E-05 1.42711E-05 1.42711E-05 3.5536E-05 3.5536E-05 3.5536E-05 3.76518E-05 3.76518E-05 3.76518E-05 3.76518E-05 1.65414E-06 3.44042E-06 3.44042E-06 1.14254E-08 1.01024E-08</td>	Regulation of osteoblast differentiation         Regulation of heart contraction         Osteoblast development         Regulation of striated muscle contraction by calcium ion signaling         Regulation of cardiac muscle contraction by calcium ion signaling         Regulation of cardiac muscle contraction         Response to inactivity         Response to muscle inactivity involved in regulation of muscle adaptation         Response to stimulus involved in regulation of muscle adaptation         Response to muscle inactivity involved in regulation of muscle adaptation         Response to denervation involved in regulation of muscle adaptation         A band         Deacetylase activity         Protein deacetylase activity         Negative regulation of osteoblast differentiation         Regulation of glycolytic process         Regulation of callular carbohydrate metabolic process         Negative regulation of carbohydrate metabolic process         Negative regulation of carbohydrate metabolic process         Negative regulation of nucleoside metabolic process         Negative regulation of nucleoside metabolic process         Negative regulation of nucleoside metabolic process         Negative regulation of nucleoside metabolic process         Negative regulation of nucleoside metabolic process         Negative regula	3 2 6 2 5 3 1 1 3 5 5 3 7 1 3 5 3 7 1 1 6 5 7 4 6 3 12 4 7 8 3		<ol> <li>53</li> <li>157</li> <li>178</li> <li>33</li> <li>63</li> <li>25</li> <li>52</li> <li>10</li> <li>7</li> <li>11</li> <li>7</li> <li>44</li> <li>41</li> <li>73</li> <li>56</li> <li>67</li> <li>57</li> <li>25</li> <li>30</li> <li>36</li> <li>37</li> <li>8</li> <li>40</li> <li>12</li> </ol>	45,240         45,240	46 46 46 46 46 46 46 46 46 46 46 46 46 4	GSJWF2           A2A2R6, H0Y7E8, H0Y7F4, P63092, Q5JWD1, Q5JWE9, Q5JWF2           QSJWF2, C9J0X4, F5GX36, F5H0B1, P56524           P51787, C9J0X4, F5GX36, F5H0B1, P56524           <	GNAS, GNAS, GNAS, GNAS, GNAS, GNAS, GNAS         GNAS, HDAC4, HDAC4, HDAC4, HDAC4         KGNQ1, HDAC4, HDAC4, HDAC4, HDAC4	7.0211844.9690574.7879446.8973555.9644697.2978936.241318.6198219.1343949.1343949.1343949.1343946.5841975.7519256.1343945.875666.1088597.2978937.0348596.7718246.7322968.9417496.6198218.3567875.9875536.656347	2.43723E-111 5.56829E-05 9.84102E-05 5.03412E-06 1.65414E-06 2.70438E-05 3.27042E-08 6.30331E-09 6.30331E-09 6.30331E-09 1.42711E-05 1.42711E-05 1.42711E-05 3.5536E-05 3.5536E-05 3.5536E-05 3.76518E-05 3.76518E-05 3.76518E-05 3.76518E-05 1.65414E-06 3.44042E-06 3.44042E-06 1.14254E-08 1.01024E-08
AC: 0008016         AC: 0002076         AC: 0006942         AC: 0010882         AC: 00114874         AC: 0014874         AC: 0043502         AC: 0043502         AC: 0043558         AC: 0045668         AC: 0045668         AC: 0045668         AC: 0045668         AC: 0045912         AC: 0051193         AC: 0051195	functionBiologicalprocess <td>Regulation of osteoblast differentiation         Regulation of heart contraction         Osteoblast development         Regulation of striated muscle contraction by         calcium ion signaling         Regulation of cardiac muscle contraction by         calcium ion signaling         Regulation of cardiac muscle contraction         Response to inactivity         Response to muscle inactivity involved in regulation of         Response to denervation involved in regulation of         Muscle adaptation         Regulation of muscle adaptation         Regulation of muscle adaptation         Regulation of muscle adaptation         Regulation of nucleo stativity         Protein deacetylase activity         Actomyosin         Negative regulation of cellular carbohydrate metabolic process         Regulation of nucleoside metabolic process         Negative regulation of carbohydrate metabolic process         Negative regulation of carbohydrate metabolic process         Negative regulation of nucleoside metabolic process         Regulation of cofactor metabolic process         Negative regulation of nucleoside metabolic process         Negative regulation of nucleoside metabolic process         Negative regulation of nucleoside metabolic process         Negative regulation of nucleoside metabolic proces</td> <td>3 2 6 2 5 3 1 1 3 5 5 3 7 1 1 6 5 7 4 6 3 12 4 7 8 3 6</td> <td></td> <td><ol> <li>53</li> <li>157</li> <li>178</li> <li>33</li> <li>63</li> <li>25</li> <li>10</li> <li>7</li> <li>11</li> <li>7</li> <li>44</li> <li>41</li> <li>73</li> <li>56</li> <li>67</li> <li>57</li> <li>25</li> <li>30</li> <li>36</li> <li>37</li> <li>8</li> <li>40</li> <li>12</li> <li>39</li> <li>8</li> </ol></td> <td>45,240         45,240</td> <td>46 46 46 46 46 46 46 46 46 46 46 46 46 4</td> <td>GSJWF2           A2A2R6, H0Y7E8, H0Y7F4, P63092, Q5JWD1, Q5JWE9, QSJWF2           QSJWF2, C9J0X4, F5GX36, F5H0B1, P56524           P51787, C9J0X4, F5GX36, F5H0B1, P56524           C3J0X4, F5GX36, F5H0B1, P56524           &lt;</td> <td>GNAS, GNAS, GNAS, GNAS, GNAS, GNAS, GNAS         GNAS, HDAC4, HDAC4, HDAC4, HDAC4         KCNQ1, HDAC4, HDAC4, HDAC4, HDAC4         HDAC4, HDAC4, HDAC4, HDAC4</td> <td>7.0211844.9690574.7879446.8973555.9644697.2978936.241318.6198219.1343949.1343949.1343949.1343946.4823189.1343946.5841975.7519256.1343945.875666.1088597.2978937.0348596.7718246.6198218.9417496.6563478.9417496.6563478.941749</td> <td>2.43723E-111 5.56829E-05 9.84102E-05 5.03412E-06 5.28453E-05 1.65414E-06 3.27042E-08 6.30331E-09 6.30331E-09 6.30331E-09 1.42711E-05 1.42711E-05 1.10087E-05 1.10087E-05 3.5536E-05 3.5536E-05 3.76518E-05 3.76518E-05 3.76518E-05 1.65414E-06 3.44042E-06 1.65414E-06 3.44042E-06 1.14254E-08</td>	Regulation of osteoblast differentiation         Regulation of heart contraction         Osteoblast development         Regulation of striated muscle contraction by         calcium ion signaling         Regulation of cardiac muscle contraction by         calcium ion signaling         Regulation of cardiac muscle contraction         Response to inactivity         Response to muscle inactivity involved in regulation of         Response to denervation involved in regulation of         Muscle adaptation         Regulation of muscle adaptation         Regulation of muscle adaptation         Regulation of muscle adaptation         Regulation of nucleo stativity         Protein deacetylase activity         Actomyosin         Negative regulation of cellular carbohydrate metabolic process         Regulation of nucleoside metabolic process         Negative regulation of carbohydrate metabolic process         Negative 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C3J0X4, F5GX36, F5H0B1, P56524           <	GNAS, GNAS, GNAS, GNAS, GNAS, GNAS, GNAS         GNAS, HDAC4, HDAC4, HDAC4, HDAC4         KCNQ1, HDAC4, HDAC4, HDAC4, HDAC4	7.0211844.9690574.7879446.8973555.9644697.2978936.241318.6198219.1343949.1343949.1343949.1343946.4823189.1343946.5841975.7519256.1343945.875666.1088597.2978937.0348596.7718246.6198218.9417496.6563478.9417496.6563478.941749	2.43723E-111 5.56829E-05 9.84102E-05 5.03412E-06 5.28453E-05 1.65414E-06 3.27042E-08 6.30331E-09 6.30331E-09 6.30331E-09 1.42711E-05 1.42711E-05 1.10087E-05 1.10087E-05 3.5536E-05 3.5536E-05 3.76518E-05 3.76518E-05 3.76518E-05 1.65414E-06 3.44042E-06 1.65414E-06 3.44042E-06 1.14254E-08
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<li>7</li> <li>44</li> <li>41</li> <li>73</li> <li>66</li> <li>67</li> <li>57</li> <li>44</li> <li>41</li> <li>73</li> <li>62</li> </ol></td> <td>45,240         45,240</td> <td>46 46 46 46 46 46 46 46 46 46 46 46 46 4</td> <td>GSJWF2           A2A2R6, H0Y7E8, H0Y7F4, P63092, Q5JWD1, Q5JWE9, Q5JWF2           QSJWF2, C9J0X4, F5GX36, F5H0B1, P56524           P51787, C9J0X4, F5GX36, F5H0B1, P56524           &lt;</td> <td>GNAS, GNAS, GNAS, GNAS, GNAS, GNAS, GNAS         GNAS, HDAC4, HDAC4, HDAC4, HDAC4         KGNQ1, HDAC4, HDAC4, HDAC4, HDAC4         HDAC4, HDAC4, HDAC4, HDAC4</td> <td>7.0211844.9690574.7879446.8973555.9644697.2978936.241318.6198219.1343949.1343949.1343949.1343946.5841975.7519256.1343945.875666.1088597.2978937.0348596.7718246.7322968.9417496.6198218.3567875.9875536.656347</td> <td>2.43723E-111 5.56829E-05 9.84102E-05 5.03412E-06 5.28453E-05 1.65414E-06 2.70438E-05 3.27042E-08 6.30331E-09 6.30331E-09 6.30331E-09 1.42711E-05 1.42711E-05 1.42711E-05 3.5536E-05 3.5536E-05 3.5536E-05 3.76518E-05 3.76518E-05 3.76518E-05 3.76518E-05 1.65414E-06 3.44042E-06 3.44042E-06 1.14254E-08 1.01024E-08</td>	Regulation of osteoblast differentiation         Regulation of heart contraction         Osteoblast development         Regulation of striated muscle contraction by calcium ion signaling         Regulation of cardiac muscle contraction by calcium ion signaling         Regulation of cardiac muscle contraction         Response to inactivity         Response to muscle inactivity involved in regulation of muscle adaptation         Response to stimulus involved in regulation of muscle adaptation         Response to muscle inactivity involved in regulation of muscle adaptation         Response to denervation involved in regulation of muscle adaptation         A band         Deacetylase activity         Protein deacetylase activity         Negative regulation of osteoblast differentiation         Regulation of glycolytic process         Regulation of callular carbohydrate metabolic process         Negative regulation of carbohydrate metabolic process         Negative regulation of carbohydrate metabolic process         Negative regulation of nucleoside metabolic process         Negative regulation of nucleoside metabolic process         Negative regulation of nucleoside metabolic process         Negative regulation of nucleoside metabolic process         Negative regulation of nucleoside metabolic process         Negative regula	3 2 6 2 5 3 1 1 3 5 5 3 7 1 3 5 3 7 1 1 6 5 7 4 6 3 12 4 7 8 3		<ol> <li>53</li> <li>157</li> <li>178</li> <li>33</li> <li>63</li> <li>25</li> <li>52</li> <li>10</li> <li>7</li> <li>11</li> <li>7</li> <li>44</li> <li>41</li> <li>73</li> <li>66</li> <li>67</li> <li>57</li> <li>44</li> <li>41</li> <li>73</li> <li>62</li> </ol>	45,240         45,240	46 46 46 46 46 46 46 46 46 46 46 46 46 4	GSJWF2           A2A2R6, H0Y7E8, H0Y7F4, P63092, Q5JWD1, Q5JWE9, Q5JWF2           QSJWF2, C9J0X4, F5GX36, F5H0B1, P56524           P51787, C9J0X4, F5GX36, F5H0B1, P56524           <	GNAS, GNAS, GNAS, GNAS, GNAS, GNAS, GNAS         GNAS, HDAC4, HDAC4, HDAC4, HDAC4         KGNQ1, HDAC4, HDAC4, HDAC4, HDAC4	7.0211844.9690574.7879446.8973555.9644697.2978936.241318.6198219.1343949.1343949.1343949.1343946.5841975.7519256.1343945.875666.1088597.2978937.0348596.7718246.7322968.9417496.6198218.3567875.9875536.656347	2.43723E-111 5.56829E-05 9.84102E-05 5.03412E-06 5.28453E-05 1.65414E-06 2.70438E-05 3.27042E-08 6.30331E-09 6.30331E-09 6.30331E-09 1.42711E-05 1.42711E-05 1.42711E-05 3.5536E-05 3.5536E-05 3.5536E-05 3.76518E-05 3.76518E-05 3.76518E-05 3.76518E-05 1.65414E-06 3.44042E-06 3.44042E-06 1.14254E-08 1.01024E-08
AC: 0008016         AC: 0002076         AC: 0006942         AC: 0010882         AC: 00114854         AC: 0014874         AC: 0043502         AC: 0043558         AC: 0042641         AC: 0045668         AC: 0045668         AC: 0045668         AC: 0045668         AC: 0045918         AC: 0045912         AC: 0045912         AC: 0045978         AC: 0045978         AC: 0051193         AC: 0051194	functionBiological processBiol	Regulation of osteoblast differentiation         Regulation of heart contraction         Osteoblast development         Regulation of striated muscle contraction by         calcium ion signaling         Regulation of cardiac muscle contraction by         calcium ion signaling         Regulation of cardiac muscle contraction         Response to inactivity         Response to muscle inactivity involved in regulation of         Response to denervation involved in regulation of         Muscle adaptation         Regulation of muscle adaptation         Regulation of muscle adaptation         Regulation of muscle adaptation         Regulation of nucleo stativity         Protein deacetylase activity         Actomyosin         Negative regulation of cellular carbohydrate metabolic process         Regulation of nucleoside metabolic process         Negative regulation of carbohydrate metabolic process         Negative regulation of carbohydrate metabolic process         Negative regulation of nucleoside metabolic process         Regulation of cofactor metabolic process         Negative regulation of nucleoside metabolic process         Negative regulation of nucleoside metabolic process         Negative regulation of nucleoside metabolic process         Negative regulation of nucleoside metabolic proces	3 2 6 2 5 3 1 1 3 5 5 3 7 1 1 6 5 7 4 6 3 12 4 7 8 3 6		<ol> <li>53</li> <li>157</li> <li>178</li> <li>33</li> <li>63</li> <li>25</li> <li>10</li> <li>7</li> <li>11</li> <li>7</li> <li>44</li> <li>41</li> <li>73</li> <li>56</li> <li>67</li> <li>57</li> <li>25</li> <li>30</li> <li>36</li> <li>37</li> <li>8</li> <li>40</li> <li>12</li> <li>39</li> <li>8</li> </ol>	45,240         45,240	46 46 46 46 46 46 46 46 46 46 46 46 46 4	GSJWF2           A2A2R6, H0Y7E8, H0Y7F4, P63092, Q5JWD1, Q5JWE9, QSJWF2           QSJWF2, C9J0X4, F5GX36, F5H0B1, P56524           P51787, C9J0X4, F5GX36, F5H0B1, P56524           C3J0X4, F5GX36, F5H0B1, P56524           <	GNAS, GNAS, GNAS, GNAS, GNAS, GNAS, GNAS         GNAS, HDAC4, HDAC4, HDAC4, HDAC4         KCNQ1, HDAC4, HDAC4, HDAC4, HDAC4	7.0211844.9690574.7879446.8973555.9644697.2978936.241318.6198219.1343949.1343949.1343949.1343946.4823189.1343946.5841975.7519256.1343945.875666.1088597.2978937.0348596.7718246.6198218.9417496.6563478.9417496.6563478.941749	2.43723E-111 5.56829E-05 9.84102E-05 5.03412E-06 5.28453E-05 1.65414E-06 2.70438E-05 6.30331E-09 6.30331E-09 6.30331E-09 6.30331E-09 1.42711E-05 6.30331E-09 1.42711E-05 1.10087E-05 1.3536E-05 3.76518E-05 3.76518E-05 3.76518E-05 3.76518E-05 1.65414E-06 3.44042E-06 1.65414E-06 1.14254E-08
AC: 0008016         AC: 0002076         AC: 0006942         AC: 0010882         AC: 0014854         AC: 0014870         AC: 0014870         AC: 0014874         AC: 0019213         AC: 0042641         AC: 0045668         AC: 0009118         AC: 0004577         AC: 0045980         AC: 0045978         AC: 0045978         AC: 0051193         AC: 0051193         AC: 0051193         AC: 0051193	functionBiological processBiol	Regulation of osteoblast differentiation         Regulation of heart contraction         Osteoblast development         Regulation of striated muscle contraction by calcium ion signaling         Regulation of cardiac muscle contraction by calcium ion signaling         Regulation of cardiac muscle contraction         Response to inactivity         Response to muscle inactivity involved in regulation of muscle adaptation         Response to muscle inactivity involved in regulation of muscle adaptation         Response to denervation involved in regulation of muscle adaptation         A band         Deacetylase activity         Protein deacetylase activity         Regulation of nucleoside metabolic process         Regulation of carbohydrate catabolic process         Regulation of carbohydrate metabolic process         Regulation of carbohydrate metabolic process         Regulation of carbohydrate metabolic process         Regulation of carbohydrate metabolic process         Regulation of cofactor metabolic process	3 2 6 2 5 3 1 1 3 5 5 3 7 1 1 6 5 7 4 6 3 12 4 7 8 3 6		<ol> <li>53</li> <li>157</li> <li>178</li> <li>33</li> <li>63</li> <li>25</li> <li>10</li> <li>7</li> <li>11</li> <li>7</li> <li>44</li> <li>41</li> <li>73</li> <li>56</li> <li>67</li> <li>57</li> <li>25</li> <li>30</li> <li>36</li> <li>37</li> <li>8</li> <li>40</li> <li>12</li> <li>39</li> <li>8</li> </ol>	45,240         45,240	46 46 46 46 46 46 46 46 46 46 46 46 46 4	GSJWF2           A2A2R6, H0Y7E8, H0Y7F4, P63092, Q5JWD1, Q5JWE9, QSJWF2           QSJWF2, C9J0X4, F5GX36, F5H0B1, P56524           P51787, C9J0X4, F5GX36, F5H0B1, P56524           <	GNAS, GNAS, GNAS, GNAS, GNAS, GNAS, GNAS         GNAS, HDAC4, HDAC4, HDAC4, HDAC4         KCNQ1, HDAC4, HDAC4, HDAC4, HDAC4         HDAC4, HDAC4, HDAC4, HDAC4, HDAC4         HDAC4, HDAC4, HDAC4, HDAC4 <td>7.0211844.9690574.7879446.8973555.9644697.2978936.241318.6198219.1343949.1343949.1343949.1343946.5841975.7519256.1343945.875666.1088597.2978937.0348596.7718246.7322968.9417496.6198218.3567875.9875536.6563478.9417496.656347</td> <td>2.43723E-111 5.56829E-05 9.84102E-05 5.03412E-06 5.28453E-05 1.65414E-06 2.70438E-05 6.30331E-09 6.30331E-09 6.30331E-09 1.42711E-05 6.30331E-09 1.42711E-05 3.5536E-05 3.5536E-05 3.5536E-05 3.76518E-05 3.76518E-05 3.76518E-05 3.76518E-05 3.76518E-05 3.76518E-05 1.65414E-06 3.44042E-06 1.14254E-08 1.01024E-08 1.01024E-08</td>	7.0211844.9690574.7879446.8973555.9644697.2978936.241318.6198219.1343949.1343949.1343949.1343946.5841975.7519256.1343945.875666.1088597.2978937.0348596.7718246.7322968.9417496.6198218.3567875.9875536.6563478.9417496.656347	2.43723E-111 5.56829E-05 9.84102E-05 5.03412E-06 5.28453E-05 1.65414E-06 2.70438E-05 6.30331E-09 6.30331E-09 6.30331E-09 1.42711E-05 6.30331E-09 1.42711E-05 3.5536E-05 3.5536E-05 3.5536E-05 3.76518E-05 3.76518E-05 3.76518E-05 3.76518E-05 3.76518E-05 3.76518E-05 1.65414E-06 3.44042E-06 1.14254E-08 1.01024E-08 1.01024E-08
GO: 0008016         GO: 0002076         GO: 0006942         GO: 0010882         GO: 0014854         GO: 0014870         GO: 0014871         GO: 0014870         GO: 0014871         GO: 0014870         GO: 0043502         GO: 0043502         GO: 0042641         GO: 0045668         GO: 0045668         GO: 0045978         GO: 0045978         GO: 0045978         GO: 0051193         GO: 0051193         GO: 0051193         GO: 0051193         GO: 0051193         GO: 0051193	functionBiological processBiol	Regulation of osteoblast differentiation         Regulation of heart contraction         Osteoblast development         Regulation of striated muscle contraction by calcium ion signaling         Regulation of cardiac muscle contraction by calcium ion signaling         Regulation of cardiac muscle contraction         Response to inactivity         Response to muscle inactivity         Response to stimulus involved in regulation of muscle adaptation         Response to denervation involved in regulation of muscle adaptation         Regulation of muscle adaptation         Aband         Deacetylase activity         Protein deacetylase activity         Regulation of glycolytic process         Regulation of cellular carbohydrate metabolic process         Regulation of cellular carbohydrate metabolic process         Negative regulation of glycolytic process         Negative regulation of suchohydrate metabolic process         Negative regulation of nucleoside metabolic process         Negative regulation of nucleoside metabolic process         Negative regulation of nucleoside metabolic process         Negative regulation of nucleoside metabolic process         Negative regulation of nucleoside metabolic process         Regulation of cofactor metabolic process         Negative regulation of colactor metabolic process <td< td=""><td>3 2 6 2 5 3 1 1 3 5 5 3 7 1 3 5 3 7 1 1 6 5 7 4 6 3 12 4 7 8 3 6 3 7</td><td></td><td><ol> <li>53</li> <li>157</li> <li>178</li> <li>33</li> <li>63</li> <li>25</li> <li>52</li> <li>10</li> <li>7</li> <li>11</li> <li>7</li> <li>44</li> <li>41</li> <li>73</li> <li>56</li> <li>67</li> <li>57</li> <li>30</li> <li>67</li> <li>57</li> <li>30</li> <li>36</li> <li>37</li> <li>8</li> <li>40</li> <li>12</li> <li>62</li> <li>39</li> <li>8</li> <li>39</li> <li>8</li> <li>39</li> <li>8</li> </ol></td><td>45,240         45,240</td><td>46 46 46 46 46 46 46 46 46 46 46 46 46 4</td><td>OSJWF2           A2A2R6, H0Y7E8, H0Y7F4, P63092, Q5JWD1, Q5JWE9, Q5JWF2           Q5JWF2, C9J0X4, F5GX36, F5H0B1, P56524           P51787, C9J0X4, F5GX36, F5H0B1, P56524           &lt;</td><td>GNAS, GNAS, GNAS, GNAS, GNAS, GNAS, GNAS         GNAS, HDAC4, HDAC4, HDAC4, HDAC4         KCNQ1, HDAC4, HDAC4, HDAC4, HDAC4         HDAC4, HDAC4, HDAC4, HDAC4</td><td>7.0211844.9690574.7879446.8973555.9644697.2978936.241318.6198219.1343949.1343949.1343946.5841975.7519256.1343945.875666.1088597.2978937.0348596.7718246.7322968.9417496.6563475.9875536.6563478.9417496.6563478.941749</td><td>2.43723E-111 5.56829E-05 9.84102E-05 5.03412E-06 5.28453E-05 1.65414E-06 2.70438E-05 6.30331E-09 6.30331E-09 6.30331E-09 1.42711E-05 6.30331E-09 1.42711E-05 3.5536E-05 3.5536E-05 3.5536E-05 3.76518E-05 3.76518E-05 3.76518E-05 3.76518E-05 1.65414E-06 3.44042E-06 1.65414E-06 1.14254E-08 1.01024E-05 5.08282E-05 9.24809E-06 1.14254E-08</td></td<>	3 2 6 2 5 3 1 1 3 5 5 3 7 1 3 5 3 7 1 1 6 5 7 4 6 3 12 4 7 8 3 6 3 7		<ol> <li>53</li> <li>157</li> <li>178</li> <li>33</li> <li>63</li> <li>25</li> <li>52</li> <li>10</li> <li>7</li> <li>11</li> <li>7</li> <li>44</li> <li>41</li> <li>73</li> <li>56</li> <li>67</li> <li>57</li> <li>30</li> <li>67</li> <li>57</li> <li>30</li> <li>36</li> <li>37</li> <li>8</li> <li>40</li> <li>12</li> <li>62</li> <li>39</li> <li>8</li> <li>39</li> <li>8</li> <li>39</li> <li>8</li> </ol>	45,240         45,240	46 46 46 46 46 46 46 46 46 46 46 46 46 4	OSJWF2           A2A2R6, H0Y7E8, H0Y7F4, P63092, Q5JWD1, Q5JWE9, Q5JWF2           Q5JWF2, C9J0X4, F5GX36, F5H0B1, P56524           P51787, C9J0X4, F5GX36, F5H0B1, P56524           <	GNAS, GNAS, GNAS, GNAS, GNAS, GNAS, GNAS         GNAS, HDAC4, HDAC4, HDAC4, HDAC4         KCNQ1, HDAC4, HDAC4, HDAC4, HDAC4	7.0211844.9690574.7879446.8973555.9644697.2978936.241318.6198219.1343949.1343949.1343946.5841975.7519256.1343945.875666.1088597.2978937.0348596.7718246.7322968.9417496.6563475.9875536.6563478.9417496.6563478.941749	2.43723E-111 5.56829E-05 9.84102E-05 5.03412E-06 5.28453E-05 1.65414E-06 2.70438E-05 6.30331E-09 6.30331E-09 6.30331E-09 1.42711E-05 6.30331E-09 1.42711E-05 3.5536E-05 3.5536E-05 3.5536E-05 3.76518E-05 3.76518E-05 3.76518E-05 3.76518E-05 1.65414E-06 3.44042E-06 1.65414E-06 1.14254E-08 1.01024E-05 5.08282E-05 9.24809E-06 1.14254E-08
GO: 0008016         GO: 0002076         GO: 0006942         GO: 0010882         GO: 0014854         GO: 0014854         GO: 0014870         GO: 0014874         GO: 0043502         GO: 0043502         GO: 0042641         GO: 0045968         GO: 0045978         GO: 0045978         GO: 0045978         GO: 0051193         GO: 10051193         GO: 10051193         GO: 10051193         GO: 10051193         GO: 10051193         GO: 10051193         GO: 10051193    <	functionBiological processBiol	Regulation of osteoblast differentiation         Regulation of heart contraction         Osteoblast development         Regulation of striated muscle contraction by calcium ion signaling         Regulation of cardiac muscle contraction by calcium ion signaling         Regulation of cardiac muscle contraction by calcium ion signaling         Response to inactivity         Response to muscle inactivity         Response to stimulus involved in regulation of muscle adaptation         Response to demervation involved in regulation of muscle adaptation         Response to demervation involved in regulation of muscle adaptation         Response to demervation involved in regulation of muscle adaptation         Aband         Deacetylase activity         Negative regulation of osteoblast differentiation         Regulation of glycolytic process         Regulation of nucleoside metabolic process         Negative regulation of carbohydrate metabolic process         Negative regulation of glycolytic process         Negative regulation of nucleoside metabolic process         Negative regulation of cofactor metabolic process	3 2 6 2 5 3 1 1 3 5 5 3 7 1 3 5 3 7 1 1 6 5 7 4 6 3 12 4 7 8 3 6 3 7 9		<ol> <li>53</li> <li>157</li> <li>178</li> <li>33</li> <li>63</li> <li>25</li> <li>52</li> <li>10</li> <li>7</li> <li>11</li> <li>7</li> <li>44</li> <li>41</li> <li>73</li> <li>56</li> <li>67</li> <li>57</li> <li>25</li> <li>30</li> <li>36</li> <li>37</li> <li>8</li> <li>40</li> <li>12</li> <li>30</li> <li>36</li> <li>37</li> <li>30</li> <li>36</li> <li>37</li> <li>30</li> <li>36</li> <li>37</li> <li>30</li> <li>31</li> <li>32</li> <li>32</li> <li>34</li> <li>35</li> <li>36</li> <li>37</li> <li>36</li> <li>37</li> <li>30</li> <li>31</li> <li>32</li> <li>32</li> <li>33</li> <li>34</li> <li>35</li> <li>36</li> <li>37</li> <li>36</li> <li>37</li> <li>30</li> <li>36</li> <li>37</li> <li>30</li> <li>36</li> <li>37</li> <li>30</li> <li>30</li> <li>31</li> <li>32</li> <li>34</li> <li>34</li> <li>35</li> <li>36</li> <li>37</li> <li>36</li> <li>36</li> <li>37</li> <li>36</li> <li>37</li></ol>	45,240         45,240	46 46 46 46 46 46 46 46 46 46 46 46 46 4	GSJWF2         A2A2R6, H0Y7E8, H0Y7F4, P63092, QSJWD1, QSJWE9, QSJWF2         QSJWF2, C9J0X4, F5GX36, F5H0B1, P56524         P51787, C9J0X4, F5GX36, F5H0B1, P56524	GNAS, GNAS, GNAS, GNAS, GNAS, GNAS, GNAS         GNAS, HDAC4, HDAC4, HDAC4, HDAC4         KCNQ1, HDAC4, HDAC4, HDAC4, HDAC4	7.0211844.9690574.7879446.8973555.9644697.2978936.241318.6198219.1343949.1343949.1343946.4823189.1343946.4823186.5841975.7519256.1343945.875666.1088597.2978937.0348596.7718246.67322968.9417496.6563478.9417496.6563478.9417496.6563478.9417496.6563478.9417496.6563478.941749	2.43723E-115.56829E-059.84102E-055.03412E-065.28453E-051.65414E-062.70438E-056.30331E-096.30331E-091.42711E-051.10087E-053.5536E-053.5536E-053.76518E-053.76518E-053.76518E-051.65414E-063.76518E-051.65414E-061.708907E-061.14254E-081.01024E-059.24809E-061.14254E-089.24809E-061.14254E-089.24809E-061.14254E-089.24809E-061.14254E-089.24809E-061.14254E-089.24809E-061.14254E-089.24809E-061.14254E-089.24809E-061.14254E-089.24809E-061.14254E-089.24809E-061.14254E-089.24809E-061.14254E-089.24809E-061.14254E-089.24809E-061.14254E-089.24809E-061.14254E-089.24809E-06
AC: 0008016         AC: 0002076         AC: 0006942         AC: 0010882         AC: 0014874         AC: 0043502         AC: 0043502         AC: 0043558         AC: 0042641         AC: 0045668         AC: 0045668         AC: 0045668         AC: 0045978         AC: 0045978         AC: 0045978         AC: 0051193         AC: 0051193         AC: 0051193         AC: 0051193         AC: 1900543         AC: 1903578	functionBiologicalprocess <td>Regulation of osteoblast differentiation         Regulation of heart contraction         Osteoblast development         Regulation of striated muscle contraction by calcium ion signaling         Regulation of cardiac muscle contraction by calcium ion signaling         Regulation of cardiac muscle contraction         Response to inactivity         Response to muscle inactivity involved in regulation of muscle adaptation         Response to stimulus involved in regulation of muscle adaptation         Response to denervation involved in regulation of muscle adaptation         Response to denervation involved in regulation of muscle adaptation         Regulation of muscle adaptation         A band         Deacetylase activity         Protein deacetylase activity         Regulation of glycolytic process         Regulation of glycolytic process         Regulation of cellular carbohydrate metabolic process         Regulation of carbohydrate metabolic process         Negative regulation of carbohydrate metabolic process         Negative regulation of nucleoside metabolic process         Regulation of cofactor metabolic process         Regulation of cofactor metabolic process         Regulation of colocaryme metabolic process         Negative regulation of colocaryme metabolic process         Regulation of coenzyme metabolic process</td> <td>3 2 6 2 5 3 1 1 3 5 5 3 7 1 3 5 3 7 1 1 6 5 7 4 6 3 12 4 7 8 3 6 3 7 9 5</td> <td></td> <td><ul> <li>53</li> <li>157</li> <li>178</li> <li>33</li> <li>63</li> <li>25</li> <li>52</li> <li>10</li> <li>7</li> <li>11</li> <li>7</li> <li>44</li> <li>41</li> <li>73</li> <li>56</li> <li>67</li> <li>57</li> <li>30</li> <li>36</li> <li>37</li> <li>8</li> <li>40</li> <li>12</li> <li>56</li> <li>30</li> <li>36</li> <li>37</li> <li>8</li> <li>40</li> <li>12</li> <li>41</li> <li>73</li> <li>56</li> <li>30</li> <li>36</li> <li>37</li> <li>44</li> <li>41</li> <li>73</li> <li>44</li> <li>41</li> <li>73</li> <li>56</li> <li>67</li> <li>30</li> <li>36</li> <li>37</li> <li>44</li> <li>41</li> <li>73</li> <li>56</li> <li>30</li> <li>31</li> <li>42</li> <li>43</li> <li>40</li> <li>44</li> <li>41</li> <li>41<!--</td--><td>45,240         45,240</td><td>46 46 46 46 46 46 46 46 46 46 46 46 46 4</td><td>OSJWF2           A2A2R6, H0Y7E8, H0Y7F4, P63092, Q5JWD1, Q5JWE9, Q5JWF2           OSJWF2, C9J0X4, F5GX36, F5H0B1, P56524           F51787, C9J0X4, F5GX36, F5H0B1, P56524           &lt;</td><td>GNAS, GNAS, GNAS, GNAS, GNAS, GNAS, GNAS         GNAS, HDAC4, HDAC4, HDAC4, HDAC4         HDAC4, HDAC4, HDAC4, HDAC4, HDAC4         HDAC4, HDAC4, HDAC4, HDAC4</td><td>7.0211844.9690574.7879446.8973555.9644697.2978936.241318.6198219.1343949.1343949.1343949.1343946.5841975.7519256.1343945.875666.1088597.2978937.0348596.7718246.6198218.9417496.6563478.9417496.6563478.9417496.6563478.9417496.0348597.034859</td><td>2.43723E-111 5.56829E-05 9.84102E-05 5.03412E-06 1.65414E-06 2.70438E-05 3.27042E-08 6.30331E-09 6.30331E-09 6.30331E-09 1.42711E-05 1.42711E-05 1.10087E-05 1.3536E-05 3.5536E-05 3.5536E-05 3.76518E-05 3.76518E-05 3.76518E-05 3.76518E-05 1.14254E-08 1.14254E-08 1.14254E-08 1.14254E-08</td></li></ul></td>	Regulation of osteoblast differentiation         Regulation of heart contraction         Osteoblast development         Regulation of striated muscle contraction by calcium ion signaling         Regulation of cardiac muscle contraction by calcium ion signaling         Regulation of cardiac muscle contraction         Response to inactivity         Response to muscle inactivity involved in regulation of muscle adaptation         Response to stimulus involved in regulation of muscle adaptation         Response to denervation involved in regulation of muscle adaptation         Response to denervation involved in regulation of muscle adaptation         Regulation of muscle adaptation         A band         Deacetylase activity         Protein deacetylase activity         Regulation of glycolytic process         Regulation of glycolytic process         Regulation of cellular carbohydrate metabolic process         Regulation of carbohydrate metabolic process         Negative regulation of carbohydrate metabolic process         Negative regulation of nucleoside metabolic process         Regulation of cofactor metabolic process         Regulation of cofactor metabolic process         Regulation of colocaryme metabolic process         Negative regulation of colocaryme metabolic process         Regulation of coenzyme metabolic process	3 2 6 2 5 3 1 1 3 5 5 3 7 1 3 5 3 7 1 1 6 5 7 4 6 3 12 4 7 8 3 6 3 7 9 5		<ul> <li>53</li> <li>157</li> <li>178</li> <li>33</li> <li>63</li> <li>25</li> <li>52</li> <li>10</li> <li>7</li> <li>11</li> <li>7</li> <li>44</li> <li>41</li> <li>73</li> <li>56</li> <li>67</li> <li>57</li> <li>30</li> <li>36</li> <li>37</li> <li>8</li> <li>40</li> <li>12</li> <li>56</li> <li>30</li> <li>36</li> <li>37</li> <li>8</li> <li>40</li> <li>12</li> <li>41</li> <li>73</li> <li>56</li> <li>30</li> <li>36</li> <li>37</li> <li>44</li> <li>41</li> <li>73</li> <li>44</li> <li>41</li> <li>73</li> <li>56</li> <li>67</li> <li>30</li> <li>36</li> <li>37</li> <li>44</li> <li>41</li> <li>73</li> <li>56</li> <li>30</li> <li>31</li> <li>42</li> <li>43</li> <li>40</li> <li>44</li> <li>41</li> <li>41<!--</td--><td>45,240         45,240</td><td>46 46 46 46 46 46 46 46 46 46 46 46 46 4</td><td>OSJWF2           A2A2R6, H0Y7E8, H0Y7F4, P63092, Q5JWD1, Q5JWE9, Q5JWF2           OSJWF2, C9J0X4, F5GX36, F5H0B1, P56524           F51787, C9J0X4, F5GX36, F5H0B1, P56524           &lt;</td><td>GNAS, GNAS, GNAS, GNAS, GNAS, GNAS, GNAS         GNAS, HDAC4, HDAC4, HDAC4, HDAC4         HDAC4, HDAC4, HDAC4, HDAC4, HDAC4         HDAC4, HDAC4, HDAC4, HDAC4</td><td>7.0211844.9690574.7879446.8973555.9644697.2978936.241318.6198219.1343949.1343949.1343949.1343946.5841975.7519256.1343945.875666.1088597.2978937.0348596.7718246.6198218.9417496.6563478.9417496.6563478.9417496.6563478.9417496.0348597.034859</td><td>2.43723E-111 5.56829E-05 9.84102E-05 5.03412E-06 1.65414E-06 2.70438E-05 3.27042E-08 6.30331E-09 6.30331E-09 6.30331E-09 1.42711E-05 1.42711E-05 1.10087E-05 1.3536E-05 3.5536E-05 3.5536E-05 3.76518E-05 3.76518E-05 3.76518E-05 3.76518E-05 1.14254E-08 1.14254E-08 1.14254E-08 1.14254E-08</td></li></ul>	45,240         45,240	46 46 46 46 46 46 46 46 46 46 46 46 46 4	OSJWF2           A2A2R6, H0Y7E8, H0Y7F4, P63092, Q5JWD1, Q5JWE9, Q5JWF2           OSJWF2, C9J0X4, F5GX36, F5H0B1, P56524           F51787, C9J0X4, F5GX36, F5H0B1, P56524           <	GNAS, GNAS, GNAS, GNAS, GNAS, GNAS, GNAS         GNAS, HDAC4, HDAC4, HDAC4, HDAC4         HDAC4, HDAC4, HDAC4, HDAC4, HDAC4	7.0211844.9690574.7879446.8973555.9644697.2978936.241318.6198219.1343949.1343949.1343949.1343946.5841975.7519256.1343945.875666.1088597.2978937.0348596.7718246.6198218.9417496.6563478.9417496.6563478.9417496.6563478.9417496.0348597.034859	2.43723E-111 5.56829E-05 9.84102E-05 5.03412E-06 1.65414E-06 2.70438E-05 3.27042E-08 6.30331E-09 6.30331E-09 6.30331E-09 1.42711E-05 1.42711E-05 1.10087E-05 1.3536E-05 3.5536E-05 3.5536E-05 3.76518E-05 3.76518E-05 3.76518E-05 3.76518E-05 1.14254E-08 1.14254E-08 1.14254E-08 1.14254E-08

# Table S3 KEGG analysis of the 10 genes with significant methylation frequence of the overlap group (≥15 counts)

#Term	Database	ID	Input number	Background number	P value	Correcte	d P value	Input	Hyperlink
Vibrio cholerae infection	KEGG PATHWAY	hsa05110	2	50	0.006229	0.308577	0.510637	ENSG00000087460, ENSG00000053918	http://www.genome.jp/kegg-bin/show_pathway?h
Gastric acid secretion	KEGG PATHWAY	hsa04971	2	74	0.012932	0.308577	0.510637	ENSG00000087460, ENSG00000053918	http://www.genome.jp/kegg-bin/show_pathway?h
Pancreatic secretion	KEGG PATHWAY	hsa04972	2	96	0.020893	0.308577	0.510637	ENSG00000087460, ENSG00000053918	http://www.genome.jp/kegg-bin/show_pathway?h
Adrenergic signaling in cardiomyocytes	KEGG PATHWAY	hsa04261	2	151	0.047242	0.308577	0.510637	ENSG00000087460, ENSG00000053918	http://www.genome.jp/kegg-bin/show_pathway?h
Alcoholism	KEGG PATHWAY	hsa05034	2	180	0.064213	0.308577	0.510637	ENSG00000087460, ENSG00000068024	http://www.genome.jp/kegg-bin/show_pathway?h
Viral carcinogenesis	KEGG PATHWAY	hsa05203	2	207	0.08156	0.308577	0.510637	ENSG00000002822, ENSG00000068024	http://www.genome.jp/kegg-bin/show_pathway?h
Type I diabetes mellitus	KEGG PATHWAY	hsa04940	1	42	0.093054	0.308577	0.510637	ENSG00000155093	http://www.genome.jp/kegg-bin/show_pathway?h
Vasopressin-regulated water reabsorption	KEGG PATHWAY	hsa04962	1	45	0.099219	0.308577	0.510637	ENSG00000087460	http://www.genome.jp/kegg-bin/show_pathway?h
Endocrine and other factor-regulated calcium reabsorption	KEGG PATHWAY	hsa04961	1	47	0.103306	0.308577	0.510637	ENSG00000087460	http://www.genome.jp/kegg-bin/show_pathway?h
Cocaine addiction	KEGG PATHWAY	hsa05030	1	49	0.107375	0.308577	0.510637	ENSG0000087460	http://www.genome.jp/kegg-bin/show_pathway?h
Ovarian steroidogenesis	KEGG PATHWAY	hsa04913	1	52	0.113444	0.308577	0.510637	ENSG0000087460	http://www.genome.jp/kegg-bin/show_pathway?h
Regulation of lipolysis in adipocytes	KEGG PATHWAY	hsa04923	1	58	0.12546	0.308577	0.510637	ENSG0000087460	http://www.genome.jp/kegg-bin/show_pathway?h
MicroRNAs in cancer	KEGG PATHWAY	hsa05206	2	273	0.128856	0.308577	0.510637	ENSG00000068024, ENSG00000168477	http://www.genome.jp/kegg-bin/show_pathway?h
Long-term depression	KEGG PATHWAY	hsa04730	1	61	0.131408	0.308577	0.510637	ENSG0000087460	http://www.genome.jp/kegg-bin/show_pathway?h
Renin secretion	KEGG PATHWAY	hsa04924	1	64	0.137317	0.308577	0.510637	ENSG00000087460	http://www.genome.jp/kegg-bin/show_pathway?h
Amphetamine addiction	KEGG PATHWAY	hsa05031	1	67	0.143185	0.308577	0.510637	ENSG00000087460	http://www.genome.jp/kegg-bin/show_pathway?h
Bile secretion	KEGG PATHWAY	hsa04976	1	71	0.150949	0.308577	0.510637	ENSG00000087460	http://www.genome.jp/kegg-bin/show_pathway?h
Thyroid hormone synthesis	KEGG PATHWAY	hsa04918	1	71	0.150949	0.308577	0.510637	ENSG00000087460	http://www.genome.jp/kegg-bin/show_pathway?h
Aldosterone synthesis and secretion	KEGG PATHWAY	hsa04925	1	80	0.168167	0.308577	0.510637	ENSG00000087460	http://www.genome.jp/kegg-bin/show_pathway?h
ECM-receptor interaction	KEGG PATHWAY	hsa04512	1	83	0.173829	0.308577	0.510637	ENSG00000168477	http://www.genome.jp/kegg-bin/show_pathway?h
Insulin secretion	KEGG PATHWAY	hsa04911	1	87	0.18132	0.308577	0.510637	ENSG0000087460	http://www.genome.jp/kegg-bin/show_pathway?h
Gap junction	KEGG PATHWAY	hsa04540	1	88	0.183182	0.308577	0.510637	ENSG0000087460	http://www.genome.jp/kegg-bin/show_pathway?h
Salivary secretion	KEGG PATHWAY	hsa04970	1	90	0.186894	0.308577	0.510637	ENSG0000087460	http://www.genome.jp/kegg-bin/show_pathway?h
Dilated cardiomyopathy	KEGG PATHWAY	hsa05414	1	90	0.186894	0.308577	0.510637	ENSG0000087460	http://www.genome.jp/kegg-bin/show_pathway?h
Protein digestion and absorption	KEGG PATHWAY	hsa04974	1	90	0.186894	0.308577	0.510637	ENSG0000053918	http://www.genome.jp/kegg-bin/show_pathway?h
Morphine addiction	KEGG PATHWAY	hsa05032	1	91	0.188744	0.308577	0.510637	ENSG0000087460	http://www.genome.jp/kegg-bin/show_pathway?h
GnRH signaling pathway	KEGG PATHWAY	hsa04912	1	92	0.19059	0.308577	0.510637	ENSG0000087460	http://www.genome.jp/kegg-bin/show_pathway?h
Circadian entrainment	KEGG PATHWAY	hsa04713	1	95	0.196102	0.308577	0.510637	ENSG0000087460	http://www.genome.jp/kegg-bin/show_pathway?h
ProgesteronE-mediated oocyte maturation	KEGG PATHWAY	hsa04914	1	97	0.199757	0.308577	0.510637	ENSG0000002822	http://www.genome.jp/kegg-bin/show_pathway?h
Endocrine resistance	KEGG PATHWAY	hsa01522	1	99	0.203395	0.308577	0.510637	ENSG0000087460	http://www.genome.jp/kegg-bin/show_pathway?h
Melanogenesis	KEGG PATHWAY	hsa04916	1	100	0.205207	0.308577	0.510637	ENSG0000087460	http://www.genome.jp/kegg-bin/show_pathway?h
Amoebiasis	KEGG PATHWAY	hsa05146	1	100	0.205207	0.308577	0.510637	ENSG00000087460	http://www.genome.jp/kegg-bin/show_pathway?h
Inflammatory mediator regulation of TRP channels	KEGG PATHWAY	hsa04750	1	101	0.207016	0.308577	0.510637	ENSG00000087460	http://www.genome.jp/kegg-bin/show_pathway?h
Estrogen signaling pathway	KEGG PATHWAY	hsa04915	1	101	0.207016	0.308577	0.510637	ENSG00000087460	http://www.genome.jp/kegg-bin/show_pathway?h
Glucagon signaling pathway	KEGG PATHWAY	hsa04922	1	102	0.208821	0.308577	0.510637	ENSG0000087460	http://www.genome.jp/kegg-bin/show_pathway?h
Chagas disease (American trypanosomiasis)	KEGG PATHWAY	hsa05142	1	106	0.216	0.308577	0.510637	ENSG0000087460	http://www.genome.jp/kegg-bin/show_pathway?h
Cholinergic synapse	KEGG PATHWAY	hsa04725	1	113	0.228409	0.308577	0.510637	ENSG0000053918	http://www.genome.jp/kegg-bin/show_pathway?h
Serotonergic synapse	KEGG PATHWAY	hsa04726	1	113	0.228409	0.308577	0.510637	ENSG0000087460	http://www.genome.jp/kegg-bin/show_pathway?h
Glutamatergic synapse	KEGG PATHWAY	hsa04724	1	115	0.231919	0.308577	0.510637	ENSG0000087460	http://www.genome.jp/kegg-bin/show_pathway?h
Vascular smooth muscle contraction	KEGG PATHWAY	hsa04270	1	123	0.245803	0.308577	0.510637	ENSG0000087460	http://www.genome.jp/kegg-bin/show_pathway?h
Cell cycle	KEGG PATHWAY	hsa04110	1	124	0.247521	0.308577	0.510637	ENSG0000002822	http://www.genome.jp/kegg-bin/show_pathway?h
Platelet activation	KEGG PATHWAY	hsa04611	1	125	0.249235	0.308577	0.510637	ENSG0000087460	http://www.genome.jp/kegg-bin/show_pathway?h
Dopaminergic synapse	KEGG PATHWAY	hsa04728	1	129	0.256053	0.309646	0.509135		http://www.genome.jp/kegg-bin/show_pathway?h
Phospholipase D signaling pathway	KEGG PATHWAY	hsa04072	1	146	0.284358	0.336059	0.473584	ENSG00000087460	http://www.genome.jp/kegg-bin/show_pathway?h
Oxytocin signaling pathway	KEGG PATHWAY	hsa04921	1	160	0.306871	0.354606	0.450254	ENSG0000087460	http://www.genome.jp/kegg-bin/show_pathway?h
Calcium signaling pathway	KEGG PATHWAY	hsa04020	1	179	0.336314	0.380181	0.42001	ENSG0000087460	http://www.genome.jp/kegg-bin/show_pathway?h
cAMP signaling pathway	KEGG PATHWAY	hsa04020	1	201	0.368872	0.399073	0.398948	ENSG00000087460	
Epstein-Barr virus infection	KEGG PATHWAY	hsa04024	1	201	0.368872	0.399073	0.398948		http://www.genome.jp/kegg-bin/show_pathway?h
•									http://www.genome.jp/kegg-bin/show_pathway?h
Focal adhesion	KEGG PATHWAY	hsa04510	1	206	0.376049	0.399073	0.398948	ENSG00000168477	http://www.genome.jp/kegg-bin/show_pathway?h
Rap1 signaling pathway	KEGG PATHWAY	hsa04015	1	216	0.390165	0.405771	0.391719		http://www.genome.jp/kegg-bin/show_pathway?h
PI3K-Akt signaling pathway	KEGG PATHWAY	hsa04151	1	343	0.544312	0.554985		ENSG00000168477	http://www.genome.jp/kegg-bin/show_pathway?h
Pathways in cancer	KEGG PATHWAY	hsa05200	1	399	0.599439	0.599439	0.222255	ENSG0000087460	http://www.genome.jp/kegg-bin/show_pathway?h

?/hsa05110/hsa:2778%09red/hsa:3784%09red ?/hsa04971/hsa:2778%09red/hsa:3784%09red ?/hsa04972/hsa:2778%09red/hsa:3784%09red ?/hsa04261/hsa:2778%09red/hsa:3784%09red ?/hsa05034/hsa:9759%09red/hsa:2778%09red ?/hsa05203/hsa:9759%09red/hsa:8379%09red ?/hsa04940/hsa:5799%09red ?/hsa04962/hsa:2778%09red ?/hsa04961/hsa:2778%09red

?hsa05030/hsa:2778%09red ?hsa04913/hsa:2778%09red ?hsa04923/hsa:2778%09red ?hsa05206/hsa:9759%09red/hsa:7148%09red ?hsa04730/hsa:2778%09red ?hsa04924/hsa:2778%09red ?hsa05031/hsa:2778%09red ?hsa04976/hsa:2778%09red ?hsa04918/hsa:2778%09red ?hsa04925/hsa:2778%09red ?hsa04512/hsa:7148%09red ?hsa04911/hsa:2778%09red ?hsa04540/hsa:2778%09red ?hsa04970/hsa:2778%09red ?hsa05414/hsa:2778%09red ?hsa04974/hsa:3784%09red ?hsa05032/hsa:2778%09red ?hsa04912/hsa:2778%09red ?hsa04713/hsa:2778%09red ?hsa04914/hsa:8379%09red ?hsa01522/hsa:2778%09red ?hsa04916/hsa:2778%09red ?hsa05146/hsa:2778%09red ?hsa04750/hsa:2778%09red

?hsa04915/hsa:2778%09red ?hsa04922/hsa:2778%09red ?hsa05142/hsa:2778%09red ?hsa04725/hsa:3784%09red ?hsa04726/hsa:2778%09red ?hsa04724/hsa:2778%09red ?hsa04270/hsa:2778%09red ?hsa04110/hsa:8379%09red ?hsa04611/hsa:2778%09red ?hsa04728/hsa:2778%09red ?hsa04072/hsa:2778%09red ?hsa04921/hsa:2778%09red /?hsa04020/hsa:2778%09red ?hsa04024/hsa:2778%09red ?hsa05169/hsa:9759%09red ?hsa04510/hsa:7148%09red ?hsa04015/hsa:2778%09red ?hsa04151/hsa:7148%09red ?hsa05200/hsa:2778%09red

982 Genes Diff score Chromosome Position Methylation status P value (B vs. C) P value (A vs. B) High-GpG ZNF323 131.89468 6 28431998 4.16001E-07 1.55395E-07 ASAH1 130.81353 8 17986262 2.01169E-07 4.1218E-07 High-GpG FAM111A 130.45708 11 58666572 High-GpG 1.21744E-05 7.39343E-09 121207392 MAD2L1 129.33632 5.45286E-07 2.1367E-07 4 High-GpG ATG12 8.27127E-07 127.27827 5 115205360 High-GpG 2.26256E-07 19 ZNF28 58016010 1.55587E-06 1.2067E-07 127.26429 High-GpG 26320955 5.88478E-08 HADHB 125.49116 2 High-GpG 4.79904E-06 59077027 PRKCG 125.39503 High-GpG 2.97625E-05 9.70126E-09 19 PTGES2 124.99208 9 129930459 High-GpG 8.51945E-07 3.7186E-07 AK2 124.18006 1 33275020 High-GpG 1.48229E-07 2.57668E-06 MAGOHB 123.44346 12 10657370 High-GpG 8.11057E-05 5.57958E-09 NFXL1 122.4017 47611255 1.88006E-06 3.05955E-07 4 High-GpG MOBKL3 120.93052 2 198088826 High-GpG 2.86446E-06 2.81777E-07 FAM76A 120.92863 1 27925162 1.06657E-06 7.57092E-07 High-GpG SUPT4H1 119.87514 17 53784566 High-GpG 1.36289E-05 7.55137E-08 PFN4 24199741 5.71282E-06 2.30761E-07 118,79988 2 High-GpG NTAN1 117.88967 15057701 High-GpG 1.57434E-06 1.03261E-06 16 ETNK1 117.59242 12 22669361 High-GpG 3.17717E-06 5.47921E-07 RALY 117.18969 32046086 9.3884E-06 2.03442E-07 20 High-GpG CCND1 116.8124 69164711 High-GpG 1.57231E-06 1.32502E-06 11 ASAP3 116.03716 23683861 7.38714E-05 3.37139E-08 1 High-GpG ERCC4 115.92696 16 13921604 High-GpG 2.69769E-07 9.46918E-06 UBE2K 39375775 0.000128084 2.08286E-08 115.73845 4 High-GpG KIAA1324L 86526859 115.34069 7 3.39017E-06 8.62402E-07 High-GpG AP1AR 115.30214 4 113372285 High-GpG 4.0348E-06 7.31079E-07 7 7188867 C1GALT1 114.78336 High-GpG 4.95185E-06 6.71268E-07 114.77977 96365157 NCAPH 2 6.31399E-05 5.26889E-08 High-GpG 114.74176 GCSH 79687498 High-GpG 4.30184E-07 7.80136E-06 16 DHCR24 55125751 1.87238E-05 1.92263E-07 114.43711 1 High-GpG HNRNPA1 114.07533 52960808 0.000139304 2.80869E-08 12 High-GpG GPR109A -90.42935 121755189 7.59402E-06 0.000119287 12 Low-CpG RGPD3 -91.08637 2 106451234 Low-CpG 4.72388E-05 1.64841E-05 -92.50327 34251672 0.00010681 5.2609E-06 C17orf98 17 Low-CpG AP1B1 -93.62296 28115355 2.05317E-05 2.11484E-05 22 Low-CpG DSCR8 -93.67115 21 38415359 Low-CpG 0.002349546 1.82768E-07 1.29544E-05 SNORD89 2 101256138 2.65111E-05 -94.64155 Low-CpG MTL5 68275537 3.81515E-05 -95.11474 11 Low-CpG 8.07261E-06 WRB -95.16274 39672973 1.04278E-05 2.92101E-05 21 Low-CpG 100866990 0.000157631 1.76669E-06 NALCN -95.55199 13 Low-CpG ZNF100 21725295 1.15163E-05 1.55412E-05 -97.47202 19 Low-CpG 28567843 PHACTR4 7.41887E-06 2.28407E-05 -97.70953 Low-CpG 1 1.62138E-05 GSTM4 -97.92513 1 109998812 Low-CpG 9.94493E-06 CIB4 26718375 0.000282136 3.64575E-07 -99.87754 2 Low-CpG TMBIM4 -100.22459 64851491 3.88671E-06 2.4432E-05 12 Low-CpG LOC339535 -103.632 1 236716068 Low-CpG 5.41422E-06 8.0032E-06 SNORD115-38 -103.94379 3.08714E-06 1.30636E-05 15 23034641 Low-CpG HCCA2 1601150 1.64093E-05 1.65941E-06 -105.64957 11 Low-CpG

**Table S4** 60 genes with significant hypermethylation and hypomethylation of overlap genes between B (pericarcinous tissues) *vs.* C (pancreatic cancer tissue) and A (blood) *vs.* B (pericarcinous tissues)

PARP4	-105.90702	13	23979063	Low-CpG	2.30641E-05	1.11266E-06
DLGAP2	-106.78054	8	1442761	Low-CpG	1.34894E-06	1.5558E-05
TMEM22	-108.01178	3	138039519	Low-CpG	8.62848E-06	1.83184E-06
TCAM1	-109.0501	17	59288076	Low-CpG	3.68175E-06	3.38015E-06
CEP63	-111.64598	3	135690134	Low-CpG	0.000347835	1.96801E-08
PAK2	-112.77409	3	197954174	Low-CpG	5.13802E-06	1.02753E-06
FAM9A	-112.86534	Х	8729344	Low-CpG	2.79992E-06	1.84638E-06
CCDC83	-114.29396	11	85246352	Low-CpG	5.92682E-06	6.27745E-07
SNORD114-15	-115.87882	14	100508183	Low-CpG	9.26565E-06	2.78767E-07
CDCA7L	-120.37022	7	21930929	Low-CpG	2.20559E-06	4.16346E-07
WDR27	-120.65469	6	169839513	Low-CpG	5.12794E-06	1.67721E-07
BECN1	-124.31615	17	38230497	Low-CpG	6.43061E-06	5.75617E-08
AGAP11	-138.8236	10	88746560	Low-CpG	8.04749E-08	1.62922E-07

GOID	Ontology	Term	Level	q	m	t	k	Gene IDs	Symbols	Log odds ratio	Р
GO: 0000045	Biological process	Autophagosome assembly	4	5	38	45,240	127	C1IDX9, O94817, K7EPZ0, K7EQQ7, Q14457	ATG12, ATG12, BECN1, BECN1, BECN1	5.550627	5.82E-05
GO: 0006914	Biological process	Autophagy	1	12	159	45,240	127	C1IDX9, O94817, E7EV84, K7ELY9, K7EMA2, K7EN35, K7EPZ0, K7EQQ7, K7ER46, K7ERY0, K7ESG3, Q14457	ATG12, ATG12, BECN1, BE	4.748706	3.84E-10
O:1905037	Biological process	Autophagosome organization	2	5	38	45,240	127	C1IDX9, O94817, K7EPZ0, K7EQQ7, Q14457	ATG12, ATG12, BECN1, BECN1, BECN1	5.550627	5.82E-05
iO: 0003857	Molecular function	3-hydroxyacyl-CoA dehydrogenase activity	1	4	13	45,240	127	C9JE81, C9JEY0, C9K0M0, P55084	HADHB, HADHB, HADHB, HADHB	6.776187	3.76E-05
O: 0003988	Molecular function	Acetyl-CoA C-acyltransferase activity	1	4	10	45,240	127	C9JE81, C9JEY0, C9K0M0, P55084	HADHB, HADHB, HADHB, HADHB	7.154699	1.67E-05
iO: 0004300	Molecular function	Enoyl-CoA hydratase activity	1	4	8	45,240	127	C9JE81, C9JEY0, C9K0M0, P55084	HADHB, HADHB, HADHB, HADHB	7.476627	6.38E-06
O: 0016507	Cellular component	Mitochondrial fatty acid beta-oxidation multienzyme complex	8	4	5	45,240	127	C9JE81, C9JEY0, C9K0M0, P55084	HADHB, HADHB, HADHB, HADHB	8.154699	6.42E-07
O: 0036125	Cellular component	Fatty acid beta- oxidation multienzyme complex	1	4	5	45,240	127	C9JE81, C9JEY0, C9K0M0, P55084	HADHB, HADHB, HADHB, HADHB	8.154699	6.42E-07
GO: 0016508	Molecular function	Long-chain-enoyl-CoA hydratase activity	1	4	6	45,240	127	C9JE81, C9JEY0, C9K0M0, P55084	HADHB, HADHB, HADHB, HADHB	7.891664	1.6E-06
O: 0016509	Molecular function	Long-chain-3- hydroxyacyl-CoA dehydrogenase activity	1	4	5	45,240	127	C9JE81, C9JEY0, C9K0M0, P55084	HADHB, HADHB, HADHB, HADHB	8.154699	6.42E-07
iO: 0005960	Cellular component	Glycine cleavage complex	5	4	5	45,240	127	H3BNV1, H3BQ30, H3BUG8, P23434	GCSH, GCSH, GCSH, GCSH	8.154699	6.42E-07

Table S5 Gene ontology annotation of 60 genes with significantly hypermethylation and hypomethylation of overlap genes between B (pericarcinous tissues) vs. C (pancreatic car	ncer tissue) and a (blood) vs. B (pericarcinous tissues)
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Statistical test method: hypergeometric test/Fisher's exact test. FDR correction method: Benjamini and Hochberg.

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| #Term<br>Regulation of autophagy   |   
   
   
   
   
   
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|  | Database<br>KEGG PATHWAY  
   
   
   
   
   
   | ID<br>hsa04140  
   | Input<br>number<br>2  
   
   
   
   
   
   | Background<br>number<br>40  
  | P value<br>0.023689   | Corrected<br>P value<br>0.583858   
  | Input<br>ENSG00000126581,   | Hyperlink<br>http://www.genome.jp/kegg-bin/show   |   |  
   
   
   
   
   
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| Non-small cell lung cancer   | KEGG PATHWAY  
   
   
   
   
   
   | hsa05223  
   | 2   
   
   
   
   
   
   | 58  
  | 0.045599  | 0.583858   
  | ENSG00000145782<br>ENSG00000126583,   | pathway?hsa04140/hsa:9140%09red/<br>hsa:8678%09red<br>http://www.genome.jp/kegg-bin/show  |   |  
   
   
   
   
   
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| Glioma   | KEGG PATHWAY  
   
   
   
   
   
   | hsa05214  
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   | 67  
  | 0.058495  | 0.583858   
  | ENSG00000110092<br>ENSG00000126583,   | pathway?hsa05223/hsa:595%09red/<br>hsa:5582%09red<br>http://www.genome.jp/kegg-bin/show.  |   |  
   
   
   
   
   
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| ErbB signaling pathway   | KEGG PATHWAY  
   
   
   
   
   
   | hsa04012  
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   | 90  
  | 0.096076  | 0.583858   
  | ENSG00000110092<br>ENSG00000126583,   | pathway?hsa05214/hsa:595%09red/<br>hsa:5582%09red<br>http://www.genome.jp/kegg-bin/show.  |   |  
   
   
   
   
   
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| Fc gamma R-mediated  | KEGG PATHWAY  
   
   
   
   
   
   | hsa04666  
   | 2   
   
   
   
   
   
   | 96  
  | 0.106773  | 0.583858   
  | ENSG00000180370<br>ENSG00000088280,   | pathway?hsa04012/hsa:5062%09red/<br>hsa:5582%09red<br>http://www.genome.jp/kegg-bin/show.   |   |  
   
   
   
   
   
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| phagocytosis<br>Steroid biosynthesis   | KEGG PATHWAY  
   
   
   
   
   
   | hsa00100  
   | 1   
   
   
   
   
   
   | 20  
  | 0.112548  | 0.583858   
  | ENSG00000126583<br>ENSG00000116133  | pathway?hsa04666/hsa:55616%09rec<br>hsa:5582%09red<br>http://www.genome.jp/kegg-bin/show.   |   |  
   
   
   
   
   
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| Focal adhesion   | KEGG PATHWAY  
   
   
   
   
   
   | hsa04510  
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   | 206   
  | 0.11596   | 0.583858   
  | ENSG00000126583,<br>ENSG00000180370,  | pathway?hsa00100/hsa:1718%09red<br>http://www.genome.jp/kegg-bin/show<br>pathway?hsa04510/hsa:595%09red/  |   |  
   
   
   
   
   
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| Fatty acid elongation  | KEGG PATHWAY  
   
   
   
   
   
   | hsa00062  
   | 1   
   
   
   
   
   
   | 25  
  | 0.137434  | 0.583858   
  | ENSG00000110092<br>ENSG00000138029  | hsa:5062%09red/hsa:5582%09red<br>http://www.genome.jp/kegg-bin/show.<br>pathway?hsa00062/hsa:3032%09red   |   |  
   
   
   
   
   
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| Glyoxylate and<br>dicarboxylate metabolism   | KEGG PATHWAY  
   
   
   
   
   
   | hsa00630  
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   | 28  
  | 0.152032  | 0.583858   
  | ENSG00000140905   | http://www.genome.jp/kegg-bin/show<br>pathway?hsa00630/hsa:2653%09red   |   |  
   
   
   
   
   
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| Thyroid hormone signaling<br>oathway   | KEGG PATHWAY  
   
   
   
   
   
   | hsa04919  
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   | 121   
  | 0.154242  | 0.583858   
  | ENSG00000126583,<br>ENSG00000110092   | http://www.genome.jp/kegg-bin/show<br>pathway?hsa04919/hsa:595%09red/<br>hsa:5582%09red   |   |  
   
   
   
   
   
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| Thyroid cancer   | KEGG PATHWAY  
   
   
   
   
   
   | hsa05216  
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   | 29  
  | 0.156843  | 0.583858   
  | ENSG00000110092   | http://www.genome.jp/kegg-bin/show<br>pathway?hsa05216/hsa:595%09red  |   |  
   
   
   
   
   
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| Sphingolipid<br>signaling pathway  | KEGG PATHWAY  
   
   
   
   
   
   | hsa04071  
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   | 123   
  | 0.1582  | 0.583858   
  | ENSG00000126583,<br>ENSG00000104763   | http://www.genome.jp/kegg-bin/show<br>pathway?hsa04071/hsa:427%09red/<br>hsa:5582%09red   |   |  
   
   
   
   
   
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| Cell cycle   | KEGG PATHWAY  
   
   
   
   
   
   | hsa04110  
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   | 124   
  | 0.160187  | 0.583858   
  | ENSG00000110092,<br>ENSG00000164109   | http://www.genome.jp/kegg-bin/show<br>pathway?hsa04110/hsa:595%09red/<br>hsa:4085%09red   |   |  
   
   
   
   
   
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| _ysosome   | KEGG PATHWAY  
   
   
   
   
   
   | hsa04142  
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   | 124   
  | 0.160187  | 0.583858   
  | ENSG00000104763,<br>ENSG00000100280   | http://www.genome.jp/kegg-bin/show<br>pathway?hsa04142/hsa:162%09red/<br>hsa:427%09red  |   |  
   
   
   
   
   
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| Mucin type O-Glycan<br>piosynthesis<br>Base excision repair  | KEGG PATHWAY<br>KEGG PATHWAY  
   
   
   
   
   
   | hsa00512<br>hsa03410  
   | 1   
   
   
   
   
   
   | 31<br>33  
  | 0.166384<br>0.175818  | 0.583858<br>0.583858   
  | ENSG00000106392<br>ENSG00000102699  | http://www.genome.jp/kegg-bin/show.<br>pathway?hsa00512/hsa:56913%09rec<br>http://www.genome.jp/kegg-bin/show.  |   |  
   
   
   
   
   
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| Apoptosis-multiple species   | KEGG PATHWAY  
   
   
   
   
   
   | hsa04215  
   | 1   
   
   
   
   
   
   | 33  
  | 0.175818  | 0.583858   
  | ENSG00000126581   | pathway?hsa03410/hsa:143%09red<br>http://www.genome.jp/kegg-bin/show.<br>pathway?hsa04215/hsa:8678%09red  |   |  
   
   
   
   
   
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| African trypanosomiasis  | KEGG PATHWAY  
   
   
   
   
   
   | hsa05143  
   | 1   
   
   
   
   
   
   | 34  
  | 0.180495  | 0.583858   
  | ENSG00000126583   | http://www.genome.jp/kegg-bin/show<br>pathway?hsa05143/hsa:5582%09red   |   |  
   
   
   
   
   
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| FoxO signaling pathway   | KEGG PATHWAY  
   
   
   
   
   
   | hsa04068  
   | 2   
   
   
   
   
   
   | 135   
  | 0.18232   | 0.583858   
  | ENSG00000110092,<br>ENSG00000145782   | http://www.genome.jp/kegg-bin/show<br>pathway?hsa04068/hsa:9140%09red/<br>hsa:595%09red   |   |  
   
   
   
   
   
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| Spliceosome  | KEGG PATHWAY  
   
   
   
   
   
   | hsa03040  
   | 2   
   
   
   
   
   
   | 136   
  | 0.184355  | 0.583858   
  | ENSG00000111196,<br>ENSG00000135486   | http://www.genome.jp/kegg-bin/show.<br>pathway?hsa03040/hsa:55110%09rec<br>hsa:3178%09red   |   |  
   
   
   
   
   
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| Nnt signaling pathway  | KEGG PATHWAY  
   
   
   
   
   
   | hsa04310  
   | 2   
   
   
   
   
   
   | 142   
  | 0.196631  | 0.583858   
  | ENSG00000126583,<br>ENSG00000110092   | http://www.genome.jp/kegg-bin/show_<br>pathway?hsa04310/hsa:595%09red/<br>hsa:5582%09red  |   |  
   
   
   
   
   
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| Glycine, serine and threoning<br>netabolism  |   
   
   
   
   
   
   | hsa00260  
   | 1   
   
   
   
   
   
   | 40  
  | 0.20801   | 0.583858   
  | ENSG00000140905   | http://www.genome.jp/kegg-bin/show<br>pathway?hsa00260/hsa:2653%09red   |   |  
   
   
   
   
   
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| lepatitis B  | KEGG PATHWAY  
   
   
   
   
   
   | hsa05161  
   | 2   
   
   
   
   
   
   | 148   
  | 0.209005  | 0.583858   
  | ENSG00000126583,<br>ENSG00000110092   | http://www.genome.jp/kegg-bin/show<br>pathway?hsa05161/hsa:595%09red/<br>hsa:5582%09red   |   |  
   
   
   
   
   
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| Bladder cancer<br>AldosteronE-regulated  | KEGG PATHWAY<br>KEGG PATHWAY  
   
   
   
   
   
   | hsa05219<br>hsa04960  
   | 1   
   
   
   
   
   
   | 41<br>41  
  | 0.212505<br>0.212505  | 0.583858<br>0.583858   
  | ENSG00000110092<br>ENSG00000126583  | http://www.genome.jp/kegg-bin/show.<br>pathway?hsa05219/hsa:595%09red<br>http://www.genome.jp/kegg-bin/show.  |   |  
   
   
   
   
   
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| sodium reabsorption  | KEGG PATHWAY  
   
   
   
   
   
   | hsa00071  
   | 1   
   
   
   
   
   
   | 45  
  | 0.230236  | 0.583858   
  | ENSG00000138029   | pathway?hsa04960/hsa:5582%09red<br>http://www.genome.jp/kegg-bin/show<br>pathway?hsa00071/hsa:3032%09red  |   |  
   
   
   
   
   
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| Dxytocin signaling<br>bathway  | KEGG PATHWAY  
   
   
   
   
   
   | hsa04921  
   | 2   
   
   
   
   
   
   | 160   
  | 0.233969  | 0.583858   
  | ENSG00000126583,<br>ENSG00000110092   | http://www.genome.jp/kegg-bin/show<br>pathway?hsa04921/hsa:595%09red/   |   |  
   
   
   
   
   
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| Hedgehog signaling<br>bathway  | KEGG PATHWAY  
   
   
   
   
   
   | hsa04340  
   | 1   
   
   
   
   
   
   | 46  
  | 0.234606  | 0.583858   
  | ENSG00000110092   | hsa:5582%09red<br>http://www.genome.jp/kegg-bin/show<br>pathway?hsa04340/hsa:595%09red  |   |  
   
   
   
   
   
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| Nucleotide excision<br>epair   | KEGG PATHWAY  
   
   
   
   
   
   | hsa03420  
   | 1   
   
   
   
   
   
   | 46  
  | 0.234606  | 0.583858   
  | ENSG00000175595   | http://www.genome.jp/kegg-bin/show,<br>pathway?hsa03420/hsa:2072%09red  |   |  
   
   
   
   
   
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| Endocrine and other<br>actor-regulated<br>calcium reabsorption   | KEGG PATHWAY  
   
   
   
   
   
   | hsa04961  
   | 1   
   
   
   
   
   
   | 47  
  | 0.238952  | 0.583858   
  | ENSG00000126583   | http://www.genome.jp/kegg-bin/show<br>pathway?hsa04961/hsa:5582%09red   |   |  
   
   
   
   
   
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| Sphingolipid metabolism<br>/aline, leucine and   | KEGG PATHWAY  
   
   
   
   
   
   | hsa00600<br>hsa00280  
   | 1<br>1  
   
   
   
   
   
   | 47<br>48  
  | 0.238952<br>0.243273  | 0.583858<br>0.583858   
  | ENSG00000104763<br>ENSG00000138029  | http://www.genome.jp/kegg-bin/show.<br>pathway?hsa00600/hsa:427%09red<br>http://www.genome.jp/kegg-bin/show.  |   |  
   
   
   
   
   
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| aine, leacine and<br>soleucine degradation<br>Fatty acid metabolism  | KEGG PATHWAY  
   
   
   
   
   
   | hsa01212  
   | 1   
   
   
   
   
   
   | 48  
  | 0.243273  | 0.583858   
  | ENSG00000138029   | http://www.genome.jp/kegg-bin/show<br>pathway?hsa00280/hsa:3032%09red<br>http://www.genome.jp/kegg-bin/show<br>pathway?hsa01212/hsa:3032%09red  |   |  
   
   
   
   
   
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| Glutathione metabolism   | KEGG PATHWAY  
   
   
   
   
   
   | hsa00480  
   | 1   
   
   
   
   
   
   | 51  
  | 0.256091  | 0.583858   
  | ENSG00000168765   | pathway?hsa01212/hsa:3032%09red<br>http://www.genome.jp/kegg-bin/show<br>pathway?hsa00480/hsa:2948%09red  |   |  
   
   
   
   
   
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| RNA transport  | KEGG PATHWAY  
   
   
   
   
   
   | hsa03013  
   | 2   
   
   
   
   
   
   | 171   
  | 0.257003  | 0.583858   
  | ENSG00000153165,<br>ENSG00000111196   | http://www.genome.jp/kegg-bin/show.<br>pathway?hsa03013/hsa:653489%09re<br>hsa:55110%09red  |   |  
   
   
   
   
   
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  |
| Endometrial cancer   | KEGG PATHWAY  
   
   
   
   
   
   | hsa05213  
   | 1   
   
   
   
   
   
   | 54  
  | 0.268693  | 0.583858   
  | ENSG00000175595   | http://www.genome.jp/kegg-bin/show.<br>pathway?hsa05213/hsa:595%09red   |   |  
   
   
   
   
   
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| <sup>-</sup> anconi anemia pathway<br>/iral myocarditis  | KEGG PATHWAY<br>KEGG PATHWAY  
   
   
   
   
   
   | hsa03460<br>hsa05416  
   | 1<br>1  
   
   
   
   
   
   | 56<br>57  
  | 0.276976<br>0.281083  | 0.583858<br>0.583858   
  | ENSG00000175595<br>ENSG00000110092  | http://www.genome.jp/kegg-bin/show,<br>pathway?hsa03460/hsa:2072%09red<br>http://www.genome.jp/kegg-bin/show,   |   |  
   
   
   
   
   
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  |
| Acute myeloid leukemia   | KEGG PATHWAY  
   
   
   
   
   
   | hsa05221  
   | 1   
   
   
   
   
   
   | 59  
  | 0.289227  | 0.583858   
  | ENSG00000110092   | pathway?hsa05416/hsa:595%09red<br>http://www.genome.jp/kegg-bin/show<br>pathway?hsa05221/hsa:595%09red  |   |  
   
   
   
   
   
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  |
| ong-term depression  |   
   
   
   
   
   
   | hsa04730  
   | 1   
   
   
   
   
   
   | 61  
  | 0.297279  | 0.583858   
  | ENSG00000126583   | http://www.genome.jp/kegg-bin/show<br>pathway?hsa04730/hsa:5582%09red   |   |  
   
   
   
   
   
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| /EGF signaling pathway<br>Arachidonic acid   | KEGG PATHWAY  
   
   
   
   
   
   | hsa04370<br>hsa00590  
   | 1   
   
   
   
   
   
   | 64<br>64  
  | 0.309188  | 0.583858<br>0.583858   
  | ENSG00000126583<br>ENSG00000148334  | http://www.genome.jp/kegg-bin/show<br>pathway?hsa04370/hsa:5582%09red<br>http://www.genome.jp/kegg-bin/show   |   |  
   
   
   
   
   
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| netabolism<br>Colorectal cancer  | KEGG PATHWAY  
   
   
   
   
   
   | hsa05210  
   | 1   
   
   
   
   
   
   | 64  
  | 0.309188  | 0.583858   
  | ENSG00000110092   | pathway?hsa00590/hsa:80142%09rec<br>http://www.genome.jp/kegg-bin/show.<br>pathway?hsa05210/hsa:595%09red   |   |  
   
   
   
   
   
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| Shigellosis  | KEGG PATHWAY  
   
   
   
   
   
   | hsa05131  
   | 1   
   
   
   
   
   
   | 66  
  | 0.317016  | 0.583858   
  | ENSG00000176732   | http://www.genome.jp/kegg-bin/show.<br>pathway?hsa05131/hsa:375189%09re   |   |  
   
   
   
   
   
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| ong-term potentiation  | KEGG PATHWAY  
   
   
   
   
   
   | hsa04720<br>hsa05031  
   | 1   
   
   
   
   
   
   | 66<br>67  
  | 0.317016  | 0.583858<br>0.583858   
  | ENSG00000126583<br>ENSG00000126583  | http://www.genome.jp/kegg-bin/show.<br>pathway?hsa04720/hsa:5582%09red<br>http://www.genome.jp/kegg-bin/show.   |   |  
   
   
   
   
   
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| Pancreatic cancer  | KEGG PATHWAY  
   
   
   
   
   
   | hsa05212  
   | 1   
   
   
   
   
   
   | 68  
  | 0.320390  | 0.583858   
  | ENSG00000120383   | pathway?hsa05031/hsa:5582%09red<br>http://www.genome.jp/kegg-bin/show   |   |  
   
   
   
   
   
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| Drug metabolism-<br>sytochrome P450  | KEGG PATHWAY  
   
   
   
   
   
   | hsa00982  
   | 1   
   
   
   
   
   
   | 68  
  | 0.324755  | 0.583858   
  | ENSG00000168765   | pathway?hsa05212/hsa:595%09red<br>http://www.genome.jp/kegg-bin/show<br>pathway?hsa00982/hsa:2948%09red   |   |  
   
   
   
   
   
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| Renal cell carcinoma   | KEGG PATHWAY  
   
   
   
   
   
   | hsa05211  
   | 1   
   
   
   
   
   
   | 69  
  | 0.328592  | 0.583858   
  | ENSG00000180370   | http://www.genome.jp/kegg-bin/show<br>pathway?hsa05211/hsa:5062%09red   |   |  
   
   
   
   
   
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| 553 signaling pathway<br>RIG-I-like receptor   | KEGG PATHWAY<br>KEGG PATHWAY  
   
   
   
   
   
   | hsa04115<br>hsa04622  
   | 1   
   
   
   
   
   
   | 69<br>70  
  | 0.328592<br>0.332408  | 0.583858<br>0.583858   
  | ENSG00000110092<br>ENSG00000145782  | http://www.genome.jp/kegg-bin/show,<br>pathway?hsa04115/hsa:595%09red<br>http://www.genome.jp/kegg-bin/show,  |   |  
   
   
   
   
   
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| ignaling pathway<br>Proteoglycans in cancer  | KEGG PATHWAY  
   
   
   
   
   
   | hsa05205  
   | 2   
   
   
   
   
   
   | 208   
  | 0.33428   | 0.583858   
  | ENSG00000126583,<br>ENSG00000110092   | pathway?hsa04622/hsa:9140%09red<br>http://www.genome.jp/kegg-bin/show<br>pathway?hsa05205/hsa:595%09red/  |   |  
   
   
   
   
   
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| Thyroid hormone<br>synthesis   | KEGG PATHWAY  
   
   
   
   
   
   | hsa04918  
   | 1   
   
   
   
   
   
   | 71  
  | 0.336201  | 0.583858   
  | ENSG00000126583   | hsa:5582%09red<br>http://www.genome.jp/kegg-bin/show<br>pathway?hsa04918/hsa:5582%09red   |   |  
   
   
   
   
   
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  |
| Metabolism of<br>kenobiotics by  | KEGG PATHWAY  
   
   
   
   
   
   | hsa00980  
   | 1   
   
   
   
   
   
   | 72  
  | 0.339974  | 0.583858   
  | ENSG00000168765   | http://www.genome.jp/kegg-bin/show.<br>pathway?hsa00980/hsa:2948%09red  |   |  
   
   
   
   
   
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  |
| cytochrome P450<br>Melanoma  | KEGG PATHWAY  
   
   
   
   
   
   | hsa05218  
   | 1   
   
   
   
   
   
   | 73  
  | 0.343725  | 0.583858   
  | ENSG00000110092   | http://www.genome.jp/kegg-bin/show<br>pathway?hsa05218/hsa:595%09red  |   |  
   
   
   
   
   
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| Gastric acid secretion   | KEGG PATHWAY  
   
   
   
   
   
   | hsa04971  
   | 1   
   
   
   
   
   
   | 74  
  | 0.347455  | 0.583858   
  | ENSG00000126583   | http://www.genome.jp/kegg-bin/show<br>pathway?hsa04971/hsa:5582%09red   |   |  
   
   
   
   
   
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| Prolactin signaling pathway<br>Rap1 signaling pathway  | KEGG PATHWAY  
   
   
   
   
   
   | hsa04917<br>hsa04015  
   | 1<br>2  
   
   
   
   
   
   | 74<br>216   
  | 0.347455<br>0.350752  | 0.583858<br>0.583858   
  | ENSG00000110092<br>ENSG00000176732,   | http://www.genome.jp/kegg-bin/show.<br>pathway?hsa04917/hsa:595%09red<br>http://www.genome.jp/kegg-bin/show.  |   |  
   
   
   
   
   
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| Chronic myeloid leukemia   | KEGG PATHWAY  
   
   
   
   
   
   | hsa05220  
   | 1   
   
   
   
   
   
   | 75  
  | 0.351164  | 0.583858   
  | ENSG00000126583<br>ENSG00000110092  | pathway?hsa04015/hsa:375189%09re<br>hsa:5582%09red<br>http://www.genome.jp/kegg-bin/show.   |   |  
   
   
   
   
   
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| Platinum drug resistance   | KEGG PATHWAY  
   
   
   
   
   
   | hsa01524  
   | 1   
   
   
   
   
   
   | 76  
  | 0.354852  | 0.583858   
  | ENSG00000168765   | pathway?hsa05220/hsa:595%09red<br>http://www.genome.jp/kegg-bin/show<br>pathway?hsa01524/hsa:2948%09red   |   |  
   
   
   
   
   
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| Regulation of actin<br>sytoskeleton  | KEGG PATHWAY  
   
   
   
   
   
   | hsa04810  
   | 2   
   
   
   
   
   
   | 219   
  | 0.356894  | 0.583858   
  | ENSG00000176732,<br>ENSG00000180370   | http://www.genome.jp/kegg-bin/show<br>pathway?hsa04810/hsa:375189%09re<br>hsa:5062%09red  |   |  
   
   
   
   
   
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| Aldosterone synthesis and secretion  | KEGG PATHWAY  
   
   
   
   
   
   | hsa04925  
   | 1   
   
   
   
   
   
   | 80  
  | 0.369397  | 0.583858   
  | ENSG00000126583   | http://www.genome.jp/kegg-bin/show<br>pathway?hsa04925/hsa:5582%09red   |   |  
   
   
   
   
   
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| Chemical carcinogenesis<br>EGFR tyrosine kinase  | KEGG PATHWAY  
   
   
   
   
   
   | hsa05204<br>hsa01521  
   | 1   
   
   
   
   
   
   | 82  
  | 0.376547  | 0.583858<br>0.583858   
  | ENSG00000168765<br>ENSG00000126583  | http://www.genome.jp/kegg-bin/show.<br>pathway?hsa05204/hsa:2948%09red<br>http://www.genome.jp/kegg-bin/show.   |   |  
   
   
   
   
   
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| nhibitor resistance<br>Ras signaling pathway   | KEGG PATHWAY  
   
   
   
   
   
   | hsa04014  
   | 2   
   
   
   
   
   
   | 231   
  | 0.381248  | 0.583858   
  | ENSG00000126583,<br>ENSG00000180370   | pathway?hsa01521/hsa:5582%09red<br>http://www.genome.jp/kegg-bin/show.<br>pathway?hsa04014/hsa:5062%09red/  |   |  
   
   
   
   
   
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| Salmonella infection   | KEGG PATHWAY  
   
   
   
   
   
   | hsa05132  
   | 1   
   
   
   
   
   
   | 86  
  | 0.390606  | 0.583858   
  | ENSG00000176732   | hsa:5582%09red<br>http://www.genome.jp/kegg-bin/show  |   |  
   
   
   
   
   
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| nsulin secretion   | KEGG PATHWAY  
   
   
   
   
   
   | hsa04911  
   | 1   
   
   
   
   
   
   | 87  
  | 0.394071  | 0.583858   
  | ENSG00000126583   | pathway?hsa05132/hsa:375189%09re<br>http://www.genome.jp/kegg-bin/show<br>pathway?hsa04911/hsa:5582%09red   |   |  
   
   
   
   
   
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| GABAergic synapse  | KEGG PATHWAY  
   
   
   
   
   
   | hsa04727  
   | 1   
   
   
   
   
   
   | 88  
  | 0.397517  | 0.583858   
  | ENSG00000126583   | http://www.genome.jp/kegg-bin/show<br>pathway?hsa04727/hsa:5582%09red   |   |  
   
   
   
   
   
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| -  | KEGG PATHWAY<br>KEGG PATHWAY  
   
   
   
   
   
   | hsa05222<br>hsa04540  
   | 1   
   
   
   
   
   
   | 88<br>88  
  | 0.397517<br>0.397517  | 0.583858<br>0.583858   
  | ENSG00000110092<br>ENSG00000126583  | pathway?hsa05222/hsa:595%09red<br>http://www.genome.jp/kegg-bin/show  |   |  
   
   
   
   
   
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| Gap junction   |   
   
   
   
   
   
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  |   | http://www.genome.jp/kegg-bin/show<br>pathway?hsa04540/hsa:5582%09red<br>http://www.genome.jp/kegg-bin/show   |   |  
   
   
   
   
   
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| Gap junction<br>Salivary secretion   | KEGG PATHWAY  
   
   
   
   
   
   | hsa04540  
   | 1   
   
   
   
   
   
   | 88  
  | 0.397517  | 0.583858   
  | ENSG00000126583   | http://www.genome.jp/kegg-bin/show<br>pathway?hsa04540/hsa:5582%09red   |   |  
   
   
   
   
   
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| Gap junction<br>Salivary secretion<br>Prostate cancer<br>Norphine addiction  | KEGG PATHWAY<br>KEGG PATHWAY<br>KEGG PATHWAY<br>KEGG PATHWAY  
   
   
   
   
   
   | hsa04540<br>hsa04970<br>hsa05215<br>hsa05032  
   | 1<br>1<br>1<br>1  
   
   
   
   
   
   | 88<br>90<br>91<br>91  
  | 0.397517<br>0.40435<br>0.407737<br>0.407737   | 0.583858<br>0.583858<br>0.583858<br>0.583858   
  | ENSG00000126583<br>ENSG00000126583<br>ENSG00000110092<br>ENSG00000126583  | http://www.genome.jp/kegg-bin/show,<br>pathway?hsa04540/hsa:5582%09red<br>http://www.genome.jp/kegg-bin/show,<br>pathway?hsa04970/hsa:5582%09red<br>http://www.genome.jp/kegg-bin/show,<br>pathway?hsa05215/hsa:595%09red<br>http://www.genome.jp/kegg-bin/show,<br>pathway?hsa05032/hsa:5582%09red   |   |  
   
   
   
   
   
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| Small cell lung cancer<br>Gap junction<br>Salivary secretion<br>Prostate cancer<br>Morphine addiction<br>mRNA surveillance<br>pathway<br>Metabolic pathways  | KEGG PATHWAY<br>KEGG PATHWAY<br>KEGG PATHWAY  
   
   
   
   
   
   | hsa04540<br>hsa04970<br>hsa05215  
   | 1<br>1<br>1   
   
   
   
   
   
   | 88<br>90<br>91  
  | 0.397517<br>0.40435<br>0.407737   | 0.583858<br>0.583858<br>0.583858   
  | ENSG00000126583<br>ENSG00000126583<br>ENSG00000110092   | http://www.genome.jp/kegg-bin/show.pathway?hsa04540/hsa:5582%09red<br>http://www.genome.jp/kegg-bin/show.pathway?hsa04970/hsa:5582%09red<br>http://www.genome.jp/kegg-bin/show.pathway?hsa05215/hsa:595%09red<br>http://www.genome.jp/kegg-bin/show.  |   |  
   
   
   
   
   
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  |
| Gap junction<br>Salivary secretion<br>Prostate cancer<br>Morphine addiction<br>mRNA surveillance<br>pathway  | KEGG PATHWAY<br>KEGG PATHWAY<br>KEGG PATHWAY<br>KEGG PATHWAY  
   
   
   
   
   
   | hsa04540<br>hsa04970<br>hsa05215<br>hsa05032<br>hsa03015  
   | 1<br>1<br>1<br>1<br>1   
   
   
   
   
   
   | 88<br>90<br>91<br>91<br>91  
  | 0.397517<br>0.40435<br>0.407737<br>0.407737<br>0.407737   | 0.583858<br>0.583858<br>0.583858<br>0.583858<br>0.583858   
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| Bap junction<br>Balivary secretion<br>Prostate cancer<br>Morphine addiction<br>nRNA surveillance<br>bathway<br>Metabolic pathways  | KEGG PATHWAY<br>KEGG PATHWAY<br>KEGG PATHWAY<br>KEGG PATHWAY<br>KEGG PATHWAY  
   
   
   
   
   
   | hsa04540<br>hsa04970<br>hsa05215<br>hsa05032<br>hsa03015<br>hsa01100  
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  | ENSG00000126583<br>ENSG00000126583<br>ENSG00000110092<br>ENSG00000126583<br>ENSG00000139163,<br>ENSG00000139163,<br>ENSG00000148334,<br>ENSG0000016392,<br>ENSG00000104763,<br>ENSG00000138029,<br>ENSG00000140905  | http://www.genome.jp/kegg-bin/show.pathway?hsa04540/hsa:5582%09red<br>http://www.genome.jp/kegg-bin/show.pathway?hsa04970/hsa:5582%09red<br>http://www.genome.jp/kegg-bin/show.pathway?hsa05215/hsa:595%09red<br>http://www.genome.jp/kegg-bin/show.pathway?hsa05032/hsa:5582%09red<br>http://www.genome.jp/kegg-bin/show.pathway?hsa03015/hsa:55110%09red<br>http://www.genome.jp/kegg-bin/show.pathway?hsa03015/hsa:55110%09red/<br>hsa:427%09red/hsa:56913%09red/<br>hsa:80142%09red/hsa:3032%09red/<br>hsa:204%09red<br>http://www.genome.jp/kegg-bin/show.pathway?hsa04713/hsa:5582%09red/<br>http://www.genome.jp/kegg-bin/show.pathway?hsa04713/hsa:5582%09red/<br>http://www.genome.jp/kegg-bin/show.pathway?hsa04713/hsa:5582%09red/<br>http://www.genome.jp/kegg-bin/show.pathway?hsa04713/hsa:5582%09red/  |   |  
   
   
   
   
   
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  | 0.397517<br>0.40435<br>0.407737<br>0.407737<br>0.407737<br>0.412411<br>0.412411<br>0.421098<br>0.424391   | 0.583858<br>0.583858<br>0.583858<br>0.583858<br>0.583858<br>0.583858<br>0.583858   
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  | http://www.genome.jp/kegg-bin/show.<br>pathway?hsa04540/hsa:5582%09red<br>http://www.genome.jp/kegg-bin/show.<br>pathway?hsa04970/hsa:5582%09red<br>http://www.genome.jp/kegg-bin/show.<br>pathway?hsa05215/hsa:595%09red<br>http://www.genome.jp/kegg-bin/show.<br>pathway?hsa05032/hsa:5582%09red<br>http://www.genome.jp/kegg-bin/show.<br>pathway?hsa01100/hsa:2653%09red/<br>hsa:427%09red/hsa:56913%09red/<br>hsa:55500%09red/hsa:3032%09red/<br>hsa:80142%09red/hsa:1718%09red/<br>hsa:204%09red<br>http://www.genome.jp/kegg-bin/show.<br>pathway?hsa04713/hsa:5582%09red<br>http://www.genome.jp/kegg-bin/show.<br>pathway?hsa04713/hsa:5582%09red<br>http://www.genome.jp/kegg-bin/show.<br>pathway?hsa04972/hsa:5582%09red<br>http://www.genome.jp/kegg-bin/show.  |   |  
   
   
   
   
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  | 0.397517<br>0.40435<br>0.407737<br>0.407737<br>0.407737<br>0.412411<br>0.412411<br>0.421098<br>0.424391<br>0.424391<br>0.427665<br>0.432595   | 0.583858<br>0.583858<br>0.583858<br>0.583858<br>0.583858<br>0.583858<br>0.583858<br>0.583858  | ENSG0000126583<br>ENSG0000126583<br>ENSG0000110092<br>ENSG0000126583<br>ENSG00000130163<br>ENSG00000139163,<br>ENSG00000148334,<br>ENSG00000148334,<br>ENSG0000016392,<br>ENSG00000126583<br>ENSG00000126583<br>ENSG00000126583<br>ENSG00000126583   
  | http://www.genome.jp/kegg-bin/show.<br>pathway?hsa04540/hsa:5582%09red<br>http://www.genome.jp/kegg-bin/show.<br>pathway?hsa04970/hsa:5582%09red<br>http://www.genome.jp/kegg-bin/show.<br>pathway?hsa05215/hsa:595%09red<br>http://www.genome.jp/kegg-bin/show.<br>pathway?hsa05032/hsa:5582%09red<br>http://www.genome.jp/kegg-bin/show.<br>pathway?hsa03015/hsa:55110%09red/<br>http://www.genome.jp/kegg-bin/show.<br>pathway?hsa01100/hsa:2653%09red/<br>hsa:427%09red/hsa:56913%09red/<br>hsa:55500%09red/hsa:3032%09red/<br>hsa:204%09red<br>http://www.genome.jp/kegg-bin/show.<br>pathway?hsa04113/hsa:5582%09red<br>http://www.genome.jp/kegg-bin/show.<br>pathway?hsa04972/hsa:5582%09red<br>http://www.genome.jp/kegg-bin/show.<br>pathway?hsa04972/hsa:5582%09red<br>http://www.genome.jp/kegg-bin/show.<br>pathway?hsa04914/hsa:4085%09red<br>http://www.genome.jp/kegg-bin/show.<br>pathway?hsa04914/hsa:4085%09red<br>http://www.genome.jp/kegg-bin/show.<br>pathway?hsa04010/hsa:5062%09red/<br>http://www.genome.jp/kegg-bin/show.<br>pathway?hsa04010/hsa:5062%09red/  |   |  
   
   
   
   
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| Cap junction<br>Salivary secretion<br>Prostate cancer<br>Morphine addiction<br>nRNA surveillance<br>bathway<br>Metabolic pathways<br>Circadian entrainment<br>Pancreatic secretion<br>Slycerophospholipid<br>netabolism<br>Progesterone-mediated<br>bocyte maturation<br>MAPK signaling pathway  | KEGG PATHWAY<br>KEGG PATHWAY<br>KEGG PATHWAY<br>KEGG PATHWAY<br>KEGG PATHWAY<br>KEGG PATHWAY<br>KEGG PATHWAY<br>KEGG PATHWAY<br>KEGG PATHWAY  
   
   
   
   
   
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  | 0.397517<br>0.40435<br>0.407737<br>0.407737<br>0.407737<br>0.412411<br>0.412411<br>0.421098<br>0.424391<br>0.424391<br>0.427665   | 0.583858<br>0.583858<br>0.583858<br>0.583858<br>0.583858<br>0.583858<br>0.583858<br>0.583858<br>0.583858   
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   | <ul> <li>hsa04540</li> <li>hsa04970</li> <li>hsa05215</li> <li>hsa05032</li> <li>hsa03015</li> <li>hsa01100</li> <li>hsa04713</li> <li>hsa04972</li> <li>hsa04972</li> <li>hsa00564</li> <li>hsa04914</li> <li>hsa04010</li> <li>hsa01522</li> <li>hsa05166</li> </ul>  
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   | 88<br>90<br>91<br>91<br>1240<br>95<br>96<br>96<br>96<br>96<br>96<br>97<br>257<br>99<br>259  
  | 0.397517<br>0.40435<br>0.407737<br>0.407737<br>0.407737<br>0.412411<br>0.412411<br>0.421098<br>0.424391<br>0.424391<br>0.424391<br>0.423595<br>0.432595   | 0.583858<br>0.583858<br>0.583858<br>0.583858<br>0.583858<br>0.583858<br>0.583858<br>0.583858<br>0.583858<br>0.583858<br>0.583858   
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| Circadian entrainment<br>Pancreatic secretion<br>Circadian entrainment<br>Progesterone-mediated<br>pocyte maturation<br>MAPK signaling pathway<br>Cirdocrine resistance<br>Circadian entrainment<br>Circadian entrainment<br>Circ  | KEGG PATHWAY<br>KEGG PATHWAY  
   
   
   
   
   
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   | 88<br>90<br>91<br>91<br>1240<br>95<br>96<br>96<br>96<br>96<br>96<br>97<br>257<br>99<br>259<br>100<br>100<br>100   
  | 0.397517<br>0.40435<br>0.407737<br>0.407737<br>0.407737<br>0.412411<br>0.424391<br>0.424391<br>0.424391<br>0.424391<br>0.423595<br>0.432595<br>0.432595<br>0.432595<br>0.432595   | 0.583858<br>0.583858<br>0.583858<br>0.583858<br>0.583858<br>0.583858<br>0.583858<br>0.583858<br>0.583858<br>0.583858<br>0.583858<br>0.583858  | ENSG00000126583         ENSG00000126583         ENSG00000110092         ENSG00000126583         ENSG00000139163         ENSG00000148334         ENSG00000148334         ENSG00000139163         ENSG00000148334         ENSG00000148334         ENSG00000148334         ENSG00000148334         ENSG00000148334         ENSG00000148334         ENSG00000148334         ENSG00000148334         ENSG00000148334         ENSG00000126583         ENSG00000126583         ENSG00000126583         ENSG00000110092         ENSG00000110092         ENSG00000126583         ENSG00000126583         ENSG00000126583         ENSG00000126583         ENSG00000126583         ENSG00000126583         ENSG00000126583         ENSG00000126583         ENSG00000126583  
  | http://www.genome.jp/kegg-bin/show.<br>pathway?hsa04540/hsa:5582%09red<br>http://www.genome.jp/kegg-bin/show.<br>pathway?hsa05215/hsa:5582%09red<br>http://www.genome.jp/kegg-bin/show.<br>pathway?hsa05032/hsa:5582%09red<br>http://www.genome.jp/kegg-bin/show.<br>pathway?hsa03015/hsa:55110%09red<br>http://www.genome.jp/kegg-bin/show.<br>pathway?hsa01100/hsa:2653%09red/<br>hsa:55500%09red/hsa:3032%09red/<br>hsa:55500%09red/hsa:3032%09red/<br>hsa:204%09red<br>http://www.genome.jp/kegg-bin/show.<br>pathway?hsa04713/hsa:5582%09red<br>http://www.genome.jp/kegg-bin/show.<br>pathway?hsa04972/hsa:5582%09red<br>http://www.genome.jp/kegg-bin/show.<br>pathway?hsa04972/hsa:5582%09red<br>http://www.genome.jp/kegg-bin/show.<br>pathway?hsa04972/hsa:5582%09red<br>http://www.genome.jp/kegg-bin/show.<br>pathway?hsa04914/hsa:4085%09red<br>http://www.genome.jp/kegg-bin/show.<br>pathway?hsa04914/hsa:5062%09red/<br>hsa:5582%09red<br>http://www.genome.jp/kegg-bin/show.<br>pathway?hsa04010/hsa:5062%09red/<br>hsa:5582%09red<br>http://www.genome.jp/kegg-bin/show.<br>pathway?hsa04016/hsa:5582%09red<br>http://www.genome.jp/kegg-bin/show.<br>pathway?hsa05166/hsa:595%09red/<br>http://www.genome.jp/kegg-bin/show.<br>pathway?hsa05146/hsa:5582%09red<br>http://www.genome.jp/kegg-bin/show.<br>pathway?hsa05146/hsa:5582%09red<br>http://www.genome.jp/kegg-bin/show.<br>pathway?hsa05146/hsa:5582%09red<br>http://www.genome.jp/kegg-bin/show.<br>pathway?hsa05146/hsa:5582%09red<br>http://www.genome.jp/kegg-bin/show.<br>pathway?hsa05146/hsa:5582%09red<br>http://www.genome.jp/kegg-bin/show.<br>pathway?hsa05146/hsa:5582%09red<br>http://www.genome.jp/kegg-bin/show.<br>pathway?hsa05146/hsa:5582%09red<br>http://www.genome.jp/kegg-bin/show.<br>pathway?hsa05146/hsa:5582%09red   |   |  
   
   
   
   
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| Circadian entrainment<br>Pancreatic secretion<br>Circadian entrainment<br>Pancreatic secretion<br>Circadian entrainment<br>Pancreatic secretion<br>Circadian entrainment<br>Pancreatic secretion<br>Circadian entrainment<br>Circadian entrainment<br>Circadian entrainment<br>Pancreatic secretion<br>Circadian entrainment<br>Circadian entrainment<br>Circa  | KEGG PATHWAY<br>KEGG PATHWAY   
   
   
   
   
   
  | hsa04540         hsa04970         hsa05215         hsa05032         hsa03015         hsa01100         hsa04713         hsa04972         hsa04972         hsa04914         hsa04010         hsa01522         hsa05146         hsa05146  
  | 1<br>1<br>1<br>1<br>1<br>1<br>8<br>1<br>1<br>1<br>1<br>2<br>1<br>2<br>1<br>2<br>1<br>1<br>2  
   
   
   
   
   
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   | 0.397517<br>0.40435<br>0.407737<br>0.407737<br>0.407737<br>0.412411<br>0.421098<br>0.424391<br>0.424391<br>0.424391<br>0.427665<br>0.432595<br>0.432595<br>0.432595   | 0.583858<br>0.583858<br>0.583858<br>0.583858<br>0.583858<br>0.583858<br>0.583858<br>0.583858<br>0.583858<br>0.583858<br>0.583858<br>0.583858  | ENSG0000126583<br>ENSG0000126583<br>ENSG0000110092<br>ENSG0000126583<br>ENSG0000111196<br>ENSG0000148334<br>ENSG00000148334<br>ENSG000014763,<br>ENSG000014763,<br>ENSG0000126583<br>ENSG0000126583<br>ENSG0000126583<br>ENSG0000126583,<br>ENSG0000110092<br>ENSG0000110092<br>ENSG0000110092,<br>ENSG00000126583<br>ENSG0000126583  
   | http://www.genome.jp/kegg-bin/show.<br>pathway?hsa04540/hsa:5582%09red<br>http://www.genome.jp/kegg-bin/show.<br>pathway?hsa05215/hsa:5582%09red<br>http://www.genome.jp/kegg-bin/show.<br>pathway?hsa05032/hsa:5582%09red<br>http://www.genome.jp/kegg-bin/show.<br>pathway?hsa03015/hsa:55110%09red<br>http://www.genome.jp/kegg-bin/show.<br>pathway?hsa01100/hsa:2653%09red/<br>hsa:427%09red/hsa:56913%09red/<br>hsa:55500%09red/hsa:3032%09red/<br>hsa:80142%09red/hsa:3032%09red/<br>hsa:204%09red<br>http://www.genome.jp/kegg-bin/show.<br>pathway?hsa04713/hsa:5582%09red<br>http://www.genome.jp/kegg-bin/show.<br>pathway?hsa04713/hsa:5582%09red<br>http://www.genome.jp/kegg-bin/show.<br>pathway?hsa04972/hsa:5582%09red<br>http://www.genome.jp/kegg-bin/show.<br>pathway?hsa04972/hsa:5582%09red<br>http://www.genome.jp/kegg-bin/show.<br>pathway?hsa04914/hsa:4085%09red<br>http://www.genome.jp/kegg-bin/show.<br>pathway?hsa04010/hsa:5062%09red<br>http://www.genome.jp/kegg-bin/show.<br>pathway?hsa041010/hsa:5062%09red<br>http://www.genome.jp/kegg-bin/show.<br>pathway?hsa0416/hsa:5582%09red<br>http://www.genome.jp/kegg-bin/show.<br>pathway?hsa0416/hsa:5582%09red<br>http://www.genome.jp/kegg-bin/show.<br>pathway?hsa0416/hsa:5582%09red<br>http://www.genome.jp/kegg-bin/show.<br>pathway?hsa05166/hsa:5582%09red<br>http://www.genome.jp/kegg-bin/show.<br>pathway?hsa0416/hsa:5582%09red<br>http://www.genome.jp/kegg-bin/show.<br>pathway?hsa0416/hsa:5582%09red<br>http://www.genome.jp/kegg-bin/show.<br>pathway?hsa0416/hsa:5582%09red<br>http://www.genome.jp/kegg-bin/show.<br>pathway?hsa04723/hsa:5582%09red<br>http://www.genome.jp/kegg-bin/show.<br>pathway?hsa04723/hsa:5582%09red<br>http://www.genome.jp/kegg-bin/show.<br>pathway?hsa04723/hsa:5582%09red<br>http://www.genome.jp/kegg-bin/show.<br>pathway?hsa04723/hsa:5582%09red<br>http://www.genome.jp/kegg-bin/show.<br>pathway?hsa04723/hsa:5582%09red<br>http://www.genome.jp/kegg-bin/show.<br>pathway?hsa04723/hsa:5582%09red<br>http://www.genome.jp/kegg-bin/show.<br>pathway?hsa04723/hsa:5582%09red  |   |   
   
   
   
   
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| Circadian entrainment<br>Pancreatic secretion<br>Circadian entrainment<br>Circadian entrainment<br>Pancreatic secretion<br>Circadian entrainment<br>Pancreatic secretion<br>Circadian entrainment<br>Pancreatic secretion<br>Circadian entrainment<br>Pancreatic secretion<br>Circadian entrainment<br>Pancreatic secretion<br>Circadian entrainment<br>Pancreatic secretion<br>Circadian entrainment<br>Phosphatidylinositol<br>Signaling system<br>Circadian entrainment<br>Circadian entrainment<br>Circadian entrainment<br>Circadian entrainment<br>Circadian entrainment<br>Phosphatidylinositol<br>Signaling system<br>Circadian entrainment  | KEGG PATHWAY<br>KEGG PATHWAY  
   
   
   
   
   
   | hsa04540         hsa04970         hsa05215         hsa05032         hsa03015         hsa01100         hsa04713         hsa04972         hsa04972         hsa04914         hsa04010         hsa05166         hsa05146         hsa04916         hsa04713  
   | 1<br>1<br>1<br>1<br>1<br>1<br>8<br>1<br>1<br>1<br>2<br>1<br>2<br>1<br>1<br>2<br>1<br>1<br>1<br>1  
   
   
   
   
   
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  | 0.397517<br>0.40435<br>0.407737<br>0.407737<br>0.407737<br>0.412411<br>0.424391<br>0.424391<br>0.424391<br>0.427665<br>0.432595<br>0.432595<br>0.432595<br>0.436454<br>0.436454<br>0.437378<br>0.437378   | 0.583858<br>0.583858<br>0.583858<br>0.583858<br>0.583858<br>0.583858<br>0.583858<br>0.583858<br>0.583858<br>0.583858<br>0.583858<br>0.583858<br>0.583858  |
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| Cap junction<br>Salivary secretion<br>Prostate cancer<br>Morphine addiction<br>mRNA surveillance<br>bothway<br>Metabolic pathways<br>Metabolic pathways<br>Circadian entrainment<br>Pancreatic secretion<br>Clycerophospholipid<br>netabolism<br>Progesterone-mediated<br>bocyte maturation<br>MAPK signaling pathway<br>Endocrine resistance<br>Mark signaling pathway<br>Endocrine resistance<br>Mark signaling pathway<br>Endocrine resistance<br>Mark signaling pathway<br>Endocrine resistance<br>Mark signaling pathway<br>Endocrine resistance<br>AttLV-I infection<br>Amoebiasis<br>Melanogenesis<br>Melanogenesis<br>Melanogenesis<br>Choline metabolism in   | KEGG PATHWAY<br>KEGG PATHWAY  
   
   
   
   
   
   | hsa04540         hsa04970         hsa05215         hsa05032         hsa03015         hsa03015         hsa04713         hsa04972         hsa04972         hsa04914         hsa04010         hsa05146         hsa05146         hsa04713         hsa04010         hsa04010         hsa04010         hsa04010         hsa04010         hsa04010   
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   | <ul> <li>88</li> <li>90</li> <li>91</li> <li>91</li> <li>91</li> <li>1240</li> <li>95</li> <li>96</li> <li>96</li> <li>97</li> <li>257</li> <li>99</li> <li>259</li> <li>100</li> <li>101</li> <li>101</li> <li>101</li> <li>101</li> </ul>   
  | 0.397517<br>0.40435<br>0.407737<br>0.407737<br>0.407737<br>0.412411<br>0.424391<br>0.424391<br>0.424391<br>0.424391<br>0.427665<br>0.432595<br>0.432595<br>0.432595<br>0.432595<br>0.437378<br>0.437378<br>0.437378   | 0.583858<br>0.583858<br>0.583858<br>0.583858<br>0.583858<br>0.583858<br>0.583858<br>0.583858<br>0.583858<br>0.583858<br>0.583858<br>0.583858<br>0.583858<br>0.583858   
  | ENSG00000126583         ENSG00000126583         ENSG00000126583         ENSG00000126583         ENSG00000139163         ENSG00000148334         ENSG00000126583         ENSG00000126583         ENSG00000126583         ENSG00000110092         ENSG00000126583   | http://www.genome.jp/kegg-bin/show<br>pathway?hsa04540/hsa:5582%09red<br>http://www.genome.jp/kegg-bin/show<br>pathway?hsa05215/hsa:5582%09red<br>http://www.genome.jp/kegg-bin/show<br>pathway?hsa05032/hsa:5582%09red<br>http://www.genome.jp/kegg-bin/show<br>pathway?hsa03015/hsa:55110%09red<br>http://www.genome.jp/kegg-bin/show<br>pathway?hsa01100/hsa:2653%09red/<br>hsa:5500%09red/hsa:3032%09red/<br>hsa:55500%09red/hsa:3032%09red/<br>hsa:80142%09red/hsa:3032%09red/<br>hsa:204%09red<br>http://www.genome.jp/kegg-bin/show<br>pathway?hsa04713/hsa:5582%09red<br>http://www.genome.jp/kegg-bin/show<br>pathway?hsa04972/hsa:5582%09red<br>http://www.genome.jp/kegg-bin/show<br>pathway?hsa04972/hsa:5582%09red<br>http://www.genome.jp/kegg-bin/show<br>pathway?hsa04972/hsa:5582%09red<br>http://www.genome.jp/kegg-bin/show<br>pathway?hsa04914/hsa:4085%09red<br>http://www.genome.jp/kegg-bin/show<br>pathway?hsa04914/hsa:5562%09red<br>http://www.genome.jp/kegg-bin/show<br>pathway?hsa04010/hsa:5062%09red<br>http://www.genome.jp/kegg-bin/show<br>pathway?hsa05166/hsa:595%09red<br>http://www.genome.jp/kegg-bin/show<br>pathway?hsa05166/hsa:595%09red<br>http://www.genome.jp/kegg-bin/show<br>pathway?hsa05166/hsa:595%09red<br>http://www.genome.jp/kegg-bin/show<br>pathway?hsa05166/hsa:595%09red<br>http://www.genome.jp/kegg-bin/show<br>pathway?hsa05166/hsa:5582%09red<br>http://www.genome.jp/kegg-bin/show<br>pathway?hsa04750/hsa:5582%09red<br>http://www.genome.jp/kegg-bin/show<br>pathway?hsa04750/hsa:5582%09red<br>http://www.genome.jp/kegg-bin/show<br>pathway?hsa04750/hsa:5582%09red<br>http://www.genome.jp/kegg-bin/show<br>pathway?hsa04750/hsa:5582%09red<br>http://www.genome.jp/kegg-bin/show<br>pathway?hsa04750/hsa:5582%09red<br>http://www.genome.jp/kegg-bin/show<br>pathway?hsa04750/hsa:5582%09red<br>http://www.genome.jp/kegg-bin/show<br>pathway?hsa04070/hsa:5582%09red<br>http://www.genome.jp/kegg-bin/show<br>pathway?hsa04070/hsa:5582%09red<br>http://www.genome.jp/kegg-bin/show<br>pathway?hsa04070/hsa:5582%09red   |   |  
   
   
   
   
   
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| Circadian entrainment<br>Prosesterone-mediated<br>bocyte maturation<br>APK signaling pathway<br>Circadian entrainment<br>Pancreatic secretion<br>Circadian entrainment<br>Pancreatic secretion<br>Circadian entrainment<br>Pancreatic secretion<br>Circadian entrainment<br>Circadian entrainment<br>Circadi  | KEGG PATHWAY   
   
   
   
   
   
  | hsa04540         hsa04970         hsa05215         hsa05032         hsa03015         hsa01100         hsa04713         hsa04972         hsa04972         hsa04914         hsa04010         hsa05146         hsa04713         hsa04010  
  | 1<br>1<br>1<br>1<br>1<br>8<br>1<br>1<br>1<br>1<br>2<br>1<br>1<br>1<br>1<br>1<br>1<br>1<br>1<br>1   
   
   
   
   
   
  | <ul> <li>88</li> <li>90</li> <li>91</li> <li>91</li> <li>91</li> <li>1240</li> <li>95</li> <li>96</li> <li>96</li> <li>96</li> <li>97</li> <li>257</li> <li>99</li> <li>259</li> <li>100</li> <li>101</li> <li>101</li> <li>101</li> <li>101</li> <li>103</li> </ul>   
   | 0.397517<br>0.40435<br>0.407737<br>0.407737<br>0.407737<br>0.412411<br>0.424391<br>0.424391<br>0.424391<br>0.424391<br>0.427665<br>0.432595<br>0.432595<br>0.432595<br>0.432595<br>0.432595<br>0.432595<br>0.432595<br>0.432595<br>0.432595   | 0.583858<br>0.583858<br>0.583858<br>0.583858<br>0.583858<br>0.583858<br>0.583858<br>0.583858<br>0.583858<br>0.583858<br>0.583858<br>0.583858<br>0.583858<br>0.583858  | ENSG0000126583         ENSG0000126583         ENSG0000110092         ENSG0000126583         ENSG0000139163         ENSG0000148334         ENSG0000148334         ENSG0000116133         ENSG0000116392         ENSG0000148334         ENSG0000116392         ENSG0000116392         ENSG0000116392         ENSG0000116392         ENSG0000116392         ENSG0000116392         ENSG0000116392         ENSG0000116392         ENSG0000116392         ENSG00001126583         ENSG00000126583         ENSG00000110092         ENSG00000110092         ENSG00000126583         ENSG00000126583         ENSG00000126583         ENSG00000126583         ENSG00000126583         ENSG00000126583         ENSG00000126583         ENSG00000126583         ENSG00000126583  
   | http://www.genome.jp/kegg-bin/show.<br>pathway?hsa04540/hsa:5582%09red<br>http://www.genome.jp/kegg-bin/show.<br>pathway?hsa05215/hsa:5582%09red<br>http://www.genome.jp/kegg-bin/show.<br>pathway?hsa05032/hsa:5582%09red<br>http://www.genome.jp/kegg-bin/show.<br>pathway?hsa03015/hsa:55110%09red/<br>http://www.genome.jp/kegg-bin/show.<br>pathway?hsa01100/hsa:2653%09red/<br>hsa:427%09red/hsa:56913%09red/<br>hsa:55500%09red/hsa:3032%09red/<br>hsa:80142%09red/hsa:3032%09red/<br>hsa:204%09red<br>http://www.genome.jp/kegg-bin/show.<br>pathway?hsa04713/hsa:5582%09red<br>http://www.genome.jp/kegg-bin/show.<br>pathway?hsa04972/hsa:5582%09red<br>http://www.genome.jp/kegg-bin/show.<br>pathway?hsa04972/hsa:5582%09red<br>http://www.genome.jp/kegg-bin/show.<br>pathway?hsa04914/hsa:4085%09red<br>http://www.genome.jp/kegg-bin/show.<br>pathway?hsa04914/hsa:5062%09red<br>http://www.genome.jp/kegg-bin/show.<br>pathway?hsa04010/hsa:5062%09red<br>http://www.genome.jp/kegg-bin/show.<br>pathway?hsa04110/hsa:5062%09red<br>http://www.genome.jp/kegg-bin/show.<br>pathway?hsa04110/hsa:5062%09red<br>http://www.genome.jp/kegg-bin/show.<br>pathway?hsa04110/hsa:5082%09red<br>http://www.genome.jp/kegg-bin/show.<br>pathway?hsa0416/hsa:5582%09red<br>http://www.genome.jp/kegg-bin/show.<br>pathway?hsa05146/hsa:5582%09red<br>http://www.genome.jp/kegg-bin/show.<br>pathway?hsa04916/hsa:5582%09red<br>http://www.genome.jp/kegg-bin/show.<br>pathway?hsa04916/hsa:5582%09red<br>http://www.genome.jp/kegg-bin/show.<br>pathway?hsa04750/hsa:5582%09red<br>http://www.genome.jp/kegg-bin/show.<br>pathway?hsa04750/hsa:5582%09red<br>http://www.genome.jp/kegg-bin/show.<br>pathway?hsa04750/hsa:5582%09red<br>http://www.genome.jp/kegg-bin/show.<br>pathway?hsa04723/hsa:5582%09red<br>http://www.genome.jp/kegg-bin/show.<br>pathway?hsa04723/hsa:5582%09red<br>http://www.genome.jp/kegg-bin/show.<br>pathway?hsa04723/hsa:5582%09red<br>http://www.genome.jp/kegg-bin/show.<br>pathway?hsa04723/hsa:5582%09red<br>http://www.genome.jp/kegg-bin/show.<br>pathway?hsa04723/hsa:5582%09red   |   |   
   
   
   
   
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| ap junction<br>alivary secretion<br>forstate cancer<br>forstate cancer<br>forphine addiction<br>fRNA surveillance<br>athway<br>fetabolic pathways<br>detabolic pathways<br>forceatic secretion<br>alycerophospholipid<br>hetabolism<br>frogesterone-mediated<br>ocyte maturation<br>fAPK signaling pathway<br>andocrine resistance<br>fTLV-1 infection<br>falammatory mediator<br>egulation of TRP channels<br>for any system<br>falammatory mediator<br>egulation any system<br>for any system<br>falammatory mediator<br>egulation any system<br>for any system<br>for any system<br>for any system<br>falammatory mediator<br>egulation any system<br>for an  | KEGG PATHWAY  
   
   
   
   
   
   | hsa04540         hsa04970         hsa05215         hsa05032         hsa01100         hsa01100         hsa04713         hsa04972         hsa04972         hsa04914         hsa04914         hsa01522         hsa04100         hsa04102         hsa04102         hsa041522         hsa041522         hsa041522         hsa04010         hsa041522         hsa041522         hsa041522         hsa041523         hsa04916         hsa04723         hsa04070         hsa04933   
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   | <ul> <li>88</li> <li>90</li> <li>91</li> <li>91</li> <li>91</li> <li>1240</li> <li>95</li> <li>96</li> <li>96</li> <li>97</li> <li>257</li> <li>99</li> <li>259</li> <li>100</li> <li>101</li> <li>101</li> <li>101</li> <li>101</li> <li>101</li> <li>103</li> <li>104</li> </ul>  
  | 0.397517<br>0.40435<br>0.407737<br>0.407737<br>0.407737<br>0.412411<br>0.421098<br>0.424391<br>0.424391<br>0.42395<br>0.423595<br>0.432595<br>0.432595<br>0.432595<br>0.436454<br>0.437378<br>0.437378<br>0.437378<br>0.437378<br>0.437378  | 0.583858<br>0.583858<br>0.583858<br>0.583858<br>0.583858<br>0.583858<br>0.583858<br>0.583858<br>0.583858<br>0.583858<br>0.583858<br>0.583858<br>0.583858<br>0.583858<br>0.583858  | ENSG0000126583         ENSG0000126583         ENSG0000110092         ENSG00001126583         ENSG0000139163         ENSG00001141196         ENSG00000148334         ENSG00000148334         ENSG0000116133         ENSG00000148334         ENSG0000116133         ENSG0000116133         ENSG00000148334         ENSG0000116133         ENSG0000116133         ENSG00000138029         ENSG00000140905         ENSG00000126583   
  | http://www.genome.jp/kegg-bin/show<br>pathway?hsa04540/hsa:5582%09red<br>http://www.genome.jp/kegg-bin/show<br>pathway?hsa05215/hsa:5582%09red<br>http://www.genome.jp/kegg-bin/show<br>pathway?hsa05032/hsa:5582%09red<br>http://www.genome.jp/kegg-bin/show<br>pathway?hsa03015/hsa:55110%09red<br>http://www.genome.jp/kegg-bin/show<br>pathway?hsa01100/hsa:2653%09red/<br>hsa:427%09red/hsa:56913%09red/<br>hsa:55500%09red/hsa:3032%09red/<br>hsa:55500%09red/hsa:3032%09red/<br>hsa:55500%09red/hsa:5582%09red/<br>hsa:204%09red<br>http://www.genome.jp/kegg-bin/show<br>pathway?hsa04713/hsa:5582%09red<br>http://www.genome.jp/kegg-bin/show<br>pathway?hsa04713/hsa:5582%09red<br>http://www.genome.jp/kegg-bin/show<br>pathway?hsa04972/hsa:5582%09red<br>http://www.genome.jp/kegg-bin/show<br>pathway?hsa04914/hsa:4085%09red<br>http://www.genome.jp/kegg-bin/show<br>pathway?hsa04914/hsa:4085%09red<br>http://www.genome.jp/kegg-bin/show<br>pathway?hsa04914/hsa:4085%09red<br>http://www.genome.jp/kegg-bin/show<br>pathway?hsa04916/hsa:5582%09red<br>http://www.genome.jp/kegg-bin/show<br>pathway?hsa05166/hsa:5582%09red<br>http://www.genome.jp/kegg-bin/show<br>pathway?hsa05146/hsa:5582%09red<br>http://www.genome.jp/kegg-bin/show<br>pathway?hsa05146/hsa:5582%09red<br>http://www.genome.jp/kegg-bin/show<br>pathway?hsa05146/hsa:5582%09red<br>http://www.genome.jp/kegg-bin/show<br>pathway?hsa05146/hsa:5582%09red<br>http://www.genome.jp/kegg-bin/show<br>pathway?hsa05146/hsa:5582%09red<br>http://www.genome.jp/kegg-bin/show<br>pathway?hsa04723/hsa:5582%09red<br>http://www.genome.jp/kegg-bin/show<br>pathway?hsa04723/hsa:5582%09red<br>http://www.genome.jp/kegg-bin/show<br>pathway?hsa04723/hsa:5582%09red<br>http://www.genome.jp/kegg-bin/show<br>pathway?hsa04723/hsa:5582%09red<br>http://www.genome.jp/kegg-bin/show<br>pathway?hsa04723/hsa:5582%09red<br>http://www.genome.jp/kegg-bin/show<br>pathway?hsa04723/hsa:5582%09red<br>http://www.genome.jp/kegg-bin/show<br>pathway?hsa04070/hsa:5582%09red<br>http://www.genome.jp/kegg-bin/show<br>pathway?hsa04070/hsa:5582%09red<br>http://www.genome.jp/kegg-bin/show<br>pathway?hsa04066/hsa:5582%09red   |   |  
   
   
   
   
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| Cap junction<br>Salivary secretion<br>Prostate cancer<br>Aorphine addiction<br>NRNA surveillance<br>bathway<br>Aetabolic pathways<br>Circadian entrainment<br>Pancreatic secretion<br>Clycerophospholipid<br>netabolism<br>Progesterone-mediated<br>bocyte maturation<br>APK signaling pathway<br>Endocrine resistance<br>ATLV-I infection<br>APK signaling pathway<br>Endocrine resistance<br>ATLV-I infection<br>Anoebiasis<br>Aelanogenesis<br>Adelanogenesis<br>Choine metabolism in<br>cignaling system<br>AGE-RAGE signaling<br>Phosphatidylinositol<br>cignaling system<br>AGE-RAGE signaling<br>Choine metabolism in<br>cancer<br>AITL-1 signaling pathway   | KEGG PATHWAY  
   
   
   
   
   
   | hsa04540         hsa04970         hsa05215         hsa05032         hsa01100         hsa04713         hsa04972         hsa04972         hsa04972         hsa04914         hsa04914         hsa04010         hsa04913         hsa041522         hsa041523         hsa041523         hsa04723         hsa04723         hsa04070         hsa04070         hsa04066         hsa04066  
   | 1<br>1<br>1<br>1<br>1<br>1<br>1<br>1<br>1<br>1<br>1<br>1<br>1<br>1  
   
   
   
   
   
   | <ul> <li>88</li> <li>90</li> <li>91</li> <li>91</li> <li>91</li> <li>1240</li> <li>95</li> <li>96</li> <li>96</li> <li>97</li> <li>257</li> <li>99</li> <li>259</li> <li>100</li> <li>101</li> <li>101</li> <li>101</li> <li>101</li> <li>101</li> <li>103</li> <li>104</li> <li>105</li> <li>107</li> <li>273</li> </ul>   
  | 0.397517<br>0.40435<br>0.407737<br>0.407737<br>0.407737<br>0.412411<br>0.424391<br>0.424391<br>0.42395<br>0.423595<br>0.432595<br>0.432595<br>0.436454<br>0.436454<br>0.437378<br>0.437378<br>0.437378<br>0.437378<br>0.43630<br>0.440579<br>0.440579<br>0.440579<br>0.440579<br>0.440579<br>0.440579   | 0.583858<br>0.583858<br>0.583858<br>0.583858<br>0.583858<br>0.583858<br>0.583858<br>0.583858<br>0.583858<br>0.583858<br>0.583858<br>0.583858<br>0.583858<br>0.583858<br>0.583858<br>0.583858   
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| Cap junction<br>Calivary secretion<br>Prostate cancer<br>Aorphine addiction<br>PRNA surveillance<br>bathway<br>Actabolic pathways<br>Actabolic pathways<br>Circadian entrainment<br>Pancreatic secretion<br>Calveerophospholipid<br>netabolism<br>Progesterone-mediated<br>oocyte maturation<br>APK signaling pathway<br>Cindocrine resistance<br>ATLV-I infection<br>APK signaling pathway<br>Cindocrine resistance<br>ATLV-I infection<br>ADPK signaling pathway<br>Cindocannabinoid signaling<br>Prosphatidylinositol<br>ignaling system<br>AGE-RAGE signaling<br>pathway in diabetic<br>complications<br>Choline metabolism in<br>cancer<br>AIFL-1 signaling pathway<br>Cicell receptor signaling<br>pathway in cancer<br>Cicell receptor signaling<br>cathway and cancer<br>Cicell receptor signaling<br>pathway in cancer<br>Cicell receptor signaling<br>cathway in cancer<br>Cicell receptor signaling<br>cathway in cancer<br>Cicell receptor signaling<br>cathway and cancer<br>Cicell receptor signaling<br>cathway and cancer<br>Cicell receptor signaling<br>cathway in cancer  | KEGG PATHWAY  
   
   
   
   
   
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| ap junction<br>alivary secretion<br>rostate cancer<br>Aorphine addiction<br>nRNA surveillance<br>athway<br>Aetabolic pathways<br>detabolic pathways<br>detabolis pathway<br>ancreatic secretion<br>alycerophospholipid<br>hetabolism<br>rogesterone-mediated<br>ocyte maturation<br>APK signaling pathway<br>andocrine resistance<br>athur and a signaling<br>athway in diabetic<br>ophatidylinositol<br>ignaling system<br>GE_RAGE signaling<br>athway in diabetic<br>omplications<br>Choline metabolism in<br>ancer<br>IFL-1 signaling pathway<br>dicroRNAs in cancer  | KEGG PATHWAY  
   
   
   
   
   
   | hsa04540         hsa04970         hsa05215         hsa05032         hsa01100         hsa01100         hsa04972         hsa04972         hsa04972         hsa04972         hsa04972         hsa04010         hsa04914         hsa04914         hsa04916         hsa04010         hsa041522         hsa04010         hsa04010         hsa04010         hsa04010         hsa04010         hsa041522         hsa041522         hsa04010         hsa04216         hsa04723         hsa04723         hsa04723         hsa044723   
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  | 0.397517<br>0.40435<br>0.407737<br>0.407737<br>0.407737<br>0.412411<br>0.421098<br>0.424391<br>0.42391<br>0.42395<br>0.423595<br>0.432595<br>0.432595<br>0.432595<br>0.437378<br>0.437378<br>0.437378<br>0.437378<br>0.437378<br>0.437378<br>0.440579<br>0.440579<br>0.440579<br>0.440579<br>0.440579<br>0.440579<br>0.440579<br>0.440579<br>0.440579<br>0.440579<br>0.440579<br>0.440579<br>0.440579<br>0.440579<br>0.440579<br>0.440579<br>0.440579<br>0.440579<br>0.440579<br>0.440579<br>0.440579<br>0.440579<br>0.440579<br>0.440579<br>0.440579<br>0.440579<br>0.440579<br>0.440579<br>0.440579<br>0.440579<br>0.440579<br>0.440579<br>0.440579<br>0.440579<br>0.440579<br>0.440579<br>0.440579<br>0.440579<br>0.440579<br>0.440579<br>0.440579<br>0.440579<br>0.440579<br>0.440579<br>0.440579<br>0.440579<br>0.440579<br>0.440579<br>0.440579<br>0.440579<br>0.440579<br>0.440579<br>0.440579<br>0.440579<br>0.440579<br>0.440579<br>0.440579<br>0.440579<br>0.440579<br>0.440579<br>0.440579<br>0.440579<br>0.440579<br>0.440579<br>0.440579<br>0.440579<br>0.440579<br>0.440579<br>0.440579<br>0.440579<br>0.440579<br>0.440579<br>0.440579<br>0.440579<br>0.440579<br>0.440579<br>0.440579<br>0.440579<br>0.440579<br>0.440579<br>0.440579<br>0.440579<br>0.440579<br>0.440579<br>0.440579<br>0.440579<br>0.440579<br>0.440579<br>0.440579<br>0.440579<br>0.440579<br>0.440579<br>0.440579<br>0.440579<br>0.440579<br>0.440579<br>0.440579<br>0.440579<br>0.440579<br>0.440579<br>0.440579<br>0.440579<br>0.440579<br>0.440579<br>0.440579<br>0.440579<br>0.440579<br>0.440579<br>0.440579<br>0.440579<br>0.440579<br>0.440579<br>0.440579<br>0.440579<br>0.440579<br>0.440579<br>0.440579<br>0.440579<br>0.440579<br>0.440579<br>0.440579<br>0.440579<br>0.440579<br>0.440579<br>0.440579<br>0.440579<br>0.440579<br>0.440579<br>0.440579<br>0.440579<br>0.440579<br>0.440579<br>0.440579<br>0.440579<br>0.440579<br>0.440579<br>0.440579<br>0.440579<br>0.440579<br>0.440579<br>0.440579<br>0.440579<br>0.440579<br>0.440579<br>0.440579<br>0.440579<br>0.440579<br>0.440579<br>0.440579<br>0.440579<br>0.440579<br>0.440579<br>0.440579<br>0.440579<br>0.440579<br>0.440579<br>0.440579<br>0.440579<br>0.440579<br>0.440579<br>0.440579<br>0.440579<br>0.440579<br>0.440579<br>0.440579<br>0.440579<br>0.440579<br>0.440579<br>0.440579<br>0.440579<br>0.440579<br>0.440579<br>0.440579<br>0.440579<br>0.440579<br>0.440579<br>0.440579<br>0.440579<br>0.440579<br>0.440579<br>0.440579<br>0.440579<br>0.440579<br>0.440579<br>0.440579           | 0.583858<br>0.583858<br>0.583858<br>0.583858<br>0.583858<br>0.583858<br>0.583858<br>0.583858<br>0.583858<br>0.583858<br>0.583858<br>0.583858<br>0.583858<br>0.583858<br>0.583858<br>0.583858<br>0.583858<br>0.583858<br>0.583858<br>0.583858<br>0.583858<br>0.583858<br>0.583858<br>0.583858<br>0.583858<br>0.583858  |
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| Aap junction<br>Salivary secretion<br>Prostate cancer<br>Aorphine addiction<br>PRNA surveillance<br>bathway<br>Aetabolic pathways<br>Actabolic pathways<br>Actabolis pathway<br>Actabolism<br>Progesterone-mediated<br>oocyte maturation<br>APK signaling pathway<br>Cholorine resistance<br>ATLV-1 infection<br>ADPK signaling pathway<br>Chosphatidylinositol<br>ignaling system<br>AGE-RAGE signaling<br>Prosphatidylinositol<br>ignaling system<br>AGE-RAGE signaling<br>Athway in diabetic<br>complications<br>Choline metabolism in<br>ancer<br>AITLV-1 signaling pathway<br>Cell receptor signaling<br>Athway in diabetic<br>complications<br>Choline metabolism in<br>ancer<br>AITLV-1 signaling pathway<br>Cocyte meiosis<br>Choline metabolism in<br>ancer<br>Altron ADAS in cancer<br>Cholinergic synapse<br>Cholinergic synapse<br>Cholinergic synapse<br>Cholinergic synapse<br>Altamatergic synapse<br>Cholinergic synapse<br>Cholinergic synapse<br>Cholinergic synapse<br>Cholinergic synapse<br>Cholinergic synapse<br>Cholinergic synapse<br>Cholinergic synapse<br>Cholinergic synapse  | KEGG PATHWAY  
   
   
   
   
   
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   | 0.397517<br>0.40435<br>0.407737<br>0.407737<br>0.407737<br>0.412411<br>0.421098<br>0.424391<br>0.42391<br>0.42395<br>0.423595<br>0.432595<br>0.432595<br>0.436454<br>0.437378<br>0.437378<br>0.437378<br>0.437378<br>0.437378<br>0.437378<br>0.437378<br>0.437378<br>0.437378<br>0.437378<br>0.440579<br>0.440579<br>0.440579<br>0.440579<br>0.440579<br>0.440579<br>0.440579<br>0.440579<br>0.440579<br>0.440579<br>0.440579<br>0.440579<br>0.440579<br>0.440579<br>0.440579<br>0.440579   | 0.583858<br>0.583858<br>0.583858<br>0.583858<br>0.583858<br>0.583858<br>0.583858<br>0.583858<br>0.583858<br>0.583858<br>0.583858<br>0.583858<br>0.583858<br>0.583858<br>0.583858<br>0.583858<br>0.583858<br>0.583858<br>0.583858  |
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| Aap junction<br>Balivary secretion<br>Prostate cancer<br>Aorphine addiction<br>PRNA surveillance<br>bathway<br>Aetabolic pathways<br>Actabolic pathways<br>Actabolic pathways<br>Actabolis pathway<br>Actabolism<br>Progesterone-mediated<br>oocyte maturation<br>APK signaling pathway<br>APK signaling pathway<br>Actabolissis<br>Alanogenesis<br>Actorograde<br>Indocannabinoid signaling<br>Phosphatidylinositol<br>ignaling system<br>Actanogenesis<br>Actarograde<br>Indocannabinoid signaling<br>Phosphatidylinositol<br>ignaling system<br>Actarograde<br>Indocannabinoid signaling<br>Athway in ciabetic<br>omplications<br>Choline metabolism in<br>ancer<br>Actoronergic synapse<br>Cholinergic synapse<br>Actoronergic synapse<br>Actarograde<br>Actaroaction<br>Actoronergic 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| Aap junction<br>alivary secretion<br>Prostate cancer<br>Aorphine addiction<br>anRNA surveillance<br>athway<br>Aetabolic pathways<br>Aetabolic pathways<br>Actabolic pathways<br>Actabolis pathway<br>Progesterone-mediated<br>ooyte maturation<br>APK signaling pathway<br>andocrine resistance<br>ALV-1 infection<br>APK signaling pathway<br>andocannabinoid signaling<br>adhway in diabetic<br>omplications<br>Aetrograde<br>ndocannabinoid signaling<br>athway in diabetic<br>omplications<br>Choline metabolism in<br>ancer<br>AlF-1 signaling pathway<br>ActororRNAs in cancer<br>ActororRNAs in cancer<br>Actor<br>ACTORRNAS in cancer<br>Actor<br>ACTORRNAS in cancer<br>Actor<br>ACTORRNAS in cancer<br>Actor<br>ACTORRNAS in cancer<br>Actor<br>ACTORRNAS in cancer<br>Actor<br>ACTORRNAS in cancer<br>ACTORRNAS in cancer<br>A   | KEGG PATHWAYKEGG PATHWAY <td>hsa04540         hsa04970         hsa05215         hsa05032         hsa01100         hsa04713         hsa04972         hsa04972         hsa04972         hsa04972         hsa04972         hsa04010         hsa04914         hsa04913         hsa04914         hsa041522         hsa04152         hsa04152         hsa04723         hsa04724         hsa04725         hsa04724         hsa04724         hsa04724</td> <td>1<br/>1<br/>1<br/>1<br/>1<br/>1<br/>1<br/>1<br/>1<br/>1<br/>1<br/>1<br/>1<br/>1</td> <td><ul> <li>88</li> <li>90</li> <li>91</li> <li>91</li> <li>91</li> <li>1240</li> <li>95</li> <li>96</li> <li>97</li> <li>257</li> <li>99</li> <li>259</li> <li>100</li> <li>101</li> <li>101&lt;</li></ul></td> 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| Aap junction<br>Salivary secretion<br>Prostate cancer<br>Aorphine addiction<br>nRNA surveillance<br>aathway<br>Aetabolic pathways<br>Aetabolic pathways<br>Actabolic pathways<br>Actabolism<br>Progesterone-mediated<br>ooyte maturation<br>APK signaling pathway<br>Actaboliasis<br>Actoranabinoid signaling<br>adhway in diabetic<br>complications<br>Actorgrade<br>indocannabinoid signaling<br>athway in diabetic<br>complications<br>Choline metabolism in<br>ancer<br>Alf-1 signaling pathway<br>Actorary synapse<br>Cholinergic synapse<br>Actorgrade<br>athway<br>Actorary synapse<br>Actorary synapse   | KEGG PATHWAYKEGG PATHWAY <td>hsa04540         hsa04970         hsa05215         hsa05032         hsa01100         hsa04713         hsa04713         hsa04972         hsa04972         hsa04972         hsa04914         hsa04010         hsa04914         hsa04913         hsa04914         hsa04913         hsa04914         hsa041522         hsa04723         hsa04724         hsa04725         hsa04723</td> 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infection<br>Artloopenesis<br>Artangenesis<br>Artangenesis<br>Artangenesis<br>Artangenesis<br>Artangenesis<br>Artangenesis<br>Artangenesis<br>Artangenesis<br>Artangenesis<br>Artangenesis<br>Artangenesis<br>Artangenesis<br>Artangenesis<br>Artangenesis<br>Artangenesis<br>Artangenesis<br>Artangenesis<br>Artangenesis<br>Artangenesis<br>Artangenesis<br>Artangenesis<br>Artangenesis<br>Artangenesis<br>Artangenesis<br>Artangenesis<br>Artangenesis<br>Artangenesis<br>Artangenesis<br>Artangenesis<br>Artangenesis<br>Artangenesis<br>Artangenesis<br>Artangenesis<br>Artangenesis<br>Artangenesis<br>Artangenesis<br>Artangenesis<br>Artangenesis<br>Artangenesis<br>Artangenesis<br>Artangenesis<br>Artangenesis<br>Artangenesis<br>Artangenesis<br>Artangenesis<br>Artangenesis<br>Artangenesis<br>Artangenesis<br>Artangenesis<br>Artangenesis<br>Artangenesis<br>Artangenesis<br>Artangenesis<br>Artangenesis<br>Artangenesis<br>Artangenesis<br>Artangenesis<br>Artangenesis<br>Artangenesis<br>Artangenesis<br>Artangenesis<br>Artangenesis<br>Artangenesis<br>Artangenesis<br>Artangenesis<br>Artangenesis<br>Artangenesis<br>Artangenesis<br>Artangenesis<br>Artangenesis<br>Artangenesis<br>Artangenesis<br>Artangenesis<br>Artangenesis<br>Artangenesis<br>Artangenesis<br>Artangenesis<br>Artangenesis<br>Artangenesis<br>Artangenesis<br>Artangenesis<br>Artangenesis<br>Artangenesis<br>Artangenesis<br>Artangenesis<br>Artangenesis<br>Artangenesis<br>Artangenesis<br>Artangenesis<br>Artangenesis<br>Artangenesis<br>Artangenesis<br>Artangenesis<br>Artangenesis<br>Artangenesis<br>Artangenesis<br>Artangenesis<br>Artangenesis<br>Artangenesis<br>A   | KEGG PATHWAYKEGG PATHWAY <td>hsa04540         hsa04970         hsa05215         hsa03015         hsa01100         hsa04713         hsa04972         hsa04972         hsa04972         hsa04972         hsa04972         hsa04972         hsa04713         hsa04713         hsa04972         hsa04914         hsa04916         hsa041522         hsa04723         hsa04724         hsa04725         hsa04725         hsa04723         hsa04723         hsa04724         hsa04725         hsa04726         hsa04728         hsa04728         hsa04120</td> <td>1<br/>1<br/>1<br/>1<br/>1<br/>1<br/>1<br/>1<br/>1<br/>1<br/>1<br/>1<br/>1<br/>1</td> <td><ul> <li>88</li> <li>90</li> <li>91</li> <li>91</li> <li>91</li> <li>1240</li> <li>95</li> <li>96</li> <li>96</li> <li>97</li> <li>257</li> <li>99</li> <li>259</li> <li>100</li> <li>101</li> <li>103</li> <li>104</li> <li>105</li> <li>107</li> <li>273</li> <li>113</li> <li>114</li> <li>105</li> <li>107</li> <li>273</li> <li>113</li> <li>114</li> <li>105</li> 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<td>http://www.genome.jp/kegg-bin/show<br/>pathway?hsa04540/hsa:5582%09red<br/>http://www.genome.jp/kegg-bin/show<br/>pathway?hsa05032/hsa:5582%09red<br/>http://www.genome.jp/kegg-bin/show<br/>pathway?hsa05032/hsa:5582%09red<br/>http://www.genome.jp/kegg-bin/show<br/>pathway?hsa03015/hsa:55110%09red/<br/>hsa:427%09red/hsa:5613%09red/<br/>hsa:276%09red/hsa:5613%09red/<br/>hsa:276%09red/hsa:3032%09red/<br/>hsa:276%09red/hsa:5613%09red/<br/>hsa:204%09red/hsa:582%09red<br/>http://www.genome.jp/kegg-bin/show<br/>pathway?hsa04713/hsa:5582%09red<br/>http://www.genome.jp/kegg-bin/show<br/>pathway?hsa04713/hsa:5582%09red<br/>http://www.genome.jp/kegg-bin/show<br/>pathway?hsa04972/hsa:5582%09red<br/>http://www.genome.jp/kegg-bin/show<br/>pathway?hsa04916/hsa:5582%09red<br/>http://www.genome.jp/kegg-bin/show<br/>pathway?hsa04916/hsa:5582%09red<br/>http://www.genome.jp/kegg-bin/show<br/>pathway?hsa04916/hsa:5582%09red<br/>http://www.genome.jp/kegg-bin/show<br/>pathway?hsa04116/hsa:5582%09red<br/>http://www.genome.jp/kegg-bin/show<br/>pathway?hsa041522/hsa:595%09red<br/>http://www.genome.jp/kegg-bin/show<br/>pathway?hsa04156/hsa:5582%09red<br/>http://www.genome.jp/kegg-bin/show<br/>pathway?hsa04156/hsa:5582%09red<br/>http://www.genome.jp/kegg-bin/show<br/>pathway?hsa04156/hsa:5582%09red<br/>http://www.genome.jp/kegg-bin/show<br/>pathway?hsa04156/hsa:5582%09red<br/>http://www.genome.jp/kegg-bin/show<br/>pathway?hsa0470/hsa:5582%09red<br/>http://www.genome.jp/kegg-bin/show<br/>pathway?hsa0470/hsa:5582%09red<br/>http://www.genome.jp/kegg-bin/show<br/>pathway?hsa0472/hsa:5582%09red<br/>http://www.genome.jp/kegg-bin/show<br/>pathway?hsa0472/hsa:5582%09red<br/>http://www.genome.jp/kegg-bin/show<br/>pathway?hsa04472/hsa:5582%09red<br/>http://www.genome.jp/kegg-bin/show<br/>pathway?hsa0472/hsa:5582%09red<br/>http://www.genome.jp/kegg-bin/show<br/>pathway?hsa0472/hsa:5582%09red<br/>http://www.genome.jp/kegg-bin/show<br/>pathway?hsa0472/hsa:5582%09red<br/>http://www.genome.jp/kegg-bin/show<br/>pathway?hsa0472/hsa:5582%09red<br/>http://www.genome.jp/kegg-bin/show<br/>pathway?hsa0472/hsa:5582%09red<br/>http://www.genome.jp/kegg-bin/show<br/>pathway?hsa0472/hsa:5582%09red<br/>http://www.genome.jp/kegg-bin/show<br/>pathway?hsa0472/hsa:5582%09red<br/>http://www.genome.jp/kegg-bin/s</td>  
   
   
   
   
   | hsa04540         hsa04970         hsa05215         hsa03015         hsa01100         hsa04713         hsa04972         hsa04972         hsa04972         hsa04972         hsa04972         hsa04972         hsa04713         hsa04713         hsa04972         hsa04914         hsa04916         hsa041522         hsa04723         hsa04724         hsa04725         hsa04725         hsa04723         hsa04723         hsa04724         hsa04725         hsa04726         hsa04728         hsa04728         hsa04120  
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| Agap junction<br>Balivary secretion<br>Prostate cancer<br>Arrostate cancer<br>Arrophine addiction<br>INNA surveillance<br>bathway<br>Actabolic pathways<br>Actabolic pathways<br>Actabolic pathways<br>Actabolic pathways<br>Actabolis pathway<br>Progesterone-mediated<br>oocyte maturation<br>APK signaling pathway<br>Anoebiasis<br>Alanogenesis<br>Alanogenesis<br>Alanogenesis<br>Actrograde<br>Indocannabinoid signaling<br>Prosphatidylinositol<br>ignaling system<br>AGE-RAGE signaling<br>athway in diabetic<br>complications<br>Choline metabolism in<br>ancer<br>AIF-1 signaling pathway<br>Actionergic synapse<br>Choline metabolism in<br>ancer<br>AlF-1 signaling pathway<br>Actionergic synapse<br>Cholinergic synapse<br>Cholinergic synapse<br>Actionation<br>Alf-1 signaling pathway<br>Actionation<br>Alf-1 signaling pathway<br>Alf-1 signaling pathw   | KEGG PATHWAYKEGG PATHWAY <td>hsa04540           hsa04970           hsa05215           hsa05032           hsa01100           hsa04713           hsa04972           hsa04972           hsa04972           hsa04972           hsa04914           hsa04914           hsa04912           hsa04914           hsa04914           hsa04914           hsa04916           hsa04723           hsa04724           hsa04725           hsa04723           hsa04724           hsa04725           hsa04725           hsa04724           hsa04725           hsa04725           hsa04726           hsa04728           hsa04728           hsa04112           hsa04520           hsa04520           hsa04520           hsa04520           hsa04520           <t< td=""><td>1         <td< td=""><td><ul> <li>88</li> <li>90</li> <li>91</li> <li>91</li> <li>91</li> <li>1240</li> <li>95</li> <li>96</li> <li>97</li> <li>257</li> <li>99</li> <li>259</li> <li>100</li> <li>101</li> <li>103</li> <li>104</li> <li>105</li> <li>107</li> <li>273</li> <li>113</li> <li>115</li> <li>120</li> <li>120</li> <li>121</li> <li>121</li> <li>120</li> <li>123</li> <li>125</li> <li>129</li> <li>130</li> <li>137</li> 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| Bap junction         Baivary secretion         Prostate cancer         Aorphine addiction         Prostate cancer         Aorphine addiction         InRNA surveillance<br>bathway         Actabolic pathways         Actabolic pathways         Actabolic pathways         Actabolic pathways         Circadian entrainment         Pancreatic secretion         Bay cerophospholipid<br>netabolism         Progesterone-mediated<br>oocyte maturation         APK signaling pathway         Actocarine resistance         ATLV-1 infection         Amoebiasis         Actograde<br>indocarnabinoid signaling<br>oathway in diabetic<br>oomplications         Actograde<br>indocannabinoid signaling<br>oathway in diabetic<br>oomplications         Choline metabolism in<br>ancer         AGE-RAGE signaling<br>oathway         Actorgrade signaling<br>oathway         Actorgrade signaling<br>oathway         Actorgrade signaling<br>oathway         Actorgrade signaling<br>oathway         Actorgrade signaling<br>oathway         Actorgrade signaling pathway         Cooline metabolism in<br>ancer         Altroprotosis         Cacell receptor signaling<br>oathway         Actorgrade signaling pathway         Cooline regis synapse   | KEGG PATHWAYKEGG PATHWAY <td>hsa04540         hsa04970         hsa05215         hsa05032         hsa01100         hsa04713         hsa04972         hsa04972         hsa04972         hsa04914         hsa04912         hsa04010         hsa04914         hsa04912         hsa04914         hsa04916         hsa04916         hsa04723         hsa04724         hsa04725         hsa04723         hsa04724         hsa04723         hsa04724         hsa04723         hsa04723         hsa04724         hsa04723         hsa04724         hsa04723         hsa04300</td> <td>1         1      <tr td=""> <!--</td--><td><ul> <li>88</li> <li>90</li> <li>91</li> <li>91</li> <li>91</li> <li>1240</li> <li>95</li> <li>96</li> <li>97</li> <li>257</li> <li>99</li> <li>259</li> <li>100</li> <li>101</li> 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hsa04912           hsa04916           hsa041522           hsa04723           hsa04723           hsa04723           hsa04723           hsa04723           hsa04723           hsa04723           hsa04723           hsa044723           hsa04723           hsa04723           hsa04723           hsa04723           hsa04724           hsa04725           hsa04724           hsa04723           hsa04724           hsa04300           hsa044723           hsa044724           hsa04300           hsa044530           hsa044530           hsa044530           hsa044530           hsa044530           hsa044530           hsa044360   <!--</td--><td></td><td><ul> <li>88</li> <li>90</li> <li>91</li> <li>91</li> <li>91</li> <li>1240</li> <li>95</li> <li>96</li> <li>97</li> <li>257</li> <li>99</li> <li>259</li> <li>100</li> <li>101</li> <li>101</li> <li>101</li> <li>103</li> <li>104</li> <li>105</li> <li>107</li> <li>273</li> <li>113</li> <li>113</li> <li>115</li> <li>120</li> <li>120</li> <li>123</li> <li>125</li> 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<li>101&lt;</li></ul></td><td>0.3975170.401350.4077370.4077370.4124110.4210980.4230910.4235950.4325950.4311580.4373780.4373780.4364540.4364540.4373780.4373780.4363610.43637380.4405790.4405790.4373780.4373780.4373780.4405790.4405790.4333030.45300740.4776080.4776080.4776080.4776080.4980740.5065930.5122030.5232210.5243250.537350.537350.537350.537350.5390520.5393620.6397130.6397130.6397130.6397130.6397130.6397130.6417690.6397130.6417690.6417690.6417690.6417690.6417690.6417690.6417690.6417690.6417690.6417690.6417690.6417690.6417690.6417690.6417690.641769</td><td>0.5838580.6385980.</td><td>ENSGOUOUI26583ENSGOUOUI10092ENSGOUOUI14334ENSGOUOUI14334ENSGOUOUI14334ENSGOUOUI14334ENSGOUOUI14334ENSGOUOUI14334ENSGOUOUI14334ENSGOUOUI14334ENSGOUOUI14334ENSGOUOUI126583ENSGOUOUI126583ENSGOUOUI126583ENSGOUOUI126583ENSGOUOUI2</td><td>http://www.genome.jp/kegg-bin/show<br/>pathway?hsa0450/hsa:5582%09red<br/>http://www.genome.jp/kegg-bin/show<br/>pathway?hsa05215/hsa:5582%09red<br/>http://www.genome.jp/kegg-bin/show<br/>pathway?hsa0302/hsa:5582%09red<br/>http://www.genome.jp/kegg-bin/show<br/>pathway?hsa01100/hsa:55110%0%ped<br/>http://www.genome.jp/kegg-bin/show<br/>pathway?hsa01100/hsa:55110%0%ped<br/>http://www.genome.jp/kegg-bin/show<br/>pathway?hsa01100/hsa:562%09red/<br/>hsa:5500%09red/hsa:563%09red/<br/>hsa:5500%09red/hsa:562%09red/<br/>hsa:5500%09red/hsa:552%09red/<br/>hsa:5550%09red/hsa:552%09red/<br/>hsa:5550%09red/hsa:552%09red/<br/>hsa:5550%09red/hsa:552%09red/<br/>hsa:5550%09red/hsa:552%09red/<br/>http://www.genome.jp/kegg-bin/show<br/>pathway?hsa04713/hsa:5582%09red<br/>http://www.genome.jp/kegg-bin/show<br/>pathway?hsa04914/hsa:4085%09red/<br/>http://www.genome.jp/kegg-bin/show<br/>pathway?hsa04914/hsa:4085%09red/<br/>http://www.genome.jp/kegg-bin/show<br/>pathway?hsa05166/hsa:5582%09red<br/>http://www.genome.jp/kegg-bin/show<br/>pathway?hsa05166/hsa:5582%09red<br/>http://www.genome.jp/kegg-bin/show<br/>pathway?hsa0516/hsa:5582%09red<br/>http://www.genome.jp/kegg-bin/show<br/>pathway?hsa0516/hsa:5582%09red<br/>http://www.genome.jp/kegg-bin/show<br/>pathway?hsa0414/hsa:5582%09red<br/>http://www.genome.jp/kegg-bin/show<br/>pathway?hsa04750/hsa:5582%09red<br/>http://www.genome.jp/kegg-bin/show<br/>pathway?hsa04750/hsa:5582%09red<br/>http://www.genome.jp/kegg-bin/show<br/>pathway?hsa04723/hsa:5582%09red<br/>http://www.genome.jp/kegg-bin/show<br/>pathway?hsa04723/hsa:5582%09red<br/>http://www.genome.jp/kegg-bin/show<br/>pathway?hsa04723/hsa:5582%09red<br/>http://www.genome.jp/kegg-bin/show<br/>pathway?hsa04726/hsa:5582%09red<br/>http://www.genome.jp/kegg-bin/show<br/>pathway?hsa04726/hsa:5582%09red<br/>http://www.genome.jp/kegg-bin/show<br/>pathway?hsa04726/hsa:5582%09red<br/>http://www.genome.jp/kegg-bin/show<br/>pathway?hsa04726/hsa:5582%09red<br/>http://www.genome.jp/kegg-bin/show<br/>pathway?hsa04726/hsa:5582%09red<br/>http://www.genome.jp/kegg-bin/show<br/>pathway?hsa04726/hsa:5582%09red<br/>http://www.genome.jp/kegg-bin/show<br/>pathway?hsa04726/hsa:5582%09red<br/>http://www.genome.jp/kegg-bin/show<br/>pathway?hsa04516/hsa:5582%09red<br/>http://www.genome.jp/kegg-bi</td></td></tr><tr><td>Aap junction<br/>Calivary secretion<br/>Prostate cancer<br/>Aorphine
addiction<br/>ARNA surveillance<br/>athway<br/>Aetabolic pathways<br/>Actabolic pathways<br/>Actabolic pathways<br/>Circadian entrainment<br/>Pancreatic secretion<br/>Circadian entrainment<br/>Pancreatic secretion<br/>Circadian entrainment<br/>Pancreatic secretion<br/>Allocations<br/>Progesterone-mediated<br/>pocyte maturation<br/>APK signaling pathway<br/>Circocrine resistance<br/>ALLV-I infection<br/>AMPK signaling pathway<br/>Actaoogenesis<br/>Allanogenesis<br/>Allanogenesis<br/>Allanogenesis<br/>Circoline metabolism in<br/>ancer<br/>AlF-1 signaling pathway<br/>ActororRNAs in cancer<br/>AllF-1 signaling pathway<br/>ActororRNAs in cancer<br/>Circolinergic synapse<br/>Cholinergic synapse<br/>Cholinergic</td><td>REGG PATHWAYREGG PATHWAY<td>hsa04540           hsa04970           hsa05215           hsa05032           hsa01100           hsa04713           hsa04713           hsa04972           hsa04912           hsa04912           hsa04912           hsa04912           hsa04914           hsa04912           hsa04916           hsa041522           hsa04723           hsa04723           hsa04723           hsa04723           hsa04723           hsa04723           hsa04723           hsa04723           hsa044723           hsa04723           hsa04723           hsa04723           hsa04723           hsa04724           hsa04725           hsa04724           hsa04723           hsa04724           hsa04300           hsa044723           hsa044724           hsa04300           hsa044530           hsa044530           hsa044530           hsa044530           hsa044530           hsa044530           hsa044360   <!--</td--><td></td><td><ul> <li>88</li> <li>90</li> <li>91</li> <li>91</li> <li>91</li> <li>1240</li> <li>95</li> <li>96</li> <li>97</li> <li>257</li> <li>99</li> <li>259</li> <li>100</li> <li>101</li> <li>101</li> <li>101</li> <li>103</li> <li>104</li> <li>105</li> <li>107</li> <li>273</li> <li>113</li> <li>113</li> <li>115</li> <li>120</li> <li>120</li> <li>123</li> <li>125</li> 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<tr><td>Aap junction         Aaivary secretion         Prostate cancer         Aorphine addiction         Arrostate cancer         Aorphine addiction         Arrostate cancer         Aorphine addiction         Arrostate cancer         Arrostatidy in diabetic         Arrostatidy in diabetic         Arrostanat</td><td>REGG PATHWAYREGG PATHWAY<td>hsa04540         hsa04970         hsa05215         hsa01100         hsa01100         hsa04713         hsa04713         hsa04972         hsa04972         hsa041522         hsa04910         hsa041522         hsa04914         hsa04916         hsa04152         hsa04470         hsa04723         hsa04723         hsa04723         hsa04723         hsa04723         hsa04723         hsa04723         hsa044723         hsa04723         hsa04723         hsa04723         hsa04723         hsa04724         hsa04725         hsa04723         hsa04724         hsa04725         hsa04724         hsa04150         hsa04300         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| App junction<br>Salivary secretion<br>Prostate cancer<br>Arrophine addiction<br>PRNA surveillance<br>bathway<br>Actabolic pathways<br>Actabolic pathways<br>Actabolic pathways<br>Actabolic pathways<br>Actabolic pathways<br>Actabolic pathways<br>Actabolic pathways<br>Actabolic secretion<br>App of signaling pathway<br>APK signaling pathway<br>Arrogesterone-mediator<br>equation of TRP channels<br>Actrograde<br>indocannabinoid signaling<br>ACE-RAGE signaling<br>bathway in diabetic<br>complications<br>Choline metabolism in<br>ancer<br>Arrograde<br>indocannabinoid signaling<br>pathway in diabetic<br>complications<br>Choline metabolism in<br>ancer<br>AIF-1 signaling pathway<br>Actrograde<br>indignaling system<br>AGE-RAGE signaling<br>bathway in diabetic<br>complications<br>Choline metabolism in<br>ancer<br>AlF-1 signaling pathway<br>Actrograde<br>cocyte meiosis<br>Actrograde<br>Actrograde<br>Actrograde<br>Actrograde<br>Actrograde<br>andocannabinoid 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      | Aap junction<br>Salivary secretion<br>Prostate cancer<br>Aorphine addiction<br>PRNA surveillance<br>bathway<br>Aetabolic pathways<br>Aetabolic pathways<br>Aetabolic pathways<br>Aetabolic pathways<br>Aetabolis pathway<br>Progesterone-mediated<br>ooyte maturation<br>APK signaling pathway<br>Endocrine resistance<br>ATLV-I infection<br>APK signaling pathway<br>Aetanogenesis<br>Aflammatory mediator<br>egulation of TRP channels<br>Retrograde<br>indocannabinoid signaling<br>Phosphatidylinositol<br>ignaling system<br>AGE-RAGE signaling<br>athway in diabetic<br>complications<br>Choline metabolism in<br>ancer<br>AIF-1 signaling pathway<br>ic cell receptor signaling<br>athway<br>AicroRNAs in cancer<br>Actionargic synapse<br>Cholinergic synapse<br>Cholinergic synapse<br>Cholinergic synapse<br>Cholinergic synapse<br>Cholinergic synapse<br>Cholinergic synapse<br>Autora time<br>Autora time<br>Auto | REGG PATHWAYREGG PATHWAY <td>hsa04540           hsa04970           hsa05215           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          hsa01100           hsa04713           hsa04972           hsa04972           hsa04912           hsa04912           hsa04912           hsa04912           hsa04912           hsa04914           hsa04912           hsa04916           hsa04723           hsa04724           hsa04725           hsa04724           hsa04723           hsa04724           hsa04112           hsa04313           hsa044530           hsa044530           hsa04330           hsa04330           hsa04330</td> <td></td> <td><ul> <li>88</li> <li>90</li> <li>91</li> <li>91</li> <li>91</li> <li>1240</li> <li>95</li> <li>96</li> <li>97</li> <li>257</li> <li>99</li> <li>259</li> <li>100</li> <li>101</li> <li>101</li> <li>101</li> <li>101</li> <li>101</li> <li>101</li> <li>103</li> <li>104</li> <li>105</li> <li>107</li> <li>273</li> <li>113</li> <li>115</li> <li>120</li> <li>120</li> <li>121</li> <li>130</li> <li>142</li> <li>153</li> <li>155</li> <li>160</li> <li>137</li> <li>138</li> <li>139</li> <li>142</li> <li>153</li> 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<tr><td>Aap junction         Aaivary secretion         Prostate cancer         Aorphine addiction         Arrostate cancer         Aorphine addiction         Arrostate cancer         Aorphine addiction         Arrostate cancer         Arrostatidy in diabetic         Arrostatidy in diabetic         Arrostanat</td><td>REGG PATHWAYREGG PATHWAY<td>hsa04540         hsa04970         hsa05215         hsa01100         hsa01100         hsa04713         hsa04713         hsa04972         hsa04972         hsa041522         hsa04910         hsa041522         hsa04914         hsa04916         hsa04152         hsa04470         hsa04723         hsa04723         hsa04723         hsa04723         hsa04723         hsa04723         hsa04723         hsa044723         hsa04723         hsa04723         hsa04723         hsa04723         hsa04724         hsa04725         hsa04723         hsa04724         hsa04725         hsa04724         hsa04150         hsa04300         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<li>101&lt;</li></ul></td><td>0.3975170.401350.4077370.4077370.4124110.4210980.4230910.4235950.4325950.4311580.4373780.4373780.4364540.4364540.4373780.4373780.4363610.43637380.4405790.4405790.4373780.4373780.4373780.4405790.4405790.4333030.45300740.4776080.4776080.4776080.4776080.4980740.5065930.5122030.5232210.5243250.537350.537350.537350.537350.5390520.5393620.6397130.6397130.6397130.6397130.6397130.6397130.6417690.6397130.6417690.6417690.6417690.6417690.6417690.6417690.6417690.6417690.6417690.6417690.6417690.6417690.6417690.6417690.6417690.641769</td><td>0.5838580.6385980.</td><td>ENSGOUOUI26583ENSGOUOUI10092ENSGOUOUI14334ENSGOUOUI14334ENSGOUOUI14334ENSGOUOUI14334ENSGOUOUI14334ENSGOUOUI14334ENSGOUOUI14334ENSGOUOUI14334ENSGOUOUI14334ENSGOUOUI126583ENSGOUOUI126583ENSGOUOUI126583ENSGOUOUI126583ENSGOUOUI2</td><td>http://www.genome.jp/kegg-bin/show<br/>pathway?hsa0450/hsa:5582%09red<br/>http://www.genome.jp/kegg-bin/show<br/>pathway?hsa05215/hsa:5582%09red<br/>http://www.genome.jp/kegg-bin/show<br/>pathway?hsa0302/hsa:5582%09red<br/>http://www.genome.jp/kegg-bin/show<br/>pathway?hsa01100/hsa:55110%0%ped<br/>http://www.genome.jp/kegg-bin/show<br/>pathway?hsa01100/hsa:55110%0%ped<br/>http://www.genome.jp/kegg-bin/show<br/>pathway?hsa01100/hsa:562%09red/<br/>hsa:5500%09red/hsa:563%09red/<br/>hsa:5500%09red/hsa:562%09red/<br/>hsa:5500%09red/hsa:552%09red/<br/>hsa:5550%09red/hsa:552%09red/<br/>hsa:5550%09red/hsa:552%09red/<br/>hsa:5550%09red/hsa:552%09red/<br/>hsa:5550%09red/hsa:552%09red/<br/>http://www.genome.jp/kegg-bin/show<br/>pathway?hsa04713/hsa:5582%09red<br/>http://www.genome.jp/kegg-bin/show<br/>pathway?hsa04914/hsa:4085%09red/<br/>http://www.genome.jp/kegg-bin/show<br/>pathway?hsa04914/hsa:4085%09red/<br/>http://www.genome.jp/kegg-bin/show<br/>pathway?hsa05166/hsa:5582%09red<br/>http://www.genome.jp/kegg-bin/show<br/>pathway?hsa05166/hsa:5582%09red<br/>http://www.genome.jp/kegg-bin/show<br/>pathway?hsa0516/hsa:5582%09red<br/>http://www.genome.jp/kegg-bin/show<br/>pathway?hsa0516/hsa:5582%09red<br/>http://www.genome.jp/kegg-bin/show<br/>pathway?hsa0414/hsa:5582%09red<br/>http://www.genome.jp/kegg-bin/show<br/>pathway?hsa04750/hsa:5582%09red<br/>http://www.genome.jp/kegg-bin/show<br/>pathway?hsa04750/hsa:5582%09red<br/>http://www.genome.jp/kegg-bin/show<br/>pathway?hsa04723/hsa:5582%09red<br/>http://www.genome.jp/kegg-bin/show<br/>pathway?hsa04723/hsa:5582%09red<br/>http://www.genome.jp/kegg-bin/show<br/>pathway?hsa04723/hsa:5582%09red<br/>http://www.genome.jp/kegg-bin/show<br/>pathway?hsa04726/hsa:5582%09red<br/>http://www.genome.jp/kegg-bin/show<br/>pathway?hsa04726/hsa:5582%09red<br/>http://www.genome.jp/kegg-bin/show<br/>pathway?hsa04726/hsa:5582%09red<br/>http://www.genome.jp/kegg-bin/show<br/>pathway?hsa04726/hsa:5582%09red<br/>http://www.genome.jp/kegg-bin/show<br/>pathway?hsa04726/hsa:5582%09red<br/>http://www.genome.jp/kegg-bin/show<br/>pathway?hsa04726/hsa:5582%09red<br/>http://www.genome.jp/kegg-bin/show<br/>pathway?hsa04726/hsa:5582%09red<br/>http://www.genome.jp/kegg-bin/show<br/>pathway?hsa04516/hsa:5582%09red<br/>http://www.genome.jp/kegg-bi</td></td></tr> 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hsa04912           hsa04916           hsa041522           hsa04723           hsa04723           hsa04723           hsa04723           hsa04723           hsa04723           hsa04723           hsa04723           hsa044723           hsa04723           hsa04723           hsa04723           hsa04723           hsa04724           hsa04725           hsa04724           hsa04723           hsa04724           hsa04300           hsa044723           hsa044724           hsa04300           hsa044530           hsa044530           hsa044530           hsa044530           hsa044530           hsa044530           hsa044360   <!--</td--><td></td><td><ul> <li>88</li> <li>90</li> <li>91</li> <li>91</li> <li>91</li> <li>1240</li> <li>95</li> <li>96</li> <li>97</li> <li>257</li> <li>99</li> <li>259</li> <li>100</li> <li>101</li> <li>101</li> <li>101</li> <li>103</li> <li>104</li> <li>105</li> <li>107</li> <li>273</li> <li>113</li> <li>113</li> <li>115</li> <li>120</li> <li>120</li> <li>123</li> <li>125</li> <li>120</li> <li>123</li> <li>125</li> <li>129</li> <li>130</li> <li>137</li> <li>138</li> <li>139</li> <li>142</li> <li>153</li> <li>160</li> <li>177</li> <li>138</li> <li>139</li> <li>142</li> <li>153</li> <li>160</li> <li>177</li> <li>138</li> <li>139</li> <li>142</li> <li>153</li> <li>160</li> <li>177</li> <li>178</li> <li>179</li> 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      | App junction<br>Salivary secretion<br>Prostate cancer<br>Arrophine addiction<br>PRNA surveillance<br>bathway<br>Actabolic pathways<br>Actabolic pathways<br>Actabolic pathways<br>Actabolic pathways<br>Actabolic pathways<br>Actabolic pathways<br>Actabolic pathways<br>Actabolic secretion<br>App of signaling pathway<br>APK signaling pathway<br>Arrogesterone-mediator<br>equation of TRP channels<br>Actrograde<br>indocannabinoid signaling<br>ACE-RAGE signaling<br>bathway in diabetic<br>complications<br>Choline metabolism in<br>ancer<br>Arrograde<br>indocannabinoid signaling<br>pathway in diabetic<br>complications<br>Choline metabolism in<br>ancer<br>AIF-1 signaling pathway<br>Actrograde<br>indignaling system<br>AGE-RAGE signaling<br>bathway in diabetic<br>complications<br>Choline metabolism in<br>ancer<br>AlF-1 signaling pathway<br>Actrograde<br>cocyte meiosis<br>Actrograde<br>Actrograde<br>Actrograde<br>Actrograde<br>Actrograde<br>andocannabinoid signaling<br>bathway<br>Actrograde<br>andocannabinoid signaling<br>bathway<br>Actrograde<br>andocannabinoid signaling<br>athway<br>Actrograde<br>andocannabinoid signaling<br>athway<br>Actrograde<br>Actrograde<br>and 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     hsa01100           hsa04713           hsa04972           hsa04972           hsa04912           hsa04912           hsa04912           hsa04912           hsa04912           hsa04914           hsa04912           hsa04916           hsa04723           hsa04724           hsa04725           hsa04724           hsa04723           hsa04724           hsa04112           hsa04313           hsa044530           hsa044530           hsa04330           hsa04330           hsa04330</td> <td></td> <td><ul> <li>88</li> <li>90</li> <li>91</li> <li>91</li> <li>91</li> <li>1240</li> <li>95</li> <li>96</li> <li>97</li> <li>257</li> <li>99</li> <li>259</li> <li>100</li> <li>101</li> <li>101</li> <li>101</li> <li>101</li> <li>101</li> <li>101</li> <li>103</li> <li>104</li> <li>105</li> <li>107</li> <li>273</li> <li>113</li> <li>115</li> <li>120</li> <li>120</li> <li>121</li> <li>130</li> <li>142</li> <li>153</li> <li>155</li> <li>160</li> <li>137</li> <li>138</li> <li>139</li> <li>142</li> <li>153</li> 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| App junction<br>Salivary secretion<br>Prostate cancer<br>Arrophine addiction<br>PRNA surveillance<br>bathway<br>Actabolic pathways<br>Actabolic pathways<br>Actabolic pathways<br>Actabolic pathways<br>Actabolic pathways<br>Actabolic pathways<br>Actabolic pathways<br>Actabolic secretion<br>App of signaling pathway<br>APK signaling pathway<br>Arrogesterone-mediator<br>equation of TRP channels<br>Actrograde<br>indocannabinoid signaling<br>ACE-RAGE signaling<br>bathway in diabetic<br>complications<br>Choline metabolism in<br>ancer<br>Arrograde<br>indocannabinoid signaling<br>pathway in diabetic<br>complications<br>Choline metabolism in<br>ancer<br>AIF-1 signaling pathway<br>Actrograde<br>indignaling system<br>AGE-RAGE signaling<br>bathway in diabetic<br>complications<br>Choline metabolism in<br>ancer<br>AlF-1 signaling pathway<br>Actrograde<br>cocyte meiosis<br>Actrograde<br>Actrograde<br>Actrograde<br>Actrograde<br>Actrograde<br>andocannabinoid signaling<br>bathway<br>Actrograde<br>andocannabinoid signaling<br>bathway<br>Actrograde<br>andocannabinoid signaling<br>athway<br>Actrograde<br>andocannabinoid signaling<br>athway<br>Actrograde<br>Actrograde<br>and 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| Sap junction<br>Salivary secretion<br>Prostate cancer<br>Aorphine addiction<br>mRNA surveillance<br>boathway<br>Ateabolic pathways<br>Ateabolic pathways<br>Ateabolic pathways<br>Actabolic pathways<br>Circadian entrainment<br>Progesterone-mediated<br>bocyte maturation<br>APK signaling pathway<br>Endocrine resistance<br>ATLV-I infection<br>Amoebiasis<br>Aelanogenesis<br>Adelanogenesis<br>Affammatory mediator<br>egulation of TRP channels<br>Actrograde<br>andocannabinoid signaling<br>Phosphatidylinositol<br>ignaling system<br>AGE – RAGE signaling<br>athway in diabetic<br>complications<br>Choline metabolism in<br>ancer<br>AITL-1 signaling pathway<br>ActoroRNAs in cancer<br>Cholinergic synapse<br>Cholinergic synapse<br>Choli  | REGG PATHWAYREGG PATHWAY <td>hsa04540         hsa04970         hsa05215         hsa05032         hsa01100         hsa04713         hsa04972         hsa04972         hsa04972         hsa04914         hsa04912         hsa04010         hsa041522         hsa04152         hsa04152         hsa04723         hsa04724         hsa04725         hsa04723         hsa04724         hsa044726         hsa044726         hsa04723         hsa044724         hsa044726         hsa044530</td> <td></td> <td><ul> <li>88</li> <li>90</li> <li>91</li> <li>91</li> <li>91</li> <li>1240</li> <li>95</li> <li>96</li> <li>97</li> <li>257</li> <li>99</li> <li>259</li> <li>100</li> <li>101</li> <li>101</li> <li>101</li> <li>101</li> <li>101</li> <li>101</li> <li>101</li> <li>103</li> <li>104</li> <li>105</li> <li>107</li> <li>273</li> <li>113</li> <li>115</li> <li>120</li> <li>120</li> <li>123</li> <li>125</li> <li>129</li> <li>130</li> <li>137</li> <li>138</li> <li>139</li> <li>142</li> <li>153</li> <li>155</li> <li>160</li> </ul></td> <td>0.3975170.401350.4077370.4077370.4077370.4124110.4210980.4230910.4230910.42364540.4373780.4364540.4373780.4373780.4363060.4405790.4405790.4405790.4405790.4353030.4373780.4373780.430140.4303140.4405790.4405790.4405790.4532030.4532030.463060.4776080.4776080.4980740.50659360.5122030.5243210.5243210.5471160.5496960.537350.5843250.58</td> <td>0.5838580.6385980.6385980.6385980.6385980.6385980.645126</td> <td>ENSGOUODI26583ENSGOUODI10092ENSGOUODI26583ENSGOUODI39163ENSGOUODI39163SNSGOUODI16332ENSGOUODI126583ENSGOUODI26583ENSGOUODI126583ENSGOUODI265</td> <td>http://www.genome.jp/kegg-bin/show<br/>pathway?hsa04540/hsa:5582%09red<br/>http://www.genome.jp/kegg-bin/show<br/>pathway?hsa05215/hsa:5582%09red<br/>http://www.genome.jp/kegg-bin/show<br/>pathway?hsa03015/hsa:55810%09red<br/>http://www.genome.jp/kegg-bin/show<br/>pathway?hsa0315/hsa:55813%09red<br/>http://www.genome.jp/kegg-bin/show<br/>pathway?hsa01100/hsa:653%09red<br/>http://www.genome.jp/kegg-bin/show<br/>pathway?hsa04113/hsa:5582%09red<br/>http://www.genome.jp/kegg-bin/show<br/>pathway?hsa04713/hsa:5582%09red<br/>http://www.genome.jp/kegg-bin/show<br/>pathway?hsa04713/hsa:5582%09red<br/>http://www.genome.jp/kegg-bin/show<br/>pathway?hsa04713/hsa:5582%09red<br/>http://www.genome.jp/kegg-bin/show<br/>pathway?hsa04110/hsa:5500%09red<br/>http://www.genome.jp/kegg-bin/show<br/>pathway?hsa04110/hsa:5502%09red<br/>http://www.genome.jp/kegg-bin/show<br/>pathway?hsa04110/hsa:5502%09red<br/>http://www.genome.jp/kegg-bin/show<br/>pathway?hsa04110/hsa:5502%09red<br/>http://www.genome.jp/kegg-bin/show<br/>pathway?hsa04110/hsa:5582%09red<br/>http://www.genome.jp/kegg-bin/show<br/>pathway?hsa0516/hsa:5595%09red<br/>http://www.genome.jp/kegg-bin/show<br/>pathway?hsa0516/hsa:5582%09red<br/>http://www.genome.jp/kegg-bin/show<br/>pathway?hsa0516/hsa:5582%09red<br/>http://www.genome.jp/kegg-bin/show<br/>pathway?hsa04723/hsa:5582%09red<br/>http://www.genome.jp/kegg-bin/show<br/>pathway?hsa04723/hsa:5582%09red<br/>http://www.genome.jp/kegg-bin/show<br/>pathway?hsa04723/hsa:5582%09red<br/>http://www.genome.jp/kegg-bin/show<br/>pathway?hsa04723/hsa:5582%09red<br/>http://www.genome.jp/kegg-bin/show<br/>pathway?hsa04723/hsa:5582%09red<br/>http://www.genome.jp/kegg-bin/show<br/>pathway?hsa04723/hsa:5582%09red<br/>http://www.genome.jp/kegg-bin/show<br/>pathway?hsa04723/hsa:5582%09red<br/>http://www.genome.jp/kegg-bin/show<br/>pathway?hsa04723/hsa:5582%09red<br/>http://www.genome.jp/kegg-bin/show<br/>pathway?hsa04723/hsa:5582%09red<br/>http://www.genome.jp/kegg-bin/show<br/>pathway?hsa04723/hsa:5582%09red<br/>http://www.genome.jp/kegg-bin/show<br/>pathway?hsa04723/hsa:5582%09red<br/>http://www.genome.jp/kegg-bin/show<br/>pathway?hsa04723/hsa:5582%09red<br/>http://www.genome.jp/kegg-bin/show<br/>pathway?hsa04723/hsa:5582%09red<br/>http://www.genome.jp/kegg-bin/show<br/>path</td>  
   
   
   
   
   
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<li>155</li> <li>160</li> <li>177</li> </ul></td> <td>0.3975170.401350.4077370.4077370.4077370.4124110.4210980.4230910.4235950.4311580.4325950.43313780.4373780.4364540.4364540.4353030.4405790.4405790.4405790.4405790.4405790.4405790.4405790.4405790.4405790.4405790.45300740.45300740.4776080.4776080.4776080.4980740.5059360.5122030.5259360.5259360.537350.58403250.5890520.5890520.507350.587350.587350.587350.587350.5374550.5374550.5374550.5374550.5374550.5374550.5374550.5374550.5374550.5374550.5374550.5375550</td> <td>0.5838580.6385980.6385980.6385980.6385980.6385980.63706770.6706770.6706770.670677</td> <td>ENSGOUODI26583ENSGOUODI10092ENSGOUODI11092ENSGOUODI11190ENSGOUODI11193SNSGOUODI14333SNSGOUODI14332SNSGOUODI14032SNSGOUODI14032ENSGOUODI126583ENSGOUODI126583ENSGOUODI126583ENSGOUODI126583ENSGOUODI126583ENSGOUODI126583ENSGOUODI126583ENSGOUODI26583ENSGOUO</td> 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| Aap junction         Aaivary secretion         Prostate cancer         Aorphine addiction         Arrostate cancer         Aorphine addiction         Arrostate cancer         Aorphine addiction         Arrostate cancer         Arrostatidy in diabetic         Arrostatidy in diabetic         Arrostanat  | REGG PATHWAYREGG PATHWAY <td>hsa04540         hsa04970         hsa05215         hsa01100         hsa01100         hsa04713         hsa04713         hsa04972         hsa04972         hsa041522         hsa04910         hsa041522         hsa04914         hsa04916         hsa04152         hsa04470         hsa04723         hsa04723         hsa04723         hsa04723         hsa04723         hsa04723         hsa04723         hsa044723         hsa04723         hsa04723         hsa04723         hsa04723         hsa04724         hsa04725         hsa04723         hsa04724         hsa04725         hsa04724         hsa04150         hsa04300         hsa04300</td> <td>1<br/>1<br/>1<br/>1<br/>1<br/>1<br/>1<br/>1<br/>1<br/>1<br/>1<br/>1<br/>1<br/>1</td> <td><ul> <li>88</li> <li>90</li> <li>91</li> <li>91</li> <li>91</li> <li>1240</li> <li>95</li> <li>96</li> <li>97</li> <li>257</li> <li>99</li> <li>259</li> <li>100</li> <li>101</li> <li>101&lt;</li></ul></td> <td>0.3975170.401350.4077370.4077370.4124110.4210980.4230910.4235950.4325950.4311580.4373780.4373780.4364540.4364540.4373780.4373780.4363610.43637380.4405790.4405790.4373780.4373780.4373780.4405790.4405790.4333030.45300740.4776080.4776080.4776080.4776080.4980740.5065930.5122030.5232210.5243250.537350.537350.537350.537350.5390520.5393620.6397130.6397130.6397130.6397130.6397130.6397130.6417690.6397130.6417690.6417690.6417690.6417690.6417690.6417690.6417690.6417690.6417690.6417690.6417690.6417690.6417690.6417690.6417690.641769</td> <td>0.5838580.6385980.</td> <td>ENSGOUOUI26583ENSGOUOUI10092ENSGOUOUI14334ENSGOUOUI14334ENSGOUOUI14334ENSGOUOUI14334ENSGOUOUI14334ENSGOUOUI14334ENSGOUOUI14334ENSGOUOUI14334ENSGOUOUI14334ENSGOUOUI126583ENSGOUOUI126583ENSGOUOUI126583ENSGOUOUI126583ENSGOUOUI2</td> <td>http://www.genome.jp/kegg-bin/show<br/>pathway?hsa0450/hsa:5582%09red<br/>http://www.genome.jp/kegg-bin/show<br/>pathway?hsa05215/hsa:5582%09red<br/>http://www.genome.jp/kegg-bin/show<br/>pathway?hsa0302/hsa:5582%09red<br/>http://www.genome.jp/kegg-bin/show<br/>pathway?hsa01100/hsa:55110%0%ped<br/>http://www.genome.jp/kegg-bin/show<br/>pathway?hsa01100/hsa:55110%0%ped<br/>http://www.genome.jp/kegg-bin/show<br/>pathway?hsa01100/hsa:562%09red/<br/>hsa:5500%09red/hsa:563%09red/<br/>hsa:5500%09red/hsa:562%09red/<br/>hsa:5500%09red/hsa:552%09red/<br/>hsa:5550%09red/hsa:552%09red/<br/>hsa:5550%09red/hsa:552%09red/<br/>hsa:5550%09red/hsa:552%09red/<br/>hsa:5550%09red/hsa:552%09red/<br/>http://www.genome.jp/kegg-bin/show<br/>pathway?hsa04713/hsa:5582%09red<br/>http://www.genome.jp/kegg-bin/show<br/>pathway?hsa04914/hsa:4085%09red/<br/>http://www.genome.jp/kegg-bin/show<br/>pathway?hsa04914/hsa:4085%09red/<br/>http://www.genome.jp/kegg-bin/show<br/>pathway?hsa05166/hsa:5582%09red<br/>http://www.genome.jp/kegg-bin/show<br/>pathway?hsa05166/hsa:5582%09red<br/>http://www.genome.jp/kegg-bin/show<br/>pathway?hsa0516/hsa:5582%09red<br/>http://www.genome.jp/kegg-bin/show<br/>pathway?hsa0516/hsa:5582%09red<br/>http://www.genome.jp/kegg-bin/show<br/>pathway?hsa0414/hsa:5582%09red<br/>http://www.genome.jp/kegg-bin/show<br/>pathway?hsa04750/hsa:5582%09red<br/>http://www.genome.jp/kegg-bin/show<br/>pathway?hsa04750/hsa:5582%09red<br/>http://www.genome.jp/kegg-bin/show<br/>pathway?hsa04723/hsa:5582%09red<br/>http://www.genome.jp/kegg-bin/show<br/>pathway?hsa04723/hsa:5582%09red<br/>http://www.genome.jp/kegg-bin/show<br/>pathway?hsa04723/hsa:5582%09red<br/>http://www.genome.jp/kegg-bin/show<br/>pathway?hsa04726/hsa:5582%09red<br/>http://www.genome.jp/kegg-bin/show<br/>pathway?hsa04726/hsa:5582%09red<br/>http://www.genome.jp/kegg-bin/show<br/>pathway?hsa04726/hsa:5582%09red<br/>http://www.genome.jp/kegg-bin/show<br/>pathway?hsa04726/hsa:5582%09red<br/>http://www.genome.jp/kegg-bin/show<br/>pathway?hsa04726/hsa:5582%09red<br/>http://www.genome.jp/kegg-bin/show<br/>pathway?hsa04726/hsa:5582%09red<br/>http://www.genome.jp/kegg-bin/show<br/>pathway?hsa04726/hsa:5582%09red<br/>http://www.genome.jp/kegg-bin/show<br/>pathway?hsa04516/hsa:5582%09red<br/>http://www.genome.jp/kegg-bi</td>   
   
   
   
   
   
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| Aap junction<br>Calivary secretion<br>Prostate cancer<br>Aorphine addiction<br>ARNA surveillance<br>athway<br>Aetabolic pathways<br>Actabolic pathways<br>Actabolic pathways<br>Circadian entrainment<br>Pancreatic secretion<br>Circadian entrainment<br>Pancreatic secretion<br>Circadian entrainment<br>Pancreatic secretion<br>Allocations<br>Progesterone-mediated<br>pocyte maturation<br>APK signaling pathway<br>Circocrine resistance<br>ALLV-I infection<br>AMPK signaling pathway<br>Actaoogenesis<br>Allanogenesis<br>Allanogenesis<br>Allanogenesis<br>Circoline metabolism in<br>ancer<br>AlF-1 signaling pathway<br>ActororRNAs in cancer<br>AllF-1 signaling pathway<br>ActororRNAs in cancer<br>Circolinergic synapse<br>Cholinergic  | REGG PATHWAYREGG PATHWAY <td>hsa04540           hsa04970           hsa05215           hsa05032           hsa01100           hsa04713           hsa04713           hsa04972           hsa04912           hsa04912           hsa04912           hsa04912           hsa04914           hsa04912           hsa04916           hsa041522           hsa04723           hsa04723           hsa04723           hsa04723           hsa04723           hsa04723           hsa04723           hsa04723           hsa044723           hsa04723           hsa04723           hsa04723           hsa04723           hsa04724           hsa04725           hsa04724           hsa04723           hsa04724           hsa04300           hsa044723           hsa044724           hsa04300           hsa044530           hsa044530           hsa044530           hsa044530           hsa044530           hsa044530           hsa044360   <!--</td--><td></td><td><ul> <li>88</li> <li>90</li> <li>91</li> <li>91</li> <li>91</li> <li>1240</li> <li>95</li> <li>96</li> <li>97</li> <li>257</li> <li>99</li> <li>259</li> <li>100</li> <li>101</li> <li>101</li> <li>101</li> <li>103</li> <li>104</li> <li>105</li> <li>107</li> <li>273</li> <li>113</li> <li>113</li> <li>115</li> <li>120</li> <li>120</li> <li>123</li> 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