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HIGHLIGHTS

1. Solid and liquid fructose are differently absorbed by intestinal barrier
2. Solid and liquid fructose differently affects gut microbiota population
3. Altered microbiota and AGEs accumulation disrupt intestinal barrier
4. Solid fructose absorption is linked to increased hepatic inflammasome activation.

Fructose liquid and solid formulations differently affect gut integrity, microbiota composition and related liver toxicity: a comparative *in vivo* study.

Mastrocola R[1,2], Ferrocino I[3], Liberto E[4], Chiazza F[4], Cento AS[1], Collotta D[4], Querio G.[4], Nigro D[1], Bitonto V[5], Cutrin JC[5], Rantsiou K[3], Durante M[6], Masini E[6], Aragno M[1], Cordero C[4], Cocolin L[3*], Collino M[3*]

*shared senior authors of this study.

[1]Dept. of Clinical and Biological Sciences, University of Turin, Italy;

[2]Dept. Internal Medicine, University of Maastricht, The Netherlands;

[3]Dept. of Agricultural, Forest and Food Sciences, University of Turin, Italy;

[4]Dept. of Drug Science and Technology, University of Turin, Italy;

[5]Dept. of Molecular Biotechnology and Sciences for the Health, University of Turin, Italy;

[6]Dept. of Neuroscience, Psychology, Drug Research and Child Health, University of Florence, Italy.

Corresponding author:
Massimo Collino
Department of Drug Science and Technology,
University of Turin via P. Giuria 9, 10125 Torino, Italy.
Tel: +39 011 6706861 Fax: +39 011 2367955
E-mail address: massimo.collino@unito.it

Luca Cocolin
DISAFA, University of Turin
Largo Braccini 2, 10095 Grugliasco, Italy.
Tel: +39 011 6708553 Fax: +39 011 2368549
E-mail address: lucasimone.cocolin@unito.it

Running title: Liquid vs. solid fructose in gut/liver toxicity

Abstract

Despite clinical findings suggest that the form (liquid versus solid) of the sugars may significantly affect the development of metabolic diseases, no experimental data are available on the impact of their formulations on gut microbiota, integrity and hepatic outcomes.

In the present sudy, C57Bl/6j mice were fed a standard diet plus water (SD), a standard diet plus 60% fructose syrup (L-Fr), or a 60% fructose solid diet plus water (S-Fr), for 12 weeks. Gut microbiota was characterized through 16S rRNA phylogenetic profiling and shotgun sequencing of microbial genes in ileum faecal content and related volatilome profiling.

Fructose feeding led to alterations of the gut microbiota depending on the fructose formulation, with increased colonization by Clostridium, Oscillospira, and Clostridiales phyla in the S-Fr group and Bacteroides, Lactobacillus, Lachnospiraceae, and Dorea in the L-Fr. S-Fr evoked the strongest accumulation of Advanced Glycation End Products (AGEs) and barrier injury in the ileum intestinal mucosa, leading to increased lipopolysaccharide (LPS) levels in the portal plasma. These effects were associated to a stronger activation of the LPS-dependent pro-inflammatory TLR4/NLRP3 inflammasome pathway in the liver of S-Fr mice than of L-Fr mice. In contrast, L-Fr intake induced higher levels of hepatosteatosis and markers of fibrosis than S-Fr. Fructose-induced *ex novo* lipogenesis with production of SCFA and MCFA was confirmed by metagenomic analysis.

These results suggest that consumption of fructose under different forms, liquid or solid, may differently affect gut microbiota, thus leading to impairment in intestinal mucosa integrity and liver homeostasis.

Keywords: Fructose; Microbiota; Advanced Glycation End-products; Faecal volatilome; Inflammasome

1. Introduction

Over the last decades, the dietary intake of fructose has rapidly increased in industrialized countries due to changes in dietary behaviors, such as the rise in sugar-sweetened beverages and sugar-rich processed foods consumption [1, 2]. The increase in fructose consumption has been associated to higher prevalence of metabolic diseases, such as dyslipidemia, insulin resistance, high blood pressure, hepatic steatosis, and nonalcoholic fatty liver diseases (NAFLD) [3, 4], which are related to the high lipogenic power of fructose [5, 6]. The peculiar lipid deposition induced by excessive fructose consumption in ectopic tissues, such as liver and skeletal muscle, without significantly affecting body weight and adipose tissue mass, has been previously described [7-9].

Fructose is absorbed in the small intestine by the specific facilitative transporters expressed in both the apical and basolateral membrane of enterocytes [10]. After absorption, fructose is primarily metabolized in the liver which takes up at least 50% of the initial fructose flux [11].

The fructose intake exceeding the absorption capacity of small intestine passes to the large intestine where it becomes fermentable substrate for the microbiota. It has been reported that high fructose intake alters microbiota composition, resulting in reduced bacterial diversity and altered expression of genes involved in specific metabolic pathways [12].

We recently demonstrated that a high fructose intake induces Advanced Glycation End Products (AGEs) accumulation in liver, contributing to increase the endogenous synthesis of fatty acids (known as *ex novo* lipogenesis) and to intracellular lipids deposition, and evoking a pro-inflammatory response [13, 14]. Fructose-derived AGEs might also impair gut homeostasis, stimulating the growth of detrimental colonic bacteria (Clostridia and/or *Bacteroides*). So far, this hypothesis has never been investigated despite recent studies indicate that exposure to diet-derived AGEs for 2 weeks is sufficient to alter the colonic bacteria profile in humans [15]. As a consequence, increased gastrointestinal permeability may allow the translocation of toxic compounds from the gut into the circulation, activating systemic immune responses and inflammatory signals.

Another recent intriguing finding is that liquid high-sugar diets differentially modulate feeding behavior, as well as intestinal sugar transporters and hormones expression, when compared to solid high-sugar diets [16]. This experimental evidence may suggest that not only the type (e.g. fructose versus glucose), but also the form (liquid versus solid) of the sugars may significantly affect the development of obesity, insulin resistance and/or fatty liver disease. Despite the paucity of experimental data, this topic deserves better elucidation as sweeteners, including fructose, can be ingested as both liquid and solid formulations. Unfortunately, to date, the peculiar effects of intake of different forms of fructose, liquid or solid, on intestine integrity and microbiota, and hepatic outcomes have never been investigated.

Hence, the present study aimed at investigating the effects of fructose-derived AGEs on gut microbiota composition and function as well as on the impact on the intestinal barrier and the following consequences on the main target organ of fructose metabolism: the liver. Most notably, the study was designed to elucidate potential toxicological differences due to the sugar formulations.

2. Materials and Methods

2.1 Animal model and procedures

Male C57Bl/6j mice (Charles River Laboratories, Calco, Italy) of 4 weeks of age were cared in compliance with the European Council directives (No. 86/609/EEC) and with the Principles of Laboratory Animal Care (NIH No. 85–23, revised 1985). The scientific project was approved by the Ethical Committee of the Turin University (permit number: D.M. 94/2012-B). Mice were divided into three groups: a group fed with a standard diet and drinking tap water (SD group, n = 10), a group fed with a standard diet and drinking a 60% fructose (w/vol) syrup solution (L-Fr group, n = 10), and a group fed with a solid diet providing the 60% of calories from fructose and drinking tap water (S-Fr group, n = 10), for twelve weeks. Standard diet (Sniff Spezialdiäten GmbH, Soest, Germany) composition was: 62.1% of calories in carbohydrates (36.2% from corn starch, 14.9% from dextrin and 11% from sucrose), 5.1% of calories in fat, 5% of calories in fibres and 17.6% of calories from proteins. L-Fr syrup was prepared dissolving 60% of fructose in water with 3.5% citric acid as preservative. S-Fr diet (Sniff Spezialdiäten GmbH, Soest, Germany) composition was: 70% of calories in carbohydrates (8.9% from corn starch, 1% from sugar and 60% from fructose), 10% of calories in fat, and 20% of calories from proteins. The SD and S-Fr diets provided the same amount of calories (3.85 kcal/g). The percentage of fructose has been chosen according to our previous studies, in which we demonstrated that 60% fructose diet for 12 weeks was able to evoke significant derangements in key end-organs of metabolic diseases [14, 17, 18]. Mice of both S-Fr and L-Fr groups were fed with the same amount of daily fructose intake. All groups received drink and food *ad libitum*.

Body weight and food intake were recorded weekly. Fasting glycemia was measured at the start of the protocol and every 4 weeks by saphenous vein puncture using a glucometer (GlucoGmeter, Menarini Diagnostics). Urine samples were collected for 18 hours from mice in individual metabolic cages. After 12 weeks, mice were anesthetized and sacrificed by cardiac exsanguination. Blood was collected and liver and small intestine (ileum) were rapidly removed. A portion of each

tissue, liver and ileum, was cryoprotected in OCT (Optimal Cutting Temperature) compound and frozen in N_2 for cryostatic preparations. Fragments from the left lateral lobe of liver and from ileum tract of intestine were fixed overnight in 4% buffered formaldehyde solution for paraffin inclusion and morphology evaluation. Other portions of tissues and the luminal faecal content of the ileum were frozen in N_2 and stored at -80°C for analysis.

2.2 Plasma analyses

Plasma and tissue triglyceride levels (TG) were determined by standard enzymatic procedures using reagent kits (Hospitex Diagnostics, Florence, Italy). Plasma insulin level was measured using an enzyme-linked immunosorbent assay (ELISA) kit (Mercodia AB, Uppsala, Sweden). Plasma LPS levels were determined by Pierce LAL Chromogenic Endotoxin Quantitation Kit (Thermo Scientific, Waltham, MA, USA). After incubation of samples with Limulus Amebocyte Lysate (LAL), chromogenic substrate and stop reagent, we measured absorbance at 410 nm.

2.3 Urine analysis

Glucose and fructose urinary concentrations were determined by gas chromatography coupled with mass spectrometric detection (GC-MS) after suitable derivatization. Urine samples were submitted to derivatization consisting of oximation/silylation according to a reference protocol [19]: 200 µL of urine and internal standard (*p*-Chlorophenylalanine 10 g/L) were diluted with methanol and carefully mixed (Whirlimixer vortex, Fisher Scientific, Loughborough, Leicestershire, UK). Then, 30 µL of MOX were added to 20 µL of that solution and incubated for 2 hours at 60°C. Next, 30 µL of MSTFA were added and incubated at 100 °C for 60 minutes. The resulting sample was diluted in dichloromethane and immediately analyzed in duplicate or stored at -80°C until analysis. Quantitation was done by external standard calibration according to a previous study [20].

GC-MS analyses were run with an Agilent 6890 GC unit coupled to an Agilent 5975C MS detector (Agilent, Little Falls, DE, USA) operating in EI mode at 70 eV. The GC transfer line was set at

300°C. An Auto Tune option was used and the scan range was set to m/z 50-350 with a scanning rate of 2,500 amu/s. The column consisted of a 30 m × 0.25 mm d_c × 0.25 µm d_f SE52 (95% polydimethylsiloxane, 5% phenyl) from Mega (Legnano, Milan, Italy). The carrier gas was helium delivered at constant flow of 1.2 mL/min. Injection was by split/splitless injector, split mode, split ratio 1/20, injector temperature 280°C, and injection volume 2µL. The oven temperature programme was 80°C (1 min) to 300°C (10 min) at 4.0°C/min.

2.4 Histological analysis

2.4.1 Hematoxylin/eosin staining and histology score on liver sections

Liver and ileum mucosa morphology was evaluated by standard hematoxylin/eosin (H&E) staining on de-waxed 5 µm sections. The NAFLD activity score (NAS) evaluating the grade of steatosis, the umber of inflammatory foci, the presence of ballooning, and the fibrosis staging has been performed as described by Kleiner et al. [21] paralleled by the histology activity index of damage (HAID), a semi-quantitative necro-inflammatory grading based in the Knodell score system [22] which evaluates the degree of periportal interface hepatitis, focal lytic necrosis, apoptosis, and focal inflammation. Histologic scores have been performed on ten fields at 200x magnification per liver section by a blinded pathologist.

2.4.2 Oil Red O staining

Liver lipid accumulation was evaluated by Oil Red O staining on 7 µm ileum cryostatic sections. Stained tissues were viewed under an Olympus Bx4I microscope (X10 magnification) with an AxioCamMR5 photographic attachment (Zeiss, Gottingen, Germany).

2.4.3 Indirect immunofluoresce

Indirect immunofluorescence on 7 µm cryostatic sections was performed for intestinal expression and localization of GLUT-5, both intestinal and hepatic expression and localization of GLUT-2, as well as intestinal CML, CEL, and RAGE expression. Sections were blocked for 1 h with 3% BSA in PBS added with unconjugated goat anti-mouse IgG (Sigma Chemical Co., St. Louis, MO, USA)

178 to prevent interferences between endogenous mouse IgG and secondary antibody against mouse
179 IgG. Sections were then incubated overnight with primary antibodies: rabbit anti-GLUT-2 (Santa
180 Cruz Biotechnology, Dallas, Texas, USA), mouse anti-CML (R&D Systems, Inc. Mineapolis, MN,
181 USA), mouse anti-CEL (TransGenic Inc., Kobe, Japan), and mouse anti-RAGE (Abcam), and
182 subsequently for 1 h with Cy3-labeled secondary antibody (Sigma Chemical Co.). Negative controls
183 were prepared incubating sections only with secondary antibodies. Nuclei were stained with
184 Hoechst dye and sections were then examined using a Leica Olympus epifluorescence microscope
185 (Olympus Bx4I) with a photographic attachment. CML, CEL and RAGE immunoreactivity has
186 been quantified by using Image J software (NIH).
187
188 **2.5 Intestinal alkaline phosphatase (IAP) activity**
189 Alkaline phosphatase activity has been detected in ileum protein extracts with SensoLite pNPP
190 Alkaline Phosphatase colorimetric assay kit (AnaSpec Inc, Fremont, CA, USA) following
191 manufacturer's instructions for kinetic reading.
192
193 **2.6 Gene and protein expression analysis**
194 *2.6.1 Preparation of tissue extracts*
195 Cytosolic and nuclear extracts from livers were prepared as previously described [23]. Total protein
196 from intestinal tissue was obtained by the AllPrep® DNA/RNA/protein Kit (Qiagen) and protein
197 content was determined using the Bradford assay (BioRad, Hercules, CA, USA).
198 *2.6.2 Western blotting*
199 Equal amounts of proteins were separated by SDS-PAGE and electrotransferred to nitrocellulose
200 membrane (GE-Healthcare Europe, Milano, Italy). Membranes were probed with mouse anti-CML
201 (R&D Systems), rabbit anti-SCAP (Abcam), rabbit anti- SREBP1 (Abcam), rabbit anti-ACC (Cell
202 Signaling Technology, Danver, MA, USA), mouse anti-FASN (Santa Cruz Biotechnology, Dallas,
203 Texas, USA), rabbit anti-NLRP3 (Abcam), rabbit anti-caspase-1 (Abcam), mouse anti-IL-1β (Santa

Cruz Biotechnology), rabbit anti-TGF-β (Abcam), rabbit anti-SMAD (Cell Signaling), rabbit anti-pSMAD (Cell Signaling), rabbit anti-fibronectin (Abcam), rabbit anti-vimentin (Cell Signaling), rat anti-ZO-1 (Santa Cruz), mouse anti-occludin (Santa Cruz), mouse anti-TLR-4 (Santa Cruz), mouse anti-MyD88 (Santa Cruz), and rabbit anti-IRAK1 (Santa Cruz) followed by incubation with appropriated HRP-conjugated secondary antibodies (Sigma).

Proteins were detected with Clarity Western ECL substrate (BioRad) and quantified by densitometry using analytic software (Quantity-One, Bio-Rad). Results were normalized with respect to densitometric value of mouse anti-GAPDH (Santa Cruz Biotechnology) for cytosolic and total proteins, and mouse anti-histone H3 (Abcam) for nuclear proteins.

2.6.3 Real- time PCR (RT-PCR)

Total RNA was isolated from ileum and liver tissue samples. Briefly, tissue samples were collected in Allprotect Tissue Reagent and stored at -80 °C. Total RNA was then obtained by the AllPrep® DNA/RNA/protein Kit and reverse transcribed into 20 µL cDNA (complementary DNA) reaction volume, using the QuantiTect® Reverse Transcription Kit. Quantitative RT-PCR was performed for specific genes (GLUT-2, GLUT-5, occludin, and ZO-1) using the SsoFast™ EvaGreen. The transcript of the reference gene ribosomal 18s RNA (RNR18) was used to normalize mRNA data, and real-time PCR was performed by a MiniOpticon™ Real Time PCR system (Bio-Rad). The PCR protocol conditions were as follows: HotStarTaq DNA polymerase activation step at +95 °C for 30 sec, followed by 40 cycles at +95 °C for 5 seconds and +55 °C for 10 sec. All runs were performed with at least three independent cDNA preparations per sample and all samples were run in duplicate. At least two non-template controls were included in all PCR runs. The quantification data analyses were performed using the Bio-Rad CFX Manager Software version 3.0 (Bio-Rad) according to the manufacturer's instructions.

2.7 Microbiota analysis

2.7.1 Samples preparation and DNA extraction.

To reduce the inter-sample variability a pool of the faecalileum content samples from each dietary intervention was obtained (three samples pools). The faecal samples pool (100 mg) were homogenized and washed twice in 500 μL of PBS (Phosphate-Buffered Saline, pH 7.4) and DNA extraction was carried out by using MasterPure Complete DNA & RNA Purification kit (Illumina, San Diego, California). RNA was removed by a treatment with RNase (Ambion, Foster City, California) for 45 min at 37 °C. The Qubit and the Qubit DNA Assay kit (Life Technologies, Carlsbad, California) were used for quantification.

2.7.2 16S rRNA phylogenetic profiling and shotgun sequencing of microbial genes

The microbial diversity was studied by high throughput amplicon target sequencing of the amplified V3–V4 region of the 16S rRNA as reported elsewhere (Klindworth et al., 2013). The PCR products were purified by means of an Agencourt AMPure kit (Beckman Coulter, Milan, Italy), and the resulting products were tagged by using the Nextera XT Index Kit (Illumina). Sequencing was performed with a MiSeq Illumina instrument with v3 chemistry and generated 250 bp paired-end reads. The software used for the base-calling and Illumina barcode demultiplexing processes, were the MiSeq Control Soft. V2.3.0.3, the RTA v1.18.42.0 and the CASAVA v1.8.2.

DNA directly extracted from faecal samples was then subject to shotgun sequencing. Shotgun libraries were fragmented and tagged with sequencing adapters by using the TruSeqDNA library preparation kit (Illumina). Shotgun sequencing was performed with a NextSeq 500 platform (Illumina) according to the manufacturer's instructions, by G4L company (Salerno, Italy) and generated 100 bp paired-end reads.

2.7.3 Bioinformatics and data analysis

16S rRNA amplicon reads were analyzed by using QIIME 1.9.0 software (Caporaso et al., 2010). OTUs defined by a 97% of similarity were picked using the uclust pipeline and the representative sequences were submitted to the RDPII classifier to obtain the taxonomy assignment and the relative abundance of each OTU using the Greengenes 16S rRNA gene database. The whole metagenome data analysis was carried out as follows: raw reads quality (Phred scores) was

evaluated by using the FastQC toolkit (http://www.bioinformatics.babraham.ac.uk/projects/fastqc/). The raw sequences were trimmed to Qscore of 20 with the SolexaQA++ software (Cox et al., 2010). Duplicate sequences and sequences less than 50 bp were discarded by using Prinseq (Schmieder and Edwards, 2011). The obtained trimmed reads were then mapped to the draft genome of *Mus musculus* (ftp://ftp.ncbi.nlm.nih.gov/genomes/Mus_musculus/Assembled_chromosomes) by using Bowtie2 (Langmead and Salzberg, 2012) in end-to-end, sensitive mode. Clean reads were aligned against the Kyoto Encyclopedia of Genes and Genomes (KEGG) database version April 2011 by using Bowtie2 software in end-to-end, sensitive mode. The number of reads uniquely mapped to each gene in the KEGG database was extracted by using SAMtools and normalized to total read mapped to the whole catalogue.

The metabolic reconstruction of the mice faecal microbiota was performed as follow: clean non host reads were then assembled with SPAdes v3.10.0 [24] and comparison of assemblers was performed by using QUAST v4.1 [25]. Each contig was run through an automated gene annotation pipeline utilizing MetaGeneMark. The predicted genes were then aligned against the NCBI-NR database by using blastx in order to obtain the gene annotation. The number of reads mapped to each gene were then used for the metabolic pathways reconstruction based on the Kyoto Encyclopedia of Genes and Genomes (KEGG) version April 2011 and visualized by using MEGAN software v5.

The functional gene count table was internally normalized in MEGAN by checking the "use normalized count" option. Rarefaction analysis was performed based on the leaves of the tree in MEGAN.

2.7.4 Sequences accession numbers.

The 16S rRNA and the metagenome sequences are available at the Sequence Read Archive (SRA) of the National Center for Biotechnology Information (NCBI) under accession numbers SRP100599 and SRP100623, respectively.

2.8 Faecal volatilome profiling

2.8.1 Volatiles sampling by Head Space Solid-Phase Micro Extraction (HS-SPME): devices and conditions

HS-SPME analysis were carried out on a GC×GC system coupled with a time of flight mass spectrometer (TOF-MS) operating in tandem ionization mode.SPME fibers, Divinylbenzene/Carboxen/ Polydimethylsiloxane (DVB/CAR/PDMS) d_f 50/30 μm - 2 cm were from Supelco (Bellefonte, PA, USA). Fibers were conditioned before use as recommended by the manufacturer. The standard-in-fiber procedure was adopted to pre-load the ISTD (α-thujone) onto the fiber before sampling. 5.0 μL of ISTD solution (100 ppm) were placed into a 2 mL glass vial and submitted to HS-SPME at 70°C for 10 min. Faecal samples were exactly weighted (10 mg) in glass vials (2.0 mL) and submitted to manual HS-SPME sampling. After ISTD loading step, the SPME device was exposed to the sample headspace for 30 min at 70°C. Extracted analytes were recovered by thermal desorption of the fiber into the S/SL injection port of the GC×GC system at 250°C for 5 min. Each sample was analyzed in triplicate.

2.8.2 GC×GC-TOF-MS instrument set-up and analytical conditions

GC×GC analyses were performed on an Agilent 6890 GC unit coupled with a Markes BenchTOF-Select and Select-eV® option (Markes International Ltd, Llantrisant UK) operating in the EI mode at 70 and 12 eV. The transfer line was set at 250°C. TOF scan interval was set at *m/z* 35-350 with 50 Hz of sampling frequency for each ionization channel. The system was equipped with a two-stage KT 2004 loop thermal modulator (Zoex Corporation, Houston, TX) cooled with liquid nitrogen and controlled by Optimode™ V.2 (SRA Instruments, Cernusco sul Naviglio, MI, Italy). Hot jet pulse time was set at 250 ms, modulation time was 4s and cold-jet total flow progressively reduced with a linear function from 40% of Mass Flow Controller (MFC) at initial conditions to 8% at the end of the run. A deactivated fused silica capillary loop (1 m × 0.1 mm d_c) was used. The column set was configured as follows: ^{1}D SolGel-Wax column (100% polyethylene glycol) (30 m × 0.25 mm d_c, 0.25 μm d_f) from SGE Analytical Science (Ringwood, Australia) coupled with a ^{2}D

OV1701 column (86% polydimethylsiloxane, 7% phenyl, 7% cyanopropyl) (1 m × 0.1 mm d_c, 0.10 μm d_f), from J&W (Agilent, Little Falls, DE, USA).

SPME thermal desorption into the GC injector port was under the following conditions: split/splitless injector in split mode, split ratio 1:20. Carrier gas was helium at a constant flow of 1.2 mL/min. The oven temperature program was: from 40°C (1 min) to 200°C at 3°C/min and to 250°C at 10°C/min (5 min). The *n*-alkanes liquid sample solution for Linear Retention Indices determination (I^T_S) was analyzed under the following conditions: split/splitless injector in split mode, split ratio 1:50, injector temperature 250°C, injection volume 1 μL.

2.8.3 Data acquisition and data elaboration

Data were acquired by Markes TOF-DS software (Markes International Ltd, Llantrisant UK) and processed by GC Image® GC×GC Edition Software, Release 2.6 (GC Image, LLC Lincoln NE, USA). Statistical analysis was performed with XLstat (Addinsoft, New York, NY USA). Targeted analysis focused on 59 compounds identified by matching their EI-MS fragmentation pattern (NIST MS Search algorithm, ver 2.2, National Institute of Standards and Technology, Gaithersburg, MD, USA, with Direct Matching threshold 900 and Reverse Matching threshold 950) with those collected in commercial (NIST2014 and Wiley 7n) and in-house databases. As a further parameter to support identification, I^T_S were considered and experimental values compared to the tabulated ones. The list of identified analytes, retention times in the two chromatographic dimensions, experimental and tabulated I^T_S, average Normalized 2D Volume and relative standard deviation (3 analytical replicates)

is provided as supplementary material (Supplementary Table 2S and Supplementary Figure S2) together with contour plots of volatile fractions from L-Fr, S-Fr and SD diet faecal samples.

2.9 Statistical analysis

The Shapiro-Wilk test was used to assess the normality of the variable distributions. One-way ANOVA followed by Bonferroni's post-hoc test was adopted for comparison among the four

groups of animals. Data were expressed as mean ± standard deviation. Threshold for statistical significance was set to $P<0.05$. Statistical tests were performed with GraphPad Prism 6.0 software package (GraphPad Software, San Diego, CA, USA).

2.10 Materials

All compounds were purchased from Sigma Chemical Co. (St. Louis, MO, USA), unless otherwise stated.

3. Results.

3.1 General parameters.

After twelve weeks of dietary intervention, the mice exposed to liquid fructose drink (L-Fr) and the mice fed with the solid fructose diet (S-Fr) showed a significant increase in plasma fasting glucose and insulin levels, while a slight increase in liver weight was recorded in the L-Fr group, when compared to the control group (Tab. 1). However, these effects were not associated with significant changes in body weight gain and serum TG levels.

As reported in Table 2, the L-Fr group markedly reduced solid food intake to compensate the calories introduced with the fructose syrup. Thus, the total calories intake was not different among groups. Similarly, no statistically significant differences were recorded in terms of daily intake of fructose among groups.

3.2 Fructose-induced translocation of GLUT-2 and fructose urinary excretion.

In intestine of mice exposed to S-Fr or L-Fr no differences in both mRNA expression or localization of the fructose specific transporter GLUT-5 were detected (Fig. 1A), while a stronger expression of the glucose/fructose transporter GLUT-2 in the apical membrane was observed, when compared to intestine from SD mice, with maximal effect in the S-Fr group (Fig. 1B). Also in the liver, the GLUT-2 was expressed at the level of the plasma membrane according to an active uptake of sugars by the hepatocytes, with no apparent differences between the two fructose groups (Fig. 1C).

Interestingly, the fructose-induced increase in intestinal GLUT-2 apical expression was associated with higher levels of urinary excretion of fructose, but not glucose, detected in both groups of fructose mice when compared to SD, thus confirming that fructose was efficiently absorbed by intestine. However, the urinary concentration of fructose was higher in the L-Fr group than in the S-Fr, indicating that fructose was more rapidly transferred by enterocytes to the plasma through basolateral transport in the liquid form (Tab. 1).

3.3 Liquid and solid formulations of fructose differently altered microbial community profile.

Concerning gut microbiota, we performed amplicon based sequencing of the 16S rRNA and shotgun metagenomic sequencing on faecal ileum content of SD and fructose-exposed mice to examine in depth the effects of the two different forms of fructose on intestinal microbiota composition and function. A total of 56.023 raw reads (2x250bp) were obtained after sequencing. After joint, a total of 54.050 reads passed the filters applied through QIIME, with an average value of 18.674 reads/sample, and a sequence length of 456 bp. The rarefaction analysis and the estimated sample coverage indicated that there was a satisfactory coverage for all the samples (ESC average 99%). Moreover, alpha-diversity also showed that there was a higher level of complexity in S-Fr, when compared to L-Fr. Accordingly, the ß-diversity through weighted UniFrac distance matrices indicated a clear separation between the diets ($P < 0.01$).

Regarding the main operational taxonomic units (OTUs), defined at the genus or phylum level, filtered for OTUs presence > 0.2 % (Fig. 2), a remarkable individual variability of abundance was observed. S-Fr sample showed higher abundance of *Clostridium* (18% of the relative abundance), *Oscillospira* (6.2%) and *Clostridiales* phylum (32%). Mice fed with L-Fr displayed the highest abundance of *Bacteroides* (12%), *Lactobacillus* (44.8), *Lachnospiraceae* (7.25%), and *Dorea* (0.37%). Control samples were characterized by the presence of *Allobaculum* (21% of the relative abundance), *Gemella* (4%) and *Parabacteroides* (6%) (Fig. 2).

Regarding the minor OTUs fraction (< 2%), L-*Ruminococcus*, *Coprococcus* and R-*Ruminococcus* were higher in mice fed with fructose compared to standard diet. In detail, the shift in the OTUs composition resulted in an overall decrease in the Firmicutes/Bacteroidetes ratio in mice fed with fructose and the L-Fr diet showed the lowest ratio value.

3.4 Metagenomic data: comparative analysis between solid and liquid formulations of fructose

Raw reads of 29.62 Mbp were generated, which yielded 4.93 Mbp/sample. After quality trimming and host sequence removal, 1.75 Mbp of clean reads were analyzed and an average of 2.333.932

393 reads/sample were obtained. Faecal samples displayed high proportions of reads of host origin due
394 to the higher abundance of mammalian cell and the low microbial biomass. A *de novo* assembly
395 generated 439 contigs of more than 1000 bp in length, with an average N50 of 758 bp. To obtain the
396 metabolic reconstruction of the mice faecal microbiota, we classified the predicted genes by
397 aligning them to the integrated NCBI-NR database of non-redundant protein sequences. The
398 predicted genes identified were 20,972, 40% of which were assigned to KEGG pathways by
399 MEGAN. Rarefaction curves obtained through MEGAN were used to determine genes abundance
400 richness, revealing that metagenomic diversity was well represented (data not shown), although
401 mice fed with SD showed a lower diversity in genes abundance compared to fructose added diets.
402 By performing the functional characterization and gene classification of the shotgun sequence reads
403 against the KEGG database and the MetaHIT gene catalogue, we detected 2,629 KEGG orthologue
404 (KO) genes and the relative abundance of each KO term was calculated based on the total read of
405 the included catalogued reference genes, normalized to total read mapped to the whole catalogue.
406 The L2 KEGG categories aminoacid metabolism was found most abundant in L-Fr samples. On the
407 other hand S-Fr showed high abundance of genes related to carbohydrate and energy metabolism, in
408 particular genes belonging to aminosugar, fructose and galactose metabolism (Fig. 3). However,
409 genes related to glycolysis, tricarboxylic acids (TCA) and pyruvate metabolism were clearly
410 associated with L-Fr diet.
411 The metabolic reconstruction of the faecal metagenomes displayed the complete biosynthetic
412 pathways for leucine, isoleucine and valine, and data indicated that the main routes for the synthesis
413 of those branched chain aminoacids (BCAAs) were from pyruvate pathways. Going more in depth
414 into the metagenome content key enzymes responsible for the biosynthesis of BCAAs were found
415 most abundant in L-Fr diet compared to the other diets: BCAA aminotransferase [EC:2.6.1.42) can
416 lead to the interconversion between 4-Methyl-2-oxopentanoate to leucine and valine and it can
417 drive the formation of isoleucine from 3-Methyl-2-oxopentanoate (Suppl Figure 1S; Suppl Table
418 1S).

Regarding the *ex-novo* biosynthesis of fatty acid (SCFA and MCFA) mice fed with fructose showed the highest counts of key genes for the production of butanoate from acetyl-CoA route (butyrate kinase [EC:2.7.2.7]), propanoate from TCA route (acetate kinase [EC:2.7.2.1]) and MCFA (medium-chain acyl-hydrolase [EC:3.1.2.21]) (Suppl Figure 1S; Suppl Table 1S). In particular butyrate kinase was found most abundant in S-Fr diet and boosted the production of 1-butanol as confirmed by GC×GC-TOF-MS data. In addition, many genes related to peptidoglycan biosynthesis (ko00550) via aminosugar metabolism route were predominantly associated with fructose diet and in particular with L-Fr.

3.5 Solid and liquid formulations of fructose evoke different changes in faecal volatilome fingerprints.

Faecal volatilome is influenced by several factors including the gut microbiota composition thereby its fingerprint is suggestive of metabolic changes induced and/or caused by microbial activity. The faecal volatiles here detected by GC×GC-TOF-MS are listed in the Table S4 and include: hydrocarbons, alcohols (short-chain and long-chain alcohols derived from acids reduction), carbonyl derivatives (aldehydes and ketones) short-chain fatty acids (acetic, propionic, butyric above all), branched-chain fatty acids, aromatic compounds (including heterocycles) and monoterpenoids.

The relative distribution of faecal volatiles between samples proved to be informative as illustrated by the heat map of Fig. 4 where clustering is clear between diet regimens (SD *vs.* fructose enriched diets) and for compound classes that result up- or down- regulated (blue or red spots). Above all, butyric and propanoic acid esters (butyl butanoate, 2-methylbutyl propanoate, 1-butanol-3-methyl propanoate) were up-regulated in fructose enriched diets (blue spots in the heat-map for L-Fr and S-Fr samples) while free SCFAs (acetic, propanoic and butanoic acids) were more abundant in the SD mice.

Analytes with a relative standard deviation higher than the analytical repeatability were submitted to pairwise t-test (α=0.05) and those with a higher informative role (marked with a star) are shown in Fig. 5 where faecal volatilome signatures of L-Fr and S-Fr diets were compared to the SD diet. Positive coefficient of variations (CV%) indicate analytes up-regulation in fructose enriched diets while negative values relate to those analyte that were more abundant in mice fed by SD diet. Red bars correspond to analytes just revealed in specific populations. Interestingly, fructose intake up-regulated the release of SCFAs esters; in particular S-Fr induced a higher production of butyl acetate and 2-methylbutyl propanoate while L-Fr concurred also to increase butyl butanoate. On the other hand, SD mice faecal signatures were connoted by higher amounts of linear and branched chain alcohols (2-propyl heptanol, hepten-3-ol, hexanol, heptanol and octanol); several carbonyl derivatives (linear saturated aldehydes - hexanal, heptanal, octanal, nonanal - and ketones -2,3-pentanedione and 2-pentanone the latter detected only in SD samples). Meaningful differences in volatiles signatures (analytes marked with the asterisk $P<0.05$) suggest different microbial metabolism induced by diets.

3.6 Liquid fructose evoked the highest levels of lipid synthesis/accumulation in the liver and accelerated liver fibrosis.

In order to evaluate the metabolism of fructose in the liver, we analyzed the activation of the lipogenenis regulated by the Sterol Regulatory Element Binding Protein (SREBP) 1c and the SREBP Cleavage Activating Protein (SCAP) signaling pathway. In the liver of both L-Fr and S-Fr mice, SCAP was upregulated, reaching statistical significance only in L-Fr group (Fig. 6A). Accordingly, the hepatic levels of the nuclear active form of the transcription factor SREBP1c were significantly increased only in the liver of the L-Fr group. In the liver of S-Fr mice, the cytosolic inactive form of SREBP1c was prevalent with respect to the nuclear form, indicating a limited nuclear translocation and, thus, activation of the lipogenic pathway when compared to L-Fr mice liver (Fig. 6B). In keeping with the increased SREBP1c activation, a significant up-regulation of its

main target genes, acetyl Coenzyme A carboxylase (ACC) and fatty acid synthase (FAS), was recorded in L-Fr mice compared to both SD and S-Fr diet mice (Fig. 6C).

As consequence of increased *ex novo* lipid synthesis, L-Fr mice showed a significantly higher TG liver deposition with respect to both SD and S-Fr mice (Table 1). Consistently, Oil Red O staining of liver slices revealed a marked steatosis in both groups of mice exposed to fructose, compared to SD, with widely diffused microvescicular steatosis in L-Fr mice, and more focal steatosis associated to ballooning and immune cells infiltration in S-Fr mice (Fig. 6D).

When we evaluated the degree of fibrosis through the expression analysis of early specific markers, we found that transforming growth factor (TGF)-β, an inducer of fibrogenesis (Fig. 7A), small mother against decapentaplegic (SMAD), a mediator of TGF-β intracellular signaling (Fig. 7B), fibronectin and vimentin, fibrillary components of extracellular matrix (Fig. 7C) were markedly upregulated in L-Fr, compared to SD mice, while only SMAD and fibronectin were significantly increased also in the S-Fr group (Fig. 7A-C). Finally, NAS score on liver H&E stained sections indicated that both groups of mice fed the high fructose developed a relevant grade of steatosis, whereas the S-Fr group only presented a significant grade of inflammation and ballooning, compared to SD mice. Macroscopic signs of fibrosis have been observed only in few liver samples from the S-Fr group, indicative of a preliminary stage of fibrosis. In addition, the HIAD score indicated the presence of hepatocytes cytolysis induced by the fructose feeding, and confirmed the highest degree of inflammation in the liver of the S-Fr group (Fig. 7D).

3.7 Solid fructose induced the highest AGEs accumulation in the mouse gut

Fructose-administered mice showed an increased accumulation of the major AGEs, N(epsilon)-(carboxymethyl)lysine (CML) and N(epsilon)-(carboxyethyl)lysine (CEL) , in intestinal mucosa revealed by immunofluorescence. In particular, a higher accumulation of CML and CEL was detected in the villus axis and basal membranes of S-Fr mice than L-Fr groups. As consequence of AGEs accumulation, we observed an induction of AGE-receptor (RAGE) expression in the crypts

in correspondance to lymph nodes in fructose-fed mice, as shown by immunofluorescence analysis (Fig. 8A) and related quantification (Fig. 8B). These findings were confirmed by western blotting analysis, showing a significantly increased expression of CML-glycated proteins in the gut S-Fr mice (Fig. 5C)

3.8 Solid fructose impaired gut integrity leading to increased hepatic NLRP3 inflammasome activation.

In order to evaluate whether the increased protein glycation and expression of RAGE were related to intestinal mucosa damage and inflammation, we tested the impact of different fructose formulations on key components of the tight junctions (TJ) expressed in the ileum, as well as on the portal and systemic plasma levels of LPS, a marker of loss of intestinal integrity and systemic diffusion of pro-inflammatory microbial components. Our results clearly showed that mRNA expression of the epithelial TJ markers occludin and zona occludens (ZO)-1, in the ileum regions was moderately decreased in the mice under L-Fr feedings and markedly suppressed in the mice under S-Fr feeding (Fig. 9A and 9B). The reduced mRNA expression of ZO-1 and occluding in S-Fr mice was confirmed when proteins were measured by Western blot analysis (Fig. 9C and 9D). Since TJ maintain enteral epithelial barrier, their robust defect in S-Fr mice is suggestive of gut impairment and it correlates well with the massive increase in both portal plasma and systemic levels of LPS recorded in S-Fr compared to SD. In contrast, only a slight but not significant increase in LPS concentration was detected in L-Fr (Fig. 9E and 9F). The massive increase in LPS concentration in S-Fr was paralleled by a significant increase of the intestinal alkaline phosphatase (IAP), a brush–border protein involved in the LPS detoxifying cascade (Fig. 9G). However, no significant alterations of mucosa morphology in mice exposed to fructose were detectable by light microscopy (Fig. S3), thus indicating an early stage of impairment of the integrity of the ileal mucosal lining.

We then evaluated the distal (hepatic) activation of one of the best-characterized LPS-dependent inflammatory pathway, the NLRP3 inflammasome. One of the main receptor mediating LPS-induced NLRP3 activation is the TLR-4. In the liver of the fructose-fed mice we detected increased protein levels of TLR-4, reaching highest upregulation in the S-Fr group. The involvement of TLR4 receptor was confirmed by the robust overexpression of the adapter protein myeloid differentiation response gene (MyD) 88, that cluster within TLR4 to recruit IL-1 receptor-associated kinase (IRAK) 1, whose expression was massively increased in the liver of S-Fr mice (Fig. 10A-C). Consistently, the main component of the inflammasome platform, the NLRP3 protein, was upregulated in the liver of high fructose fed mice compared to SD, reaching highest levels in S-Fr group (Fig. 10D). Also the NLRP3 downstream signaling, namely the rate of caspase-1 activation, was significantly higher in the S-Fr (Fig. 10E) than in the L-Fr mice livers. Accordingly, expression of the active IL-1β protein was markedly upregulated only in the S-Fr mice liver (Fig. 10F).

4. Discussion

Several experimental studies have already demonstrated that diet composition plays an important role in the development of metabolic derangements [26, 27]. Besides, an increasing body of literature highlights a tight relationship between nutrients and modifications of the intestinal barrier and microbiota that can potentially interfere with systemic metabolism and health [28, 29]. Here we confirmed and further extended previous findings on the detrimental effects associated to chronic exposure to high fructose intake, leading to hyperglycemia and liver toxicity. Most notably, we performed a comparative study on the toxicological impact of different formulations (liquid versus solid forms) of the same dietary component. This in an important and topical issue, unfortunately largely unexplored. In fact, sugar sweetened beverages are thought to contribute to weight gain because beverages appear to suppress appetite and energy intake less than solid foods [30]. However, most recent findings show that some high-energy snack foods may deliver the same level of satiation as a sugar-containing beverage [31], thus suggesting that the identification of the range of effects evoked by either liquid or solid foods is still controversial. In our experimental model, liquid fructose intake was associated with reduced solid food consumption, resulting in no significant difference in the total caloric intake between the two fructose dietary manipulations. Thus, differences here recorded between the two fructose groups were due to formulations only not being affected by impairments in net energy stores and/or amount of fructose intake. Despite we did not highlight any behavioral and physical alterations among the groups, we cannot rule out that a decrease in solid food intake might affect outcomes by under nourishing of animals with essential micronutrients.

Interestingly, here we demonstrated, for the first time, that the fructose formulation affects its absorption by the small intestine, leading to different outcomes in liver metabolism. After ingestion, fructose is absorbed in the small intestine by the apical membrane of enterocytes through the GLUT-5 facilitative transporter, and is then transferred to the blood by the GLUT-2 transporter located in the basolateral membrane [32]. High concentrations of fructose in the intestinal lumen

559 may stimulate the translocation of GLUT-2 to the apical membrane where it becomes the main
560 sugar transporter [33-35]. Although this hypothesis is still debated [36, 37], the results here reported
561 confirm an increased expression of GLUT-2 in the apical membranes of enterocytes, without
562 modifying GLUT-5 expression and distribution. Interestingly, gut of mice chronically exposed to
563 solid fructose showed a higher expression of GLUT-2 in the apical membrane when compared to
564 gut from mice treated with liquid fructose, thus suggesting a higher fructose accumulation in the
565 enterocytes and lower rate of blood transfer. This hypothesis is confirmed by a dramatically lower
566 excretion of fructose in urine of solid fructose fed mice in comparison to liquid fructose fed mice.
567 We may, thus, speculate that the liquid fructose is more rapidly absorbed in the plasma and, thus,
568 rapidly metabolized by the liver, being the excess excreted with urine. In contrast, the solid fructose
569 is likely to be more slowly transferred to the plasma because of the basolateral-to-apical membrane
570 translocation of GLUT-2. Therefore, solid fructose may persist for longer time within the gut and,
571 thus, be metabolized by enterocytes and potentially by microbiota of the large intestine when excess
572 fructose migrates from the small intestine [38, 39]. The first evidence that fructose may affect the
573 microbiota comes from a few recent studies in rats showing that orally administered fructose
574 enhanced the abundance of *Enterobacteriaceae*, *Coprococcus*, and *Ruminococcus* and induced a
575 distinct faecal metabolome profile that is associated with fructose-induced nonalcoholic fatty liver
576 disease [40]. Here we reported, for the first time, differences in the metabolic adaptation of the
577 intestinal microbiota to dietary fructose, with significant taxonomic differences between the two
578 fructose formulations. Specifically, Bacteroides, whose increased presence has been associated to
579 an increased risk of weight gain and insulin resistance [41], was massively detected in the liquid
580 diet. Several studies on mouse gut microbiota obesity-related alterations reported robust changes in
581 the Firmicutes to Bacteroidetes ratio [41, 42]. Here we found that this ratio was lowest in the
582 intestinal microbiota of L-Fr mice. The analysis on samples from mice with SD diet was in
583 agreement with previous data for rodents under standard diet regimens with Firmicutes much more
584 abundant than Bacteroidetes, Proteobacteria and Tenericutes [43, 44]. On the contrary, we observed

585 an increase of Coprococcus and Ruminococcus genera and a decrease of Firmicutes and
586 Clostridium genera in both the fructose experimental groups when compared to SD mice. In L-Fr
587 mice we recorded the highest abundance of *Lactobacillus*, which could be a consequence of the
588 increased availability of simple sugars in the intestine of these mice [45]. Our results are in
589 agreement with the changes in the relative abundance of these taxa observed in type 2 diabetes
590 patients when compared to healthy individuals [46].
591 Both fructose diets enriched the presence of few anaerobes like *Coprococcus* and *Ruminococcus*. It
592 was recently shown that *Ruminococcus* produces propionate from fructose, whereas *Coprococcus*
593 produces butyrate from fructose [47]. Interestingly, the faecal volatilome signatures confirmed the
594 highest levels of both propionate and butyrate derivatives in mice exposed to fructose.
595 Metagenomic analysis confirmed that fructose-enriched diets could lead to *ex novo* lipogenesis with
596 the production of SCFA and MCFA, and faecal volatilome referred higher amounts of SCFA esters
597 when compared to SD mice (butyl acetate increase by 50% in S-Fr mice; 2-methylbutyl propanoate
598 by 15% in S-Fr mice and butyl butanoate with by 21 and 7% in S-Fr and L-Fr mice respectively).
599 The increased systemic bioavailability of liquid fructose and SCFA esters may account for the
600 markedly higher activation of the lipogenic pathway in the liver of the L-Fr mice, compared to S-Fr
601 mice. The activation of the SCAP/SREBP1c signaling pathway regulates the transcription of the
602 enzymes involved in the *ex novo* synthesis of fatty acids and the subsequent intracellular lipid
603 accumulation, which are peculiar aspects of fructose metabolism [13, 48]. Indeed, we found
604 significantly higher TG levels and more diffuse hepatosteatosis in the L-Fr mice than in the S-Fr,
605 associated to a stronger activation of early markers of the fibrogenic cascade, which has been
606 previously demonstrated to be affected by SREBP1c activity [49-51]. Although the histological
607 examination and related scores confirmed the development of steatosis and focal lytic necrosis, no
608 significant evidence of established fibrosis was documented, suggestive of a preliminary stage not
609 yet progressed to full-blown liver scarring. These findings are in keeping with literature data
610 reporting the appearance of macroscopic signs of fibrosis, such as collagen deposition and fibrotic

611 septa generation, only after 16-20 weeks of high fructose intake [52]. In contrast, as previously
612 documented, Ritze et al [16], briefer exposure time are sufficient to highlight differences in
613 triglyceride accumulation and hepatosteatosis, confirming that that liquid sugars were more rapidly
614 absorbed and gave greater induction of hepatic lipid accumulation compared to the solid
615 counterparts. The lowest rate of fructose absorption when the sugar is derived from solid
616 formulation is here suggested by the metabolic reconstruction of the mice faecal microbiota. This
617 analysis showed that the highest increase in genes related in carbohydrate metabolism was recorded
618 in the microbiota of mice exposed to S-Fr, suggestive of higher fructose accumulation in the gut of
619 S-Fr than of L-Fr. In contrast, an increase in aminoacid metabolism genes was recorded in the
620 microbiota of mice exposed to L-Fr. Besides, the most relevant impact of solid fructose on gut
621 toxicity is confirmed by the investigation of local accumulation of fructose-derived AGEs. Fructose
622 is a highly glycative compound [53, 54], and we have previously contributed to demonstrate that
623 high dietary fructose intake can evoke stronger AGEs accumulation and RAGE activation than
624 glucose [13]. Moreover, here we reported the highest levels of fructose-derived AGEs in intestinal
625 villi of mice fed with solid formulation. AGEs ingested with highly processed foods or locally
626 produced in the gut are slowly absorbed in the circulation and only partially excreted in urine, while
627 they are accumulated and metabolized by enterocytes and are suggested to have distal effects on
628 target organs [55]. Food-derived AGEs and glycated proteins can act in the intestine as substrate for
629 colonic bacterial fermentation, driving alterations of microbiota composition and of intestinal
630 barrier permeability [56, 57]. Accordingly, we showed here that the marked AGEs accumulation
631 detected in gut of S-Fr mice was paralleled by a robust decrease in TJ mRNA and protein
632 expression in the ileal mucosal lining and massive transfer of LPS in the portal vein plasma,
633 suggestive of increased gut permeability to bacterial components [29, 58]. A higher LPS
634 concentration was also recorded at systemic level in S-Fr mice when compared to LPS
635 concentration measured in L-Fr mice. We also measured the IAP enzyme, which has been
636 demonstrated to be the main LPS detoxifying system in the gut, likely thanks to its ability to induce

637 dephosphorylation of the lipid A moiety, the primary source of LPS endotoxic effects [59]. Several
638 studies demonstrated that IAP expression and activity is altered as result of a complex interplay
639 between dietary factors, the microbiota and the host [60]. Most notably, IAP activity has been
640 shown to be enhanced by LPS injections [61]. Here we confirmed a parallelism between highest
641 LPS plasma concentration and most intense ileal IAP activity in the S-Fr group. The increased IAP
642 activity we documented was suggestive of a dysfunctional response of the intestinal detoxifying
643 mechanisms, being insufficient to degrade the solid fructose-induced rise in LPS production, thus
644 failing to prevent its transfer to the plasma. As very recently documented [62], the association of
645 microbiota modifications with intestinal permeability leads to translocation of bacterial products
646 that signal the liver through TLR4 (that recognizes LPS, a gram-negative bacteria wall component).
647 TLR4 activation, throughout the MyD88 and IRAK-1–dependent signaling pathway, leads to
648 secretion of mature IL1β by stimulating the NLRP3 inflammasome complex assembly [63]. The
649 NLRP3 inflammasome is a pro-inflammatory complex, which senses LPS and several other stimuli
650 related to pathogen and damage-associated molecular patterns in tissues undergoing infections, cell
651 damage or metabolic imbalances [64]. The formation of the NLRP3 inflammasome complex leads
652 to the activation of caspase-1, which in turn proteolytically cleaves the precursors of pro-
653 inflammatory cytokines IL-1β. Very recently, we demonstrated that both LPS and microvesicles
654 released by cells undergoing lipotoxicity may actively contribute to pro-inflammatory responses
655 within the liver by activating in a paracrine way the multimeric protein complex NLRP3
656 inflammasome in either hepatocytes and macrophages [65]. In this pathological context, the NLRP3
657 inflammasome may act as key cross-talk mechanism between injured hepatocytes and macrophages.
658 We have previously contributed to demonstrate that hepatic NLRP3 inflammasome overactivation
659 results in a sustained release of IL-1β, an event supporting the lobular inflammation in diet-related
660 metabolic diseases [66]. Here, correlations among highest LPS concentration, most intense
661 activation of the TLR4/MyD88/IRAK1 cascade and strongest NLRP3 inflammasome
662 expression/activity in the liver of S-Fr mice was demonstrated.

According to the microbiota analysis here reported and in keeping with previously published data [67, 68], we may speculate that the increased LPS translocation as well as systemic alterations of lipid metabolism and inflammatory response, are due, at least in part, to nutrient-induced modifications of the gut microbiota composition.

In conclusion, our results convincingly show that consumption of different fructose formulations, liquid or solid, evokes different impact on gut microbiota and integrity, thus differently affecting liver homeostasis. Our results suggest that the liquid fructose formulation is more rapidly absorbed by intestine and metabolized by the liver, leading to lipogenesis. In contrast, the solid fructose formulation is slowly absorbed by enterocytes leading to AGEs accumulation and affecting gut barrier integrity, with the following hepatic activation of the LPS-dependent TLR4/NLRP3 inflammasome cascade. Overall, the combined results of the microbiota analysis, faecal volatilome profiling and molecular insights bring to the fore an original and multidisciplinary approach to determine slight, not easily detectable, differences in the toxicological impact of different dietary manipulations, including changes in nutrients formulations.

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Table 1. General parameters. Physical characteristics, plasma glucose, insulin and triglyceride, and liver triglycerides of mice exposed for 12 weeks to standard diet (SD) or 60% fructose administered in liquid (L-Fr) or solid (S-Fr) formulation. Data are means ± s.e.m. of 6-10 mice per group. Statistical significance: *P<0.05, **P<0.01, vs SD; §P<0.05, §§§P<0.001, vs L-Fr.

	SD	L-Fr	S-Fr
Starting body weight (g)	16.17 ± 1.60	16.88 ± 2.39	15.99 ± 2.38
Ending body weight (g)	29.48 ± 1.72	28.42 ± 1.44	27.70 ± 2.71
Liver-to-body weight ratio (% of body weight)	3.21 ± 0.05	3.95 ± 0.12**	2.98 ± 0.21§§§
Fasting glycaemia (mg/dL)	114.5 ± 3.5	142.6 ± 6.7*	149.0 ± 5.7**
Insulinemia (ng/dL)	59.1 ± 9.2	49.0 ± 3.0	51.8 ± 7.9
TG (mg/dL)	26.3 ± 4.8	23.1 ± 1.6	28.5 ± 2.7
Hepatic TG (mg/g tissue)	24.8 ± 2.1	40.5 ± 5.5*	26.6 ± 1.2§
Urinary Glucose (mg/dL)	120.3 ± 25.4	1417.0 ± 424.5**	520.7 ± 259.4§
Urinary Fructose (mg/dL)	415.2 ± 122.6	453.9 ± 133.0	311.0 ± 55.0

Table 2. Characteristics of dietary intervention. Daily food and drink consumption and calories intake of mice exposed for 12 weeks to standard diet (SD) or 60% fructose administered in liquid (L-Fr) or solid (S-Fr) formulation. Data are means ± s.e.m. of 6-10 mice per group. Statistical significance: *P<0.05, ***P<0.001, vs SD; §P<0.05, §§§P<0.001, vs L-Fr.

	SD	L-Fr	S-Fr
Food intake (g/die)	2.95 ± 0.07	1.76 ± 0.03***	3.25 ± 0.15§§§
Drink intake (ml/die)	2.73 ± 0.07	2.78 ± 0.18	3.59 ± 0.25*§
Calories intake (Kcal/die)	11.34 ± 0.33	12.46 ± 0.36	12.63 ± 0.43
Fructose intake (g/die)	-	1.67 ± 0.11	1.88 ± 0.09

Figure Legends

Figure 1. GLUT-5 and GLUT-2 localization in intestine and liver. Representative photomicrographs showing expression and tissue distribution of GLUT-5 and GLUT-2 evaluated by indirect immunofluorescence on cryostatic sections of ileum (A and B, respectively) and GLUT-2 evaluated in liver (C) from mice exposed to SD and liquid and solid fructose. Data are means ± s.e.m. of 6-10 mice per group. Statistical significance: ***P<0.001, vs SD; §§§P<0.001, vs L-Fr.

Figure 2. Taxonomy analysis of mice gut microbiota. Relative abundance of the major taxonomic groups detected by 16S rRNA sequencing. Only OTUs with an incidence above 0.2% are shown.

Figure 3. Functional classification of mice gut metagenome. Functional classes were determined according to the second level of the KEGG annotations.

Figure 4. Faecal volatiles distribution. Heat map based on analytes relative abundance (mean of three analytical replicates) between mice faecal samples from S-Fr, L-Fr, and SD diets. Features (analytes detected) and diet groups dendrograms are shown to make easier the location of signature similitudes-differences as a function of diet manipulation. Data were centered and normalized against row standard deviation. Color scale varies between red (low abundance) to blue (high abundance).

Figure 5. Faecal volatilome signatures. Histogram referring to Coefficients of Variation (CV%) for informative analytes detected in L-Fr, S-Fr and SD diets (data were based on analytes relative abundance). Positive CV% values indicate analytes more abundant in fructose enriched diets while negative values indicate those more abundant in the SD diet. Red bars are for analytes exclusively detected in one population while asterisk is for those that reported statistically relevant changes ($p<0.05$).

Figure 6. Hepatic activation of the SCAP/SREBP1c lipogenic pathway. Representative immunoblotting showing the expression of the activating protein SCAP (A), the cytosol-to-nuclear translocation of SREBP1c (B), and the protein expression of the SREBP1c target genes ACC and FAS (C) on liver protein extracts. Histograms report the densitometric analysis for each protein normalized for the corresponding tubulin or histone H3 content, for cytosolic or nuclear extracts, respectively, and expressed as fold of SD value. Data are means ± s.e.m. of 6-10 mice per group. Statistical significance: *P<0.05, **P<0.01, ***P<0.001, vs SD; §§§P<0.001, vs L-Fr. (D) Representative photomicrographs of Oil red O staining performed on liver cryostatic sections for the evaluation of steatosis. Ballooning of hepatocytes and inflammatory foci can be observed in the 20X magnification micrographs of S-Fr sample.

Figure 7. Hepatic activation of fibrosis. Representative immunoblotting showing the expression of TGF-β (A), total and phosphorylated SMAD (B), fibronectin and vimentin (C) on liver protein extracts. Histograms report the densitometric analysis for each protein normalized for the corresponding tubulin content and expressed as fold of SD value. (D) Representative photomicrographs at 200x magnification of H&E staining performed on liver dewaxed sections for the evaluation of histology scoring. Histograms report the single components of NAS score and fibrosis staging (left graph), and the HIAD score for necro-inflammatory grading (right graph), evaluated on 10 fields per liver section. Data are means ± s.e.m. of 4-6 mice per group. Statistical significance: *P<0.05, **P<0.01, ***P<0.001, vs SD; §P<0.05, vs L-Fr.

Figure 8. AGEs accumulation and RAGE expression in the intestine. (A) Representative photomicrographs showing expression and tissue distribution of CML, CEL and RAGE evaluated by indirect immunofluorescence on cryostatic sections of ileum from mice exposed to SD and liquid and solid fructose. Enlarged squares show details of CML distribution in the intestinal villi axis. (B)

Analysis of immunoreactivity expressed as fluorescence intensity evaluated by Image J in the entire ileum section. Data are means ± s.e.m. of 5-6 mice per group. (C) Representative immunoblotting showing the CML-glycated proteins on liver protein extracts. Histograms report the densitometric analysis expressed as fold of SD value. Data are means ± s.e.m. of 6-10 mice per group. Statistical significance: *P<0.05, **P<0.01, ***P<0.001, vs SD; §P<0.05, §§P<0.01, vs L-Fr.

Figure 9. Tight junctions markers, plasma LPS and IAP activity. Gene expression of TJ proteins occludin (A) and ZO-1 (B) evaluated by RT-PCR analysis on mRNA samples from ileum tract and related protein levels (C and D). LPS concentration evaluated in portal (E) and systemic (F) plasma by biochemical technique represents an index of intestinal permeability. Intestinal alkaline phosphatse activity evaluated in ileum extracts by kinetic assay (G). Data are means ± s.e.m. of 6-10 mice per group. Statistical significance: *P<0.05, **P<0.01, vs SD; §P<0.05, §§P<0.01, vs L-Fr.

Figure 10. TLR4 and NLRP3 inflammatory pathways activation. The signaling pathway activated by TLR4, the major receptor involved in LPS-induced NLRP3 activation in liver, has been evaluated by western blotting analysis for the protein expression of TLR4 (A), MyD88 (B), and IRAK1 (C). Activation of liver inflammatory signaling has been evaluated by protein amount of NLRP3 (D), of pro-caspase and cleaved active caspase-1 (E), and of IL-1β (F) evaluated by western blotting on liver extracts. Data are means ± s.e.m. of 6-10 mice per group. Statistical significance: *P<0.05, **P<0.01, ***P<0.001, vs SD; §P<0.05, §§P<0.01, §§§P<0.001, vs L-Fr.

Figure 1

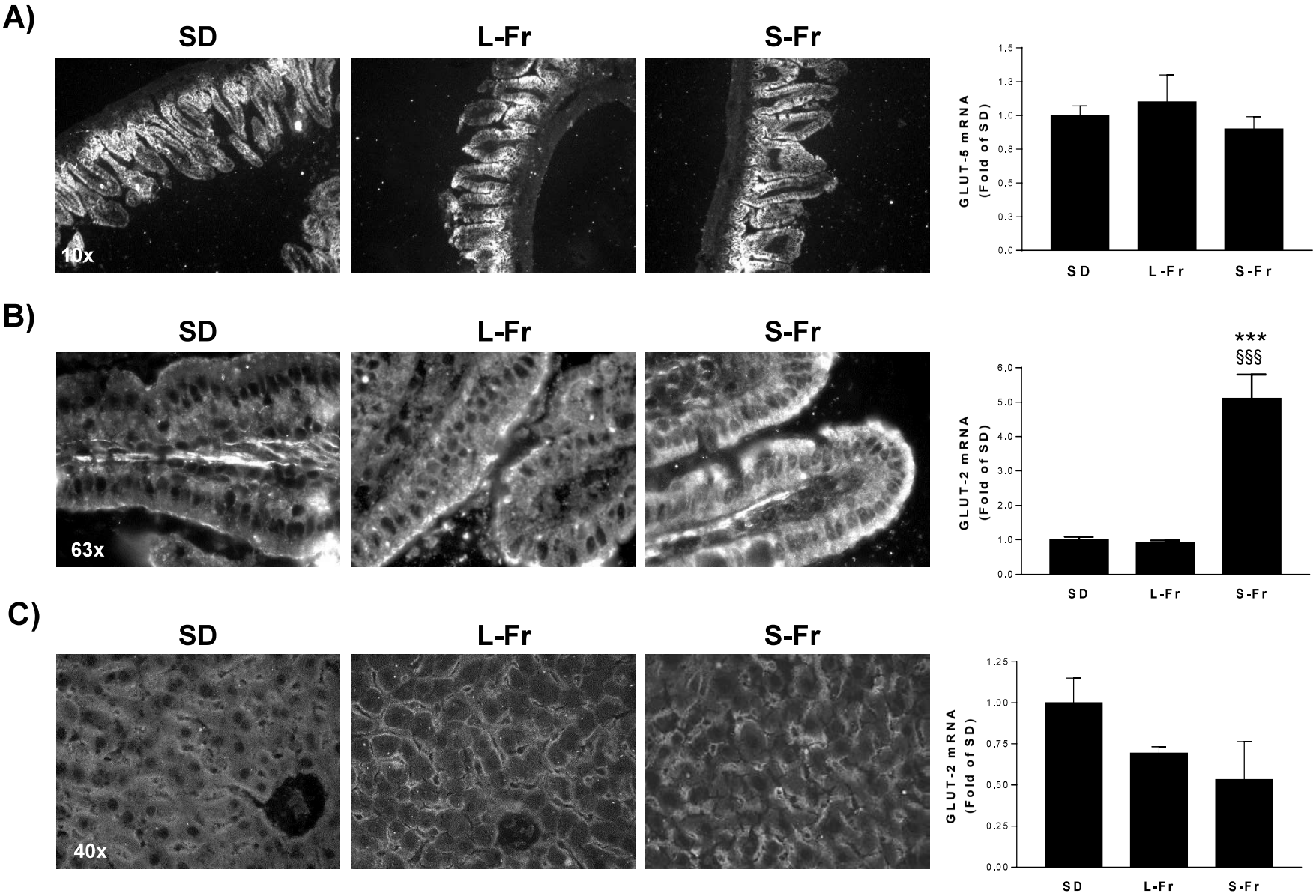
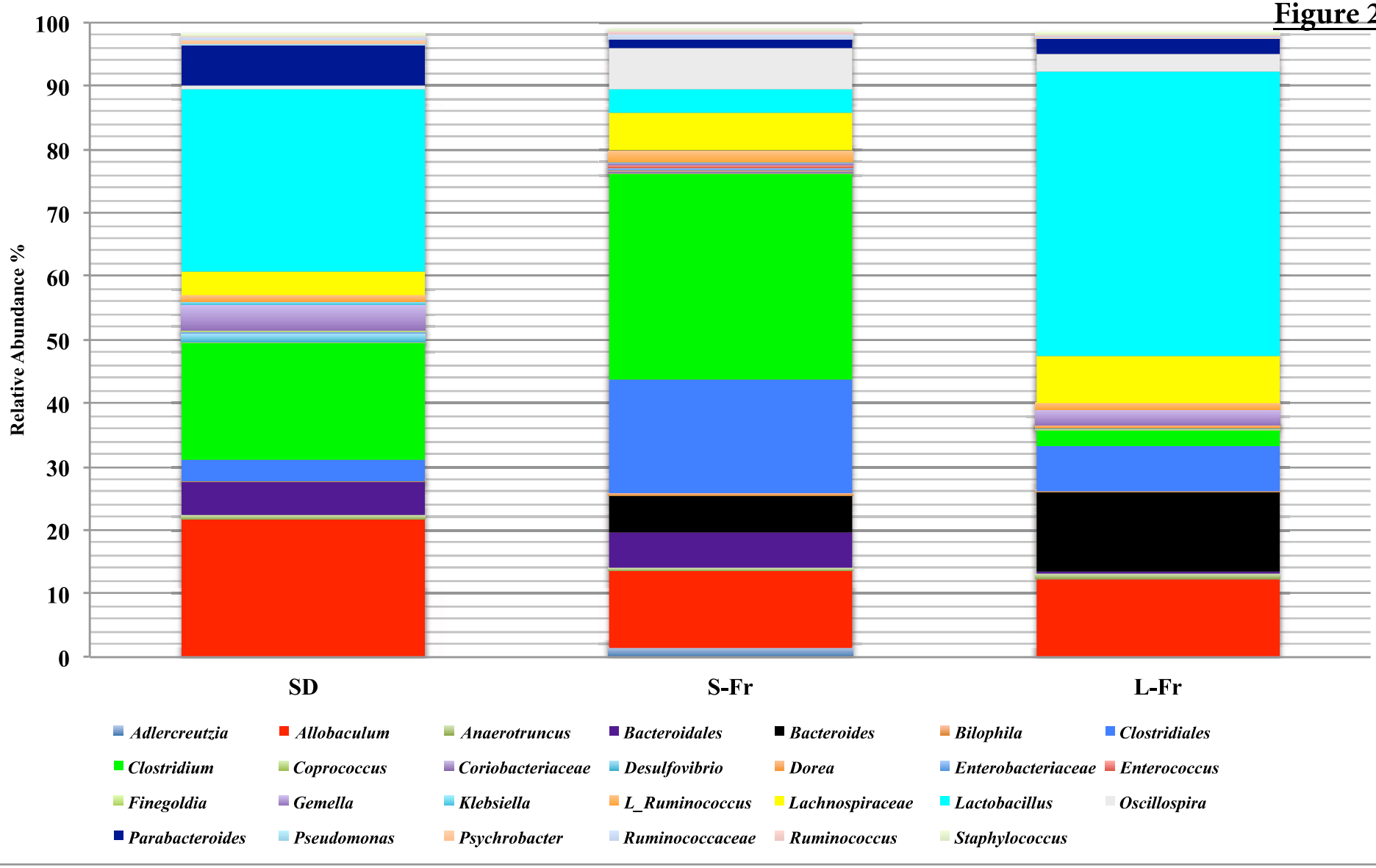

A)
SD
L-Fr
S-Fr
10x
GLUT-5 mRNA (Fold of SD)
1.5
1.3
1.0
0.8
0.5
0.3
0.0
SD
L-Fr
S-Fr
B)
SD
L-Fr
S-Fr
63x
***
§§§
GLUT-2 mRNA (Fold of SD)
6.0
5.0
4.0
3.0
2.0
1.0
0.0
SD
L-Fr
S-Fr
C)
SD
L-Fr
S-Fr
40x
GLUT-2 mRNA (Fold of SD)
1.25
1.00
0.75
0.50
0.25
0.00
SD
L-Fr
S-Fr

Figure 2


100
90
80
70
60
50
40
30
20
10
0
Relative Abundance %
SD
S-Fr
L-Fr
Adlercreutzia
Allobaculum
Anaerotruncus
Bacteroidales
Bacteroides
Bilophila
Clostridiales
Clostridium
Coprococcus
Coriobacteriaceae
Desulfovibrio
Dorea
Enterobacteriaceae
Enterococcus
Finegoldia
Gemella
Klebsiella
L_Ruminococcus
Lachnospiraceae
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Oscillospira
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Pseudomonas
Psychrobacter
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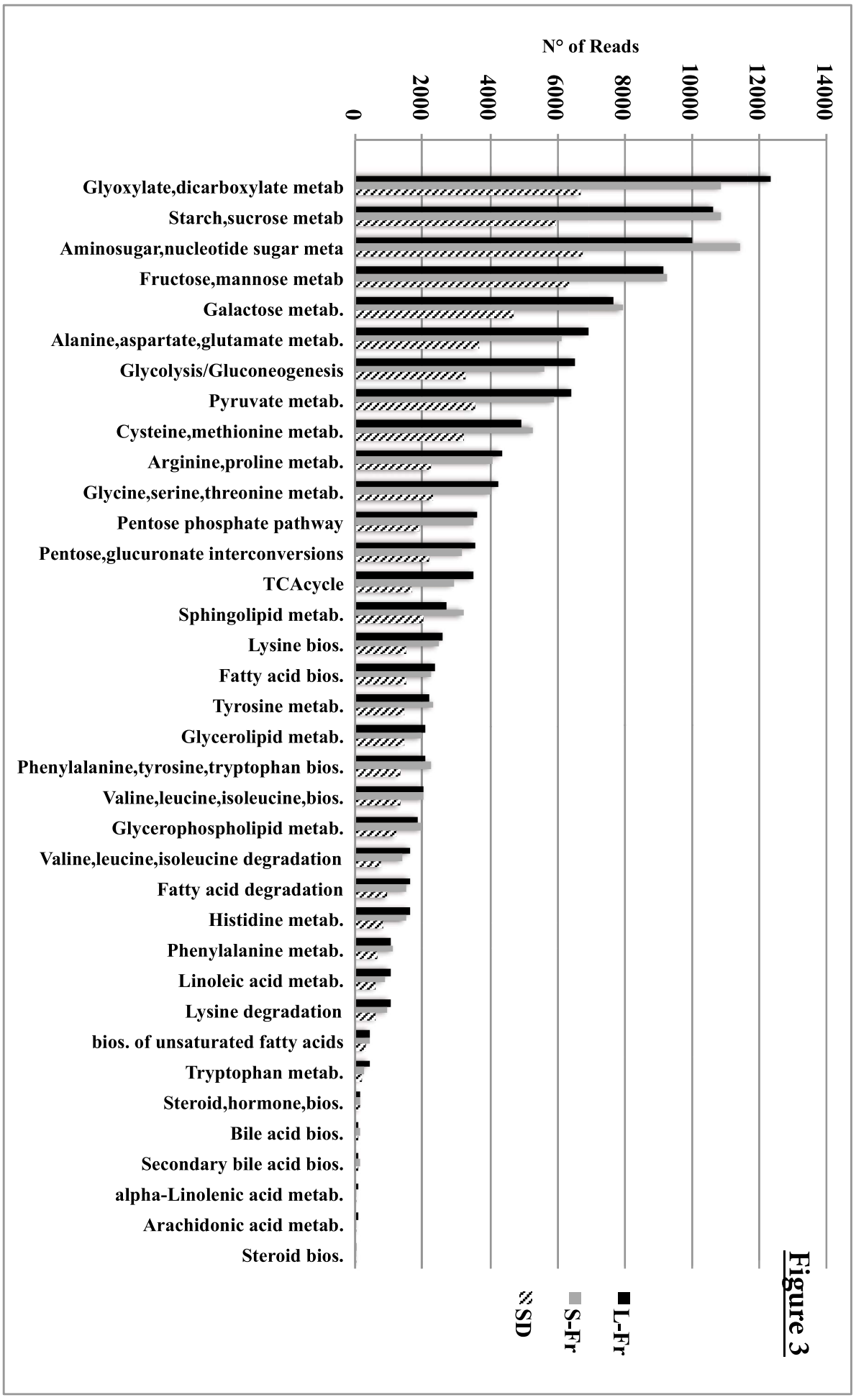
Ruminococcus
Staphylococcus


N° of Reads
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12000
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Starch,sucrose metab
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Fructose,mannose metab
Galactose metab.
Alanine,aspartate,glutamate metab.
Glycolysis/Gluconeogenesis
Pyruvate metab.
Cysteine,methionine metab.
Arginine,proline metab.
Glycine,serine,threonine metab.
Pentose phosphate pathway
Pentose,glucuronate interconversions
TCAcycle
Sphingolipid metab.
Lysine bios.
Fatty acid bios.
Tyrosine metab.
Glycerolipid metab.
Phenylalanine,tyrosine,tryptophan bios.
Valine,leucine,isoleucine,bios.
Glycerophospholipid metab.
Valine,leucine,isoleucine degradation
Fatty acid degradation
Histidine metab.
Phenylalanine metab.
Linoleic acid metab.
Lysine degradation
bios. of unsaturated fatty acids
Tryptophan metab.
Steroid,hormone,bios.
Bile acid bios.
Secondary bile acid bios.
alpha-Linolenic acid metab.
Arachidonic acid metab.
Steroid bios.
L-Fr
S-Fr
SD

Figure 3

Figure 4

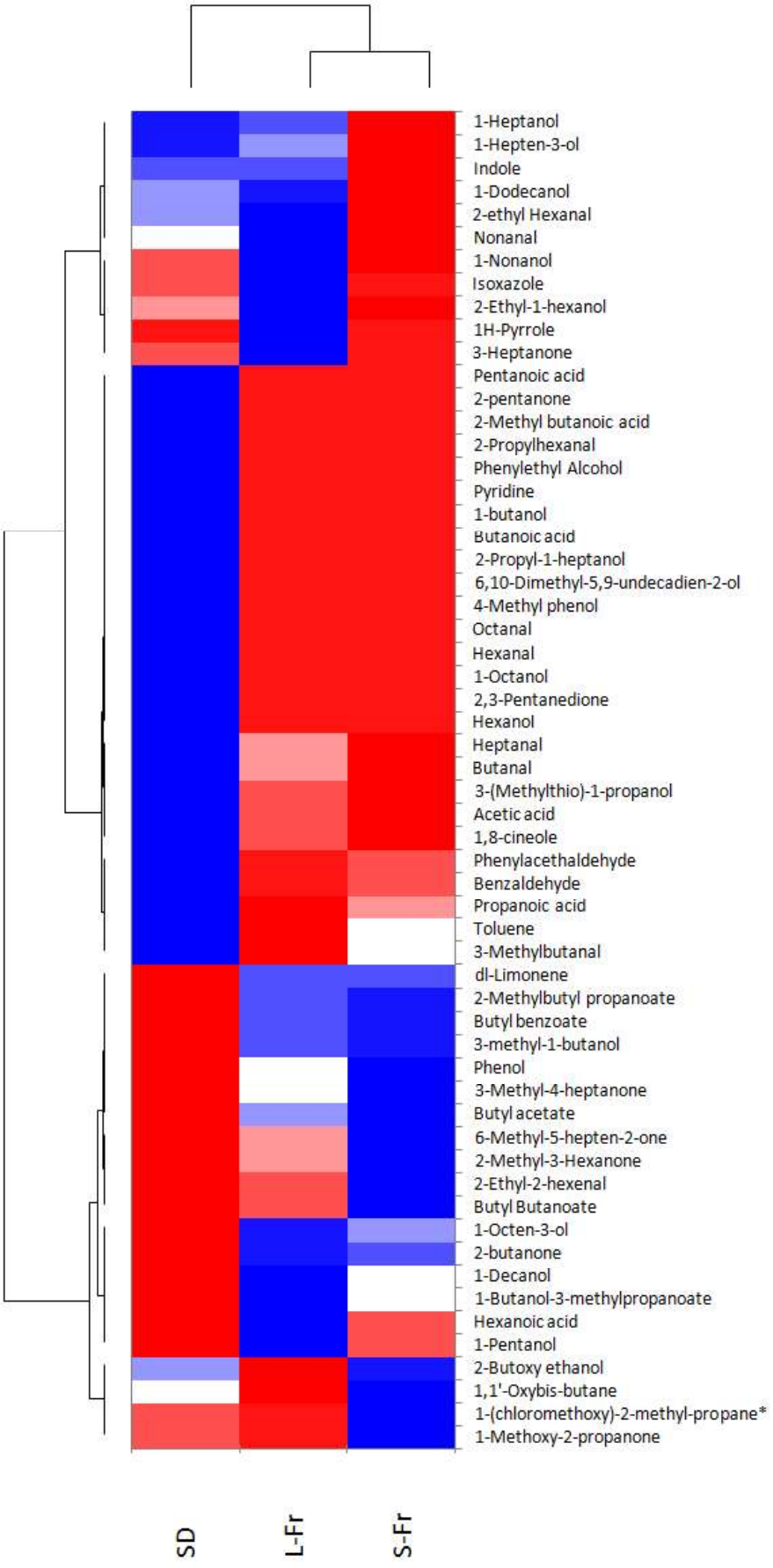

1-Heptanol
1-Hepten-3-ol
Indole
1-Dodecanol
2-ethyl Hexanal
Nonanal
1-Nonanol
Isoxazole
2-Ethyl-1-hexanol
1H-Pyrrole
3-Heptanone
Pentanoic acid
2-pentanone
2-Methyl butanoic acid
2-Propylhexanal
Phenylethyl Alcohol
Pyridine
1-butanol
Butanoic acid
2-Propyl-1-heptanol
6,10-Dimethyl-5,9-undecadien-2-ol
4-Methyl phenol
Octanal
Hexanal
1-Octanol
2,3-Pentanedione
Hexanol
Heptanal
Butanal
3-(Methylthio)-1-propanol
Acetic acid
1,8-cineole
Phenylacethaldehyde
Benzaldehyde
Propanoic acid
Toluene
3-Methylbutanal
dl-Limonene
2-Methylbutyl propanoate
Butyl benzoate
3-methyl-1-butanol
Phenol
3-Methyl-4-heptanone
Butyl acetate
6-Methyl-5-hepten-2-one
2-Methyl-3-Hexanone
2-Ethyl-2-hexenal
Butyl Butanoate
1-Octen-3-ol
2-butanone
1-Decanol
1-Butanol-3-methylpropanoate
Hexanoic acid
1-Pentanol
2-Butoxy ethanol
1,1'-Oxybis-butane
1-(chloromethoxy)-2-methyl-propane*
1-Methoxy-2-propanone
SD
L-Fr
S-Fr

Figure 5

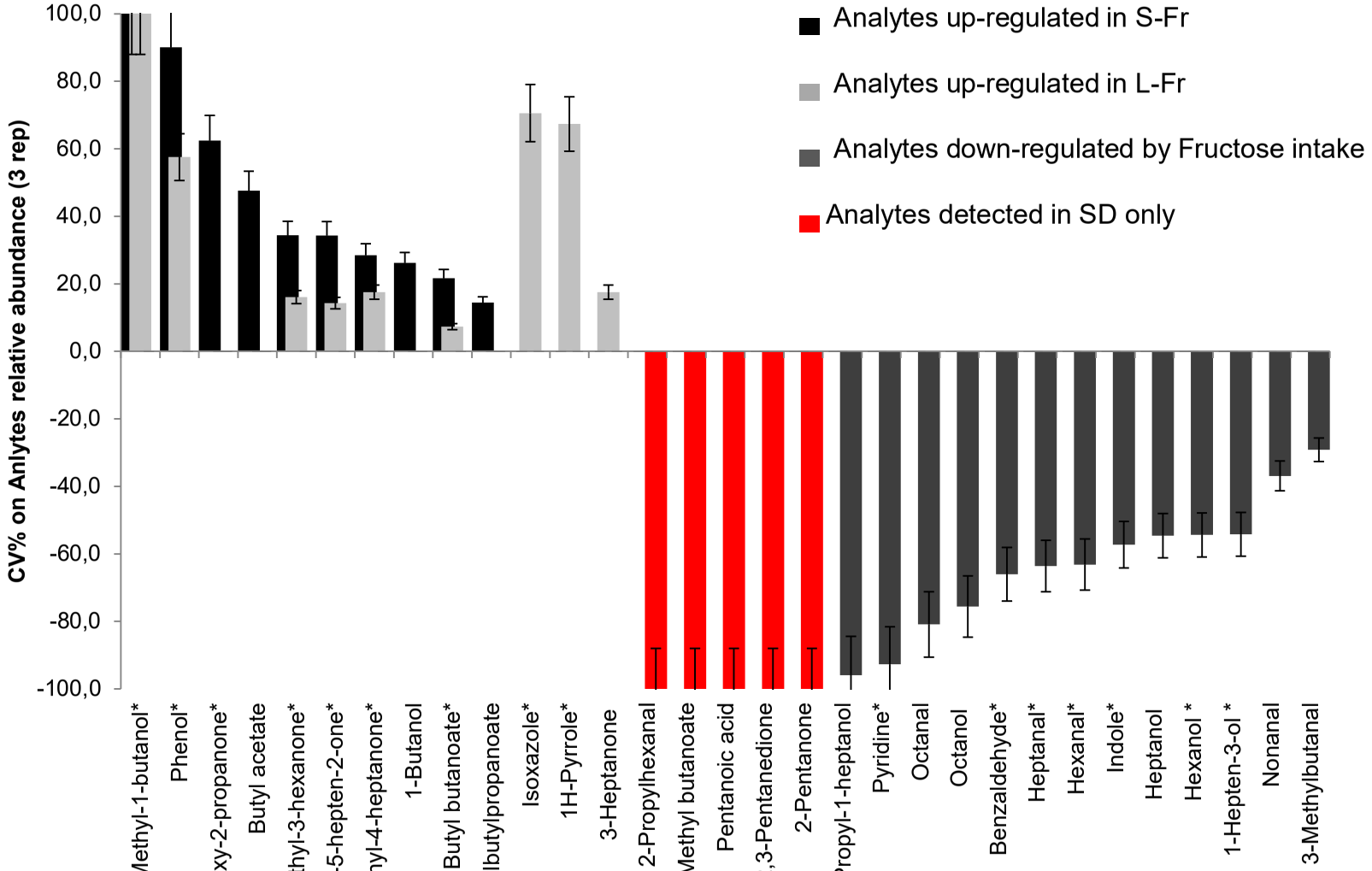

Analytes up-regulated in S-Fr
Analytes up-regulated in L-Fr
Analytes down-regulated by Fructose intake
Analytes detected in SD only
CV% on Anlytes relative abundance (3 rep)
100,0
80,0
60,0
40,0
20,0
0,0
-20,0
-40,0
-60,0
-80,0
-100,0
3-Methyl-1-butanol*
Phenol*
1-Methoxy-2-propanone*
Butyl acetate
2-Methyl-3-hexanone*
6-Methyl-5-hepten-2-one*
3-Methyl-4-heptanone*
1-Butanol
Butyl butanoate*
2-Methylbutylpropanoate
Isoxazole*
1H-Pyrrole*
3-Heptanone
2-Propylhexanal
2-Methyl butanoate
Pentanoic acid
2,3-Pentanedione
2-Pentanone
2-Propyl-1-heptanol
Pyridine*
Octanal
Octanol
Benzaldehyde*
Heptanal*
Hexanal*
Indole*
Heptanol
Hexanol *
1-Hepten-3-ol *
Nonanal
3-Methylbutanal

Figure 6

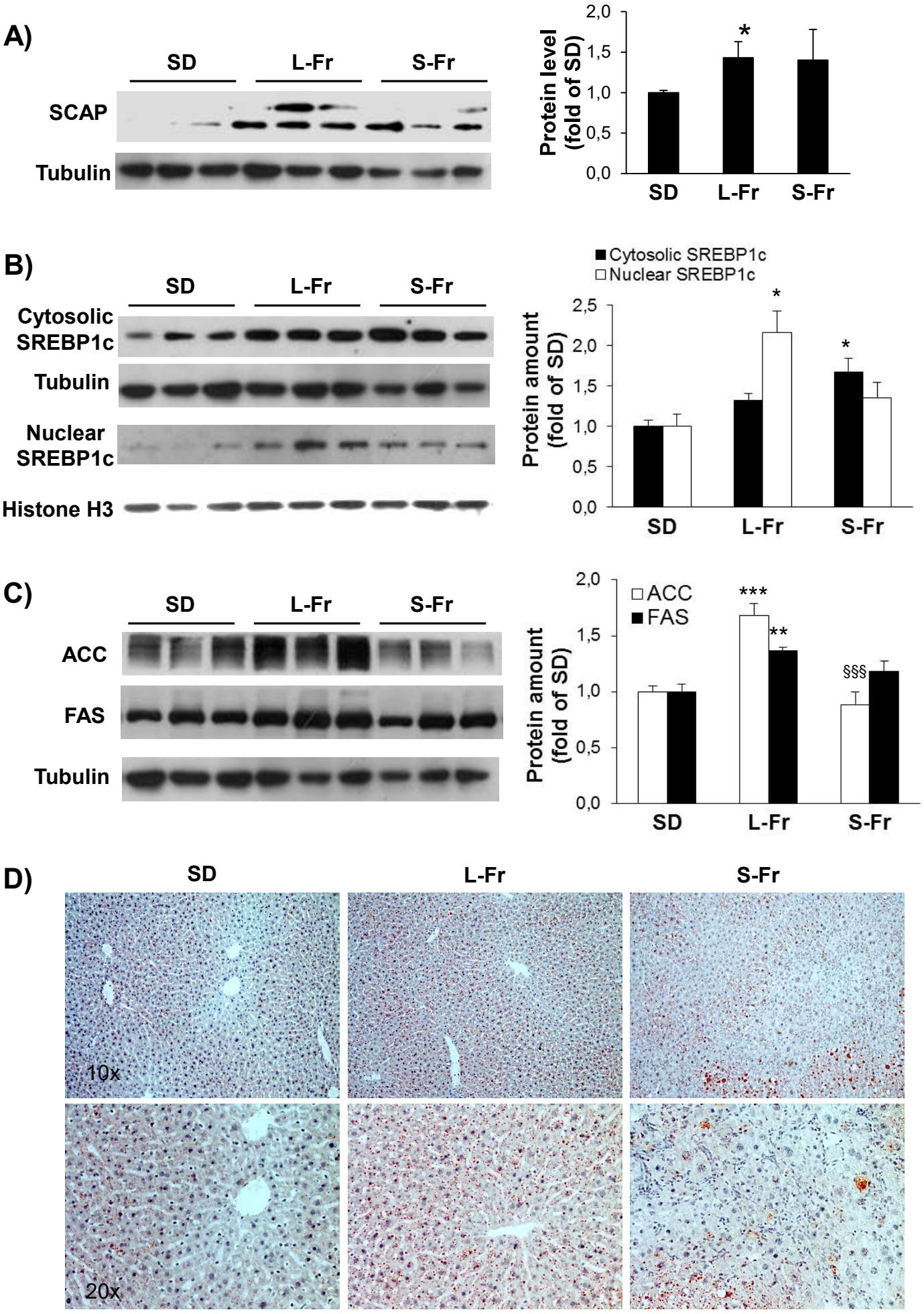

A)
SD
L-Fr
S-Fr
SCAP
Tubulin
Protein level (fold of SD)
2,0
1,5
1,0
0,5
0,0
*
SD
L-Fr
S-Fr
B)
SD
L-Fr
S-Fr
Cytosolic SREBP1c
Tubulin
Nuclear SREBP1c
Histone H3
Cytosolic SREBP1c
Nuclear SREBP1c
Protein amount (fold of SD)
2,5
2,0
1,5
1,0
0,5
0,0
*
*
SD
L-Fr
S-Fr
C)
SD
L-Fr
S-Fr
ACC
FAS
Tubulin
ACC
FAS
Protein amount (fold of SD)
2,0
1,5
1,0
0,5
0,0
***
**
§§§
SD
L-Fr
S-Fr
D)
SD
L-Fr
S-Fr
10x
20x

Figure 7

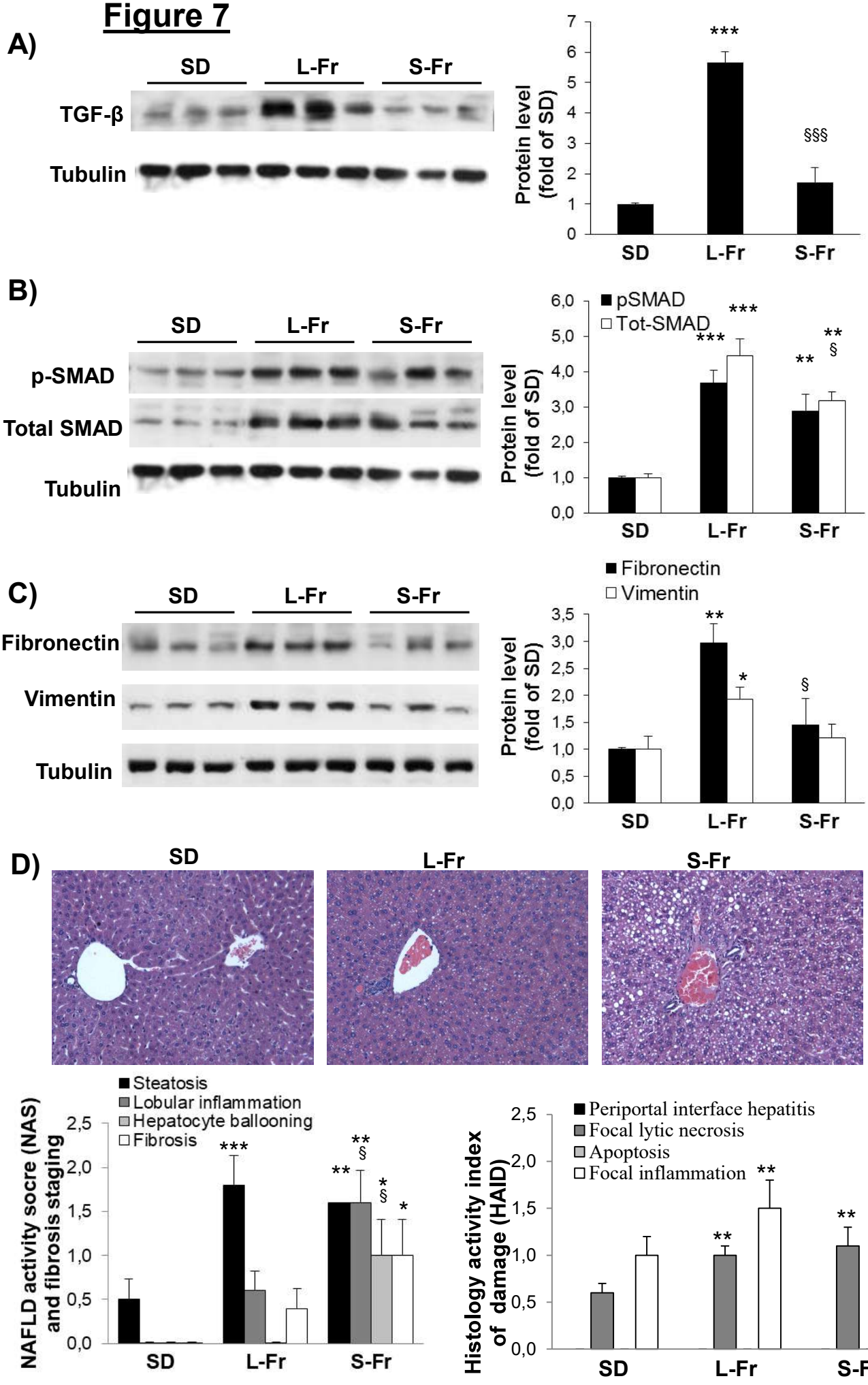
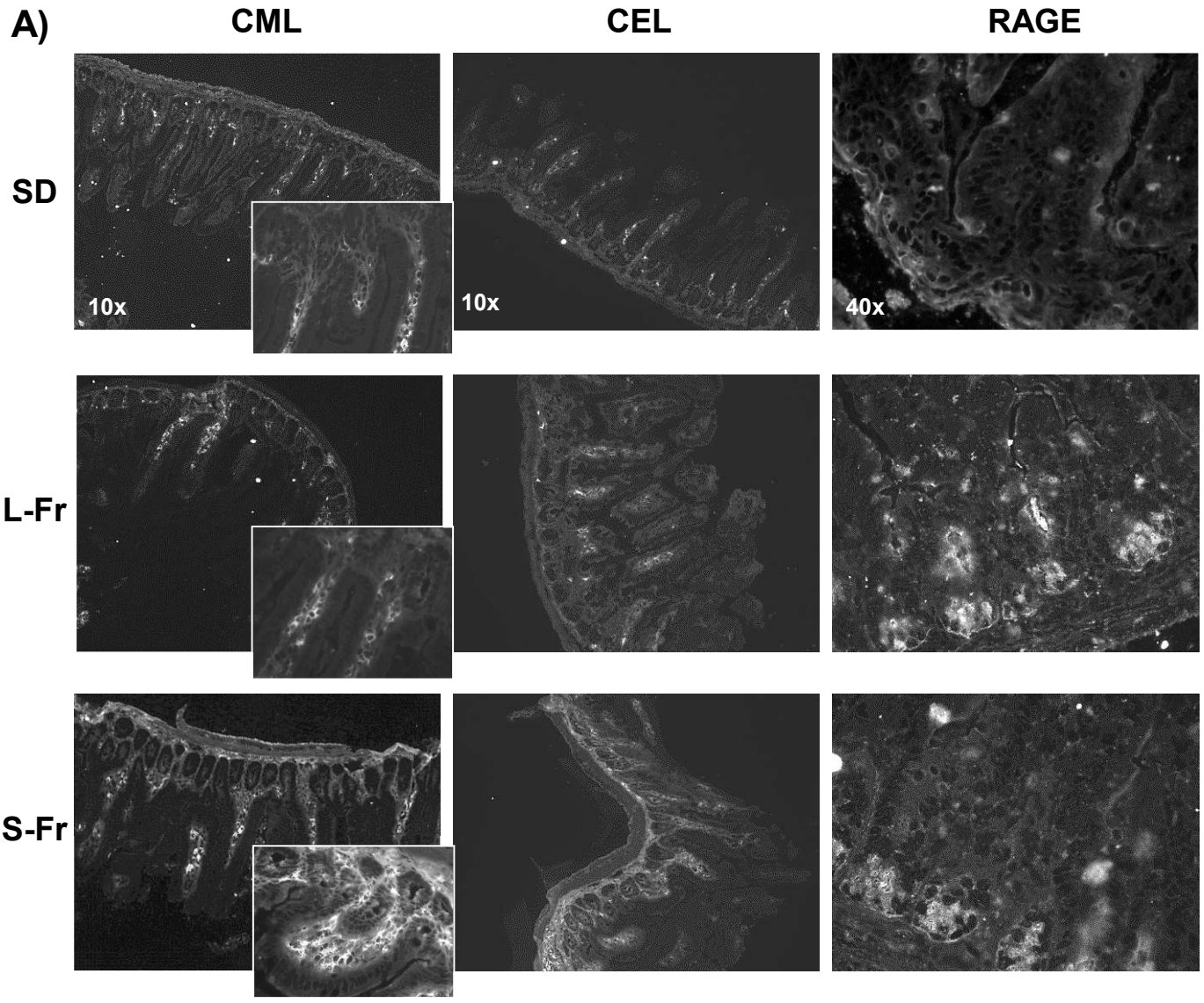
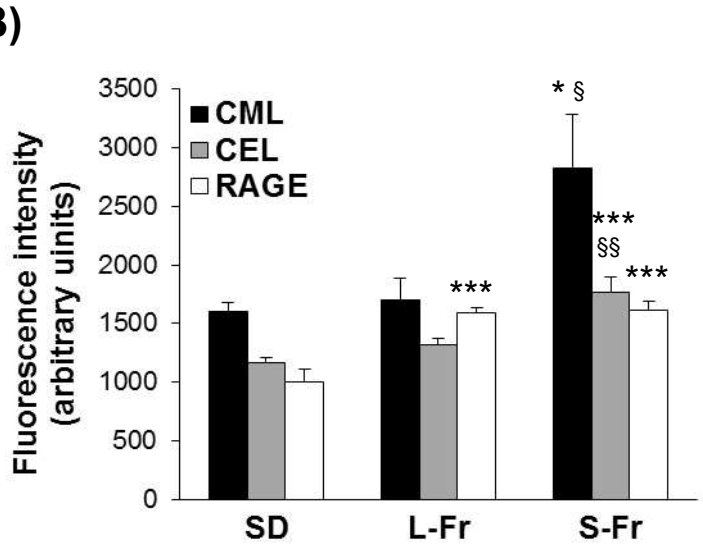

A)
SD
L-Fr
S-Fr
TGF-β
Tubulin
Protein level (fold of SD)
***
§§§
B)
p-SMAD
Total SMAD
Tubulin
pSMAD
Tot-SMAD
C)
Fibronectin
Vimentin
Tubulin
D)
Steatosis
Lobular inflammation
Hepatocyte ballooning
Fibrosis
NAFLD activity socre (NAS) and fibrosis staging
Periportal interface hepatitis
Focal lytic necrosis
Apoptosis
Focal inflammation
Histology activity index of damage (HAID)

Figure 8


A)
CML
CEL
RAGE
SD
L-Fr
S-Fr
10x
10x
40x


B)
Fluorescence intensity (arbitrary uinits)
3500
3000
2500
2000
1500
1000
500
0
CML
CEL
RAGE
* §
***
§§
***
***
SD
L-Fr
S-Fr

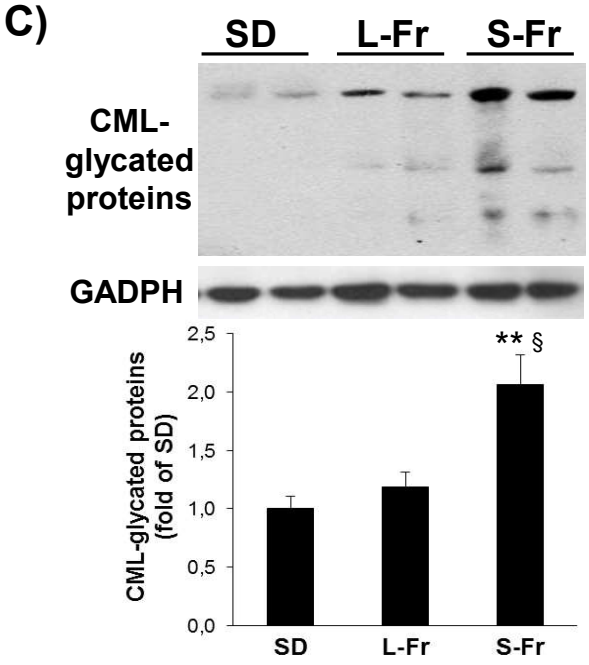

C)
SD
L-Fr
S-Fr
CML-glycated proteins
GADPH
CML-glycated proteins (fold of SD)
2,5
2,0
1,5
1,0
0,5
0,0
** §
SD
L-Fr
S-Fr

Figure 9

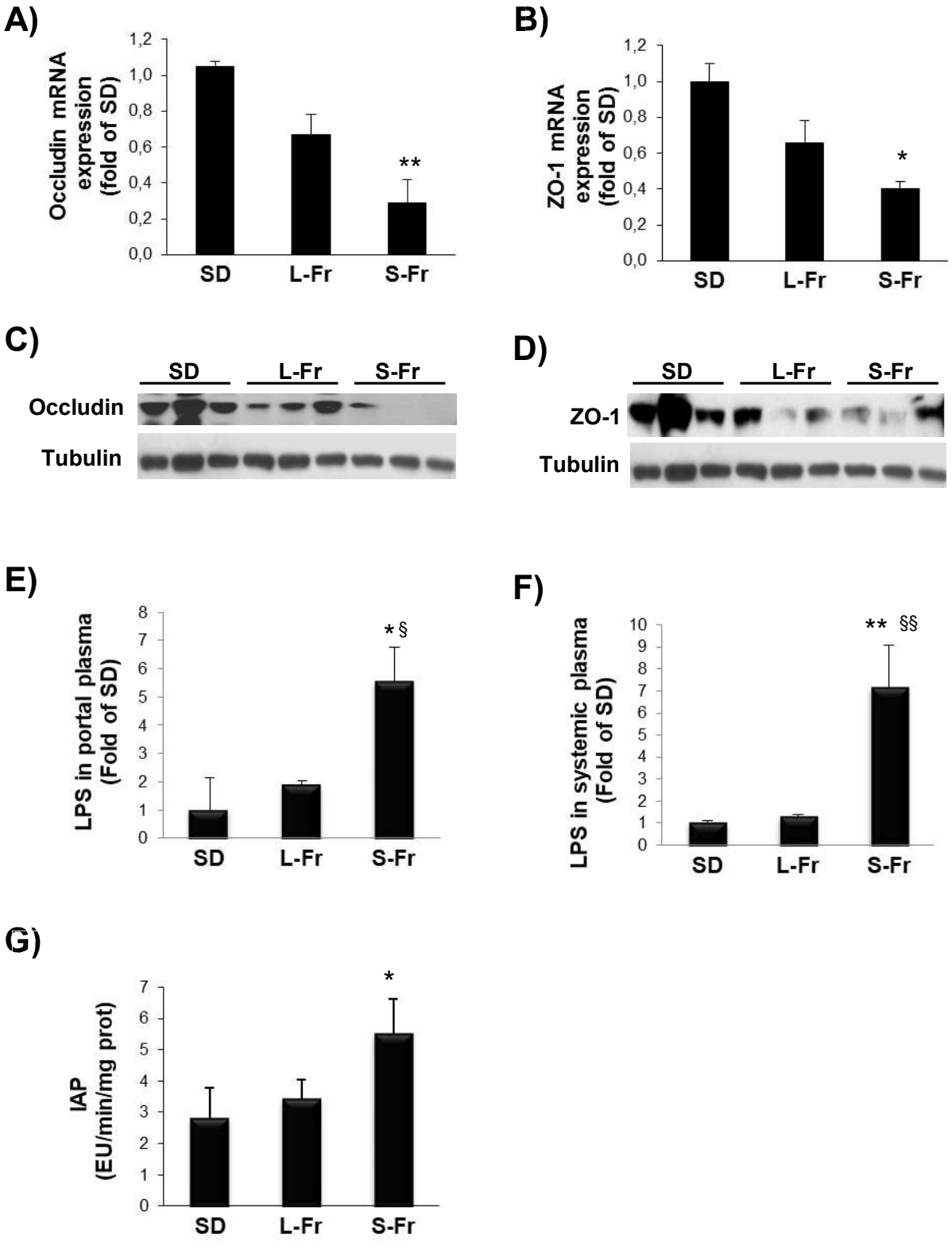
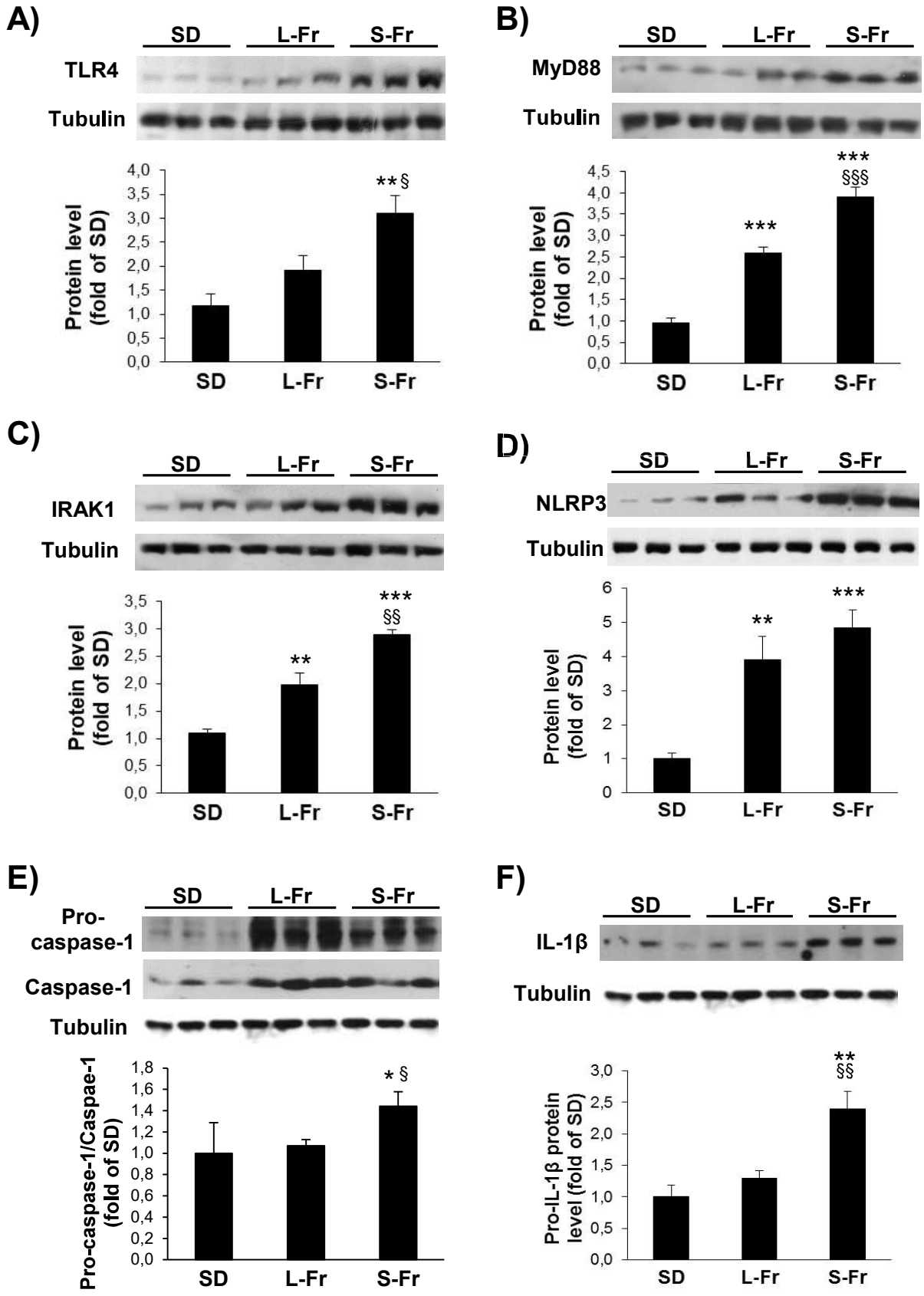
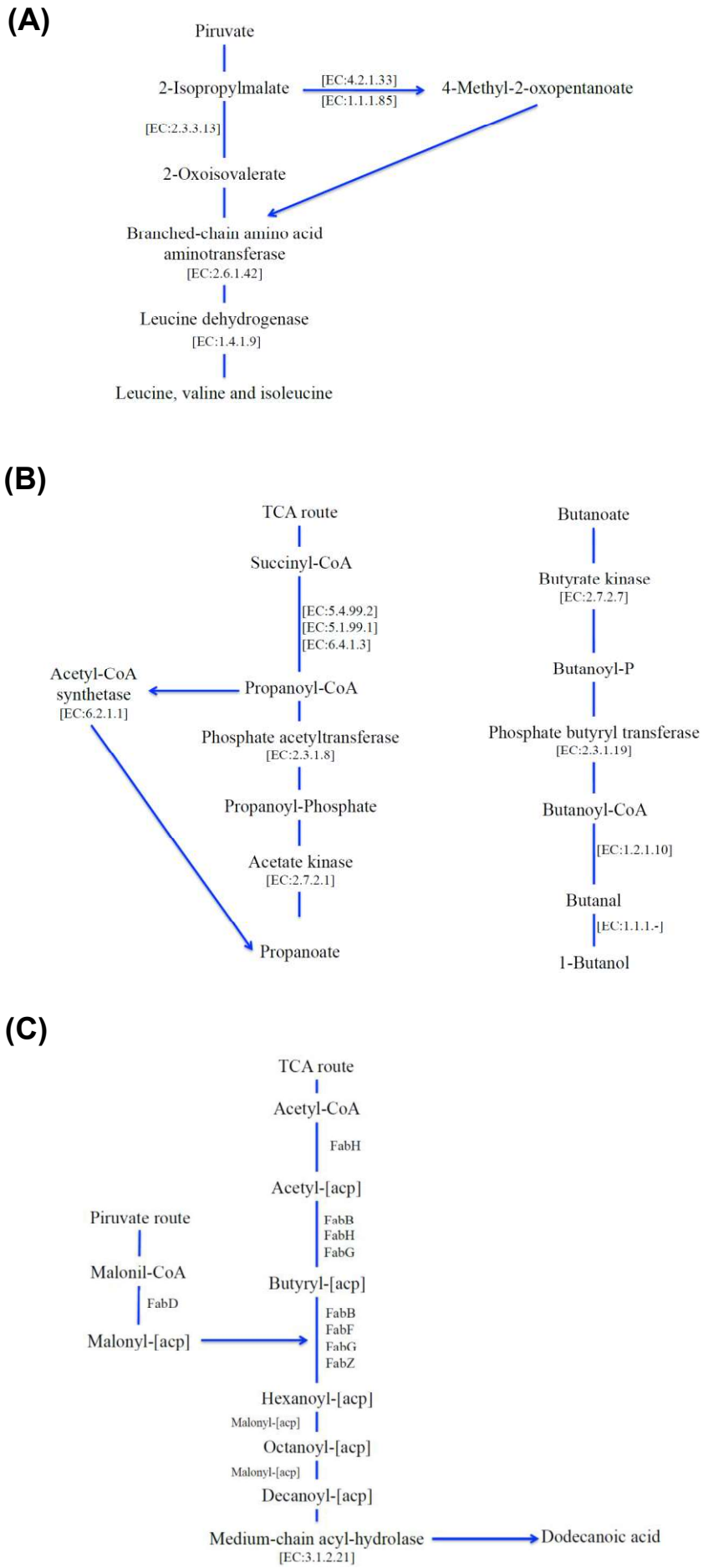

A)
Occludin mRNA expression (fold of SD)
1,2
1,0
0,8
0,6
0,4
0,2
0,0
**
SD
L-Fr
S-Fr
B)
ZO-1 mRNA expression (fold of SD)
1,2
1,0
0,8
0,6
0,4
0,2
0,0
*
SD
L-Fr
S-Fr
C)
SD
L-Fr
S-Fr
Occludin
Tubulin
D)
SD
L-Fr
S-Fr
ZO-1
Tubulin
E)
LPS in portal plasma (Fold of SD)
8
7
6
5
4
3
2
1
0
*§
SD
L-Fr
S-Fr
F)
LPS in systemic plasma (Fold of SD)
10
9
8
7
6
5
4
3
2
1
0
** §§
SD
L-Fr
S-Fr
G)
IAP (EU/min/mg prot)
7
6
5
4
3
2
1
0
*
SD
L-Fr
S-Fr

Figure 10


A)
SD
L-Fr
S-Fr
TLR4
Tubulin
Protein level (fold of SD)
**§
B)
MyD88
***
***
§§§
C)
IRAK1
**
***
§§
D)
NLRP3
**
***
E)
Pro-caspase-1
Caspase-1
Pro-caspase-1/Caspae-1 (fold of SD)
* §
F)
IL-1β
Pro-IL-1β protein level (fold of SD)
**
§§

Supplementary Figure1



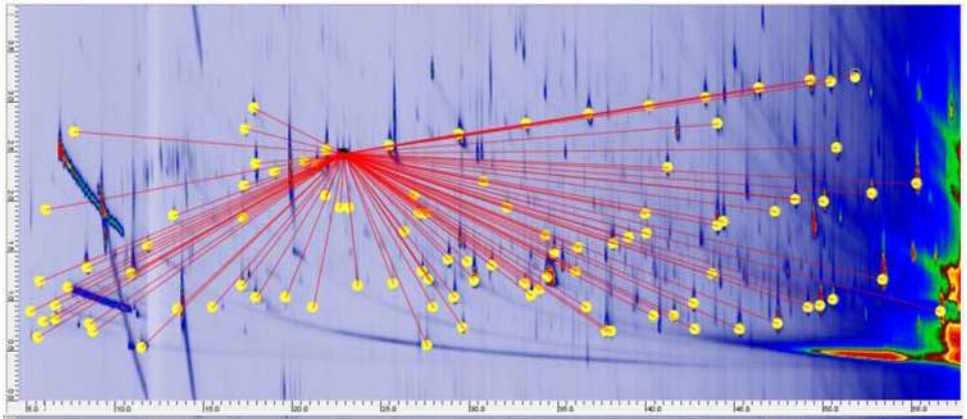


Figure S2a

S-Fr diet volatiles fingerprint
Averaged 2D plot of faeces volatiles.
Yellow circles indicate target analaytes and their relative position over the chromatographic plane. Red connection lines converge to the Internal Standard (α-Tujone) position (black circle).

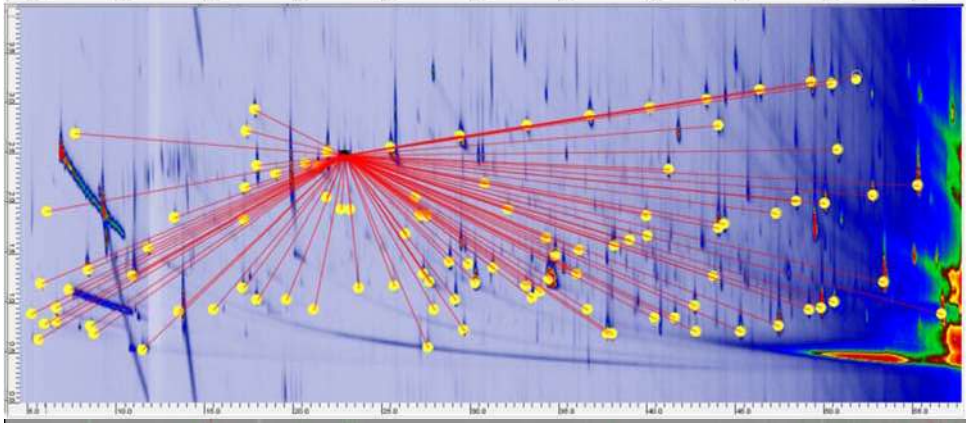


Figure S2b

L-Fr diet volatiles fingerprint
Averaged 2D plot of faeces volatiles.
Yellow circles indicate target analaytes and their relative position over the chromatographic plane. Red connection lines converge to the Internal Standard (α-Tujone) position (black circle).

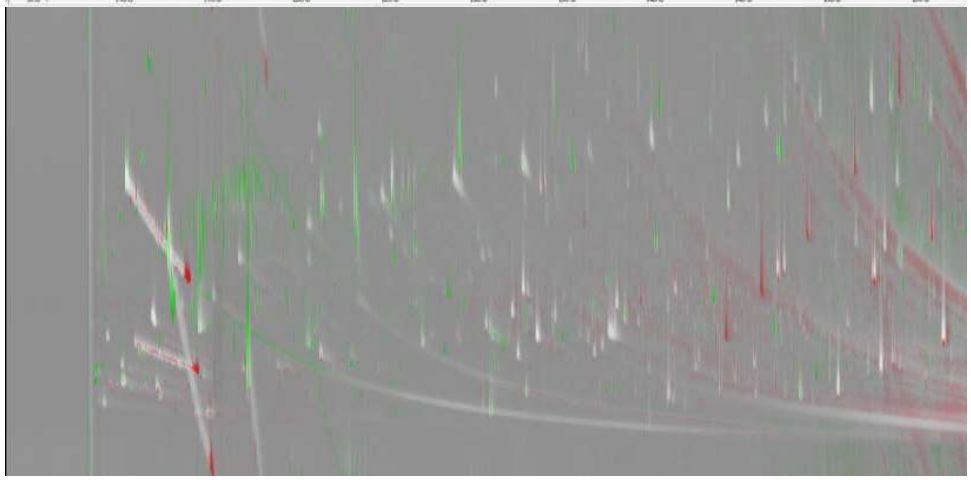
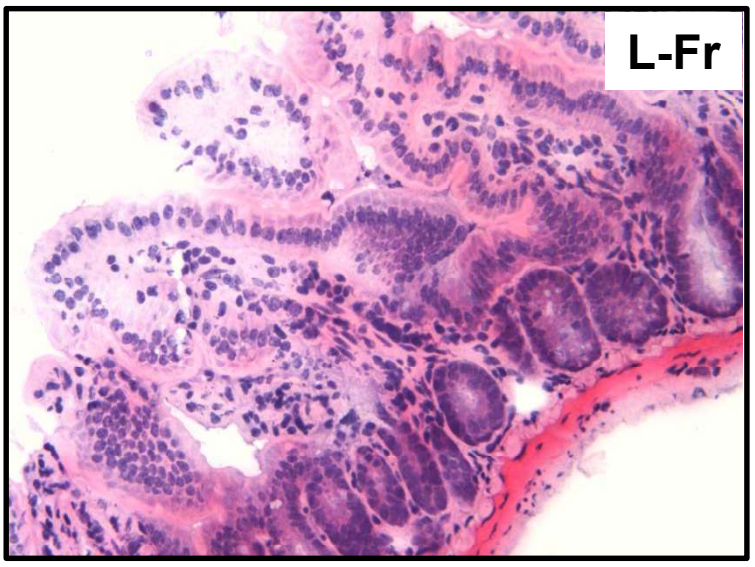


Figure S2c -Comparative visualization between S-Fr (reference) and L-Fr (analyzed) 2D patterns -Colorized fuzzy ratio rendering.
Visualization uses the Hue-Intensity-Saturation (HIS) color space to color each pixel in the retention-times plane. The method first computes the difference at each data point. The pixel hue is set to green if the difference is positive and red if it is negative (i.e., green if the value in the L-Fr chromatogram is smaller than the value in the S-Fr chromatogram and red if the value is greater). The pixel intensity is set to the larger of the two values (scaled by the largest intensity value in the chromatogram) and the pixel saturation is set to the magnitude of the difference between the data points (scaled by the magnitude of the largest difference in the chromatogram). Peaks are visible because large-valued data points yield bright pixels and small-valued data points yield dark pixels. If the difference is relatively large, the color is saturated with red or green (depending on the largest data point); if the difference is relatively small, the color saturation is low, producing a grey level from black to white depending on intensity. Peaks with large differences therefore appear red or green and peaks with small differences appear white or grey. The fuzzy difference is computed as the difference between a data point and a small region of data points in the other chromatogram (scaled by the largest fuzzy difference in the chromatogram). Thus, the colors are saturated with red or green only when the relative difference is large.

Supplementary Figure 3



kegg	fl	fs	sd
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K13734_ko05100_BacterialinvasionofepithelialcIls_Humandiseases_Infectiousdiseases_sfb1,fibronectin-bindingprotein1	0,002598332	0,002766766	0,003729112
K13735_ko05100_BacterialinvasionofepithelialcIls_Humandiseases_Infectiousdiseases_yeeJ,adhesin/invasin	0,000259315	0,000300625	0,000465101
K00558_ko05206_MicroRNAsincancer_HumanDiseases_Cancers_DNMT1,dcm,DNA(cytosine-5)-methyltransferase1[EC:2.1.1.37];K00558_ko00270_Cysteineandmethioninemetabolism_Metabolism_Aminoacidmetabolism_DNMT1,dcm,DNA(cytosine-5)-methyltrans	0,006845905	0,006201021	0,008346899
K01225_ko00500_Starchandsucrosemetabolism_Metabolism_Carbohydratemetabolism_E3.2.1.91,cellulose1,4-beta-cellobiosidase[EC:3.2.1.91]	0,001270641	0,000927351	0,000847148
K03655_ko03440_HomologousrecombinationGeneticinformationProcessing_ReplicationandRepair_recG,ATP-dependentDNAhelicaseRecG[EC:3.6.4.12]	0,011274998	0,008692639	0,009717285
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K03555_ko03430_MismatchrepairGeneticinformationProcessing_ReplicationandRepair_mutS,DNAmismatchrepairproteinMutS	0,007898722	0,01023143	0,010464769
K01190_ko00052_GalactosemetabolismMetabolism_Carbohydratemetabolism_lacZ,beta-galactosidase[EC:3.2.1.23];K01190_ko00511_OtherglycandegradationMetabolism_Glycanbiosynthesisandmetabolism_lacZ,beta-galactosidase[EC:3.2.1.23];K01190_ko006(	0,009309393	0,011021207	0,010622571
K15125_ko05133_Pertussis_HumanDiseases_Infectiousdiseases_fhaB,filamentoushemagglutinin	0,001068376	0,00099359	0,001195974
K01183_ko00520_AminosugarandnucleotidesugarmetabolismMetabolism_Carbohydratemetabolism_E3.2.1.14,chitinase[EC:3.2.1.14]	0,000663845	0,001019067	0,000872064
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K06236_ko04510_Focaladhesion_Cellgrowthanddeath_Cellularcommunity_COL1AS,collagen,typeI/II/III/V/XI/XXIV/XXVII,alpha;K06236_ko04151_PI3K-Aktsignalingpathway_Environmentalinformationprocessing_Signaltrasduction_COL1AS,collagen,typeI/II/III/V/XI/	4,66766E-05	1,5286E-05	0,000116275
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K05349_ko00940_PhenylpropanoidbiosynthesisMetabolism_BiosynthesisofothersecondarymetabolitesbglX,beta-glucosidase[EC:3.2.1.21];K05349_ko00500_StarchandsucrosemetabolismMetabolism_Carbohydratemetabolism_bglX,beta-glucosidase[EC:3.2.1.21	0,005715293	0,007240469	0,004401847
K04786_ko01053_BiosynthesisofsiderophoregroupnonribosomalpeptidesMetabolism_Metabolismofterpenoidsandpolyketidesirp1,HMWP1,yersiniabactinnonribosomalpeptide/polyketidesynthase	0,000207452	8,15253E-05	0,000141191
K14572_ko03008_RibosomebiogenesisineukaryotesGeneticinformationProcessing_Transcription_MDN1,REA1,midasin	4,14903E-05	2,03813E-05	3,32215E-05
K03332_ko00051_FructoseandmannosemetabolismMetabolism_Carbohydratemetabolism_E3.2.1.80,fructanbeta-fructosidase[EC:3.2.1.80]	0,000264501	0,000157955	0,000207634
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K01078_ko05152_TuberculosisHumanDiseases_Infectiousdiseases_E3.1.3.2,acidphosphatase[EC:3.1.3.2];K01078_ko00740_RiboflavinmetabolismMetabolism_MetabolismofcofactorsandvitaminsE3.1.3.2,acidphosphatase[EC:3.1.3.2];K01078_ko00627_Aminobe	0,000606796	0,000428008	0,000182718
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K01188_ko00940_PhenylpropanoidbiosynthesisMetabolism_BiosynthesisofothersecondarymetabolitesE3.2.1.21,beta-glucosidase[EC:3.2.1.21];K01188_ko00500_StarchandsucrosemetabolismMetabolism_Carbohydratemetabolism_E3.2.1.21,beta-glucosidase[E	0,001192847	0,001258547	0,001204279
K12681_ko05133_Pertussis_HumanDiseases_Infectiousdiseases_prn,pertactin	0,000897228	0,000636917	0,001104614
K01227_ko00511_OtherglycandegradationMetabolism_Glycanbiosynthesisandmetabolism_E3.2.1.96,mannosyl-glycoproteinendo-beta-N-acetylglucosaminidase[EC:3.2.1.96]	0,000814248	0,000973209	0,001295638
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K12373_ko04142_Lysosome_CellularProcesses_TransportandcatabolismHEXA_B,hexosaminidase[EC:3.2.1.52];K12373_ko00520_AminosugarandnucleotidesugarmetabolismMetabolism_Carbohydratemetabolism_HEXA_B,hexosaminidase[EC:3.2.1.52];K12373_k	0,003448884	0,003918312	0,004136075
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K14475_ko05143_Africantrypanosomiasis_HumanDiseases_Infectiousdiseases_ICP,inhibitorofcysteinepeptidase	0,00028006	0,000290434	0,000298993
K07258_ko01005_LipopolysaccharidebiosynthesisproteinsMetabolism_Glycanbiosynthesisandmetabolism_dacC,dacA,dacD,D-alanyl-D-alaninecarboxypeptidase(penicillin-bindingprotein5/6)[EC:3.4.16.4]	0,001815202	0,002094182	0,002267367
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K01952_ko00230_PurinemetabolismMetabolism_Nucleotidemetabolism_purL,PFAS,phosphoribosylformylglycinamidinesynthase[EC:6.3.5.3]	0,002613891	0,00267505	0,00233381
K03763_ko03030_DNAreplicationGeneticinformationProcessing_ReplicationandRepair_DPO3A2,polC,DNApolymeraseIIIsubunitalpha,Gram-positivetype[EC:2.7.7.7];K03763_ko03440_HomologousrecombinationGeneticinformationProcessing_ReplicationandRep	0,002525724	0,002802434	0,002956712
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K00284_ko00630_GlyoxylateanddicarboxylatemetabolismMetabolism_Carbohydratemetabolism_E1.4.7.1,glutamatesynthase(ferredoxin)[EC:1.4.7.1];K00284_ko00910_NitrogenmetabolismMetabolism_Energymetabolism_E1.4.7.1,glutamatesynthase(ferredoxir	0,000985395	0,000749014	0,000863759
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K01209_ko00520_AminosugarandnucleotidesugarmetabolismMetabolism_Carbohydratemetabolism_E3.2.1.55,abfA,alpha-N-arabinofuranosidase[EC:3.2.1.55]	0,002318272	0,002649574	0,001702601
K02316_ko03030_DNAreplicationGeneticinformationProcessing_ReplicationandRepair_dnaG,DNAprimase[EC:2.7.7.-]	0,003583727	0,004438036	0,003604531
K00265_ko00250_Alanine,aspartateandglutamatemetabolismMetabolism_Aminoacidmetabolism_gltB,glutamatesynthase(NADPH/NADH)largechain[EC:1.4.1.131.4.1.14];K00265_ko00910_NitrogenmetabolismMetabolism_Energymetabolism_gltB,glutamatesyn	0,00050307	0,000708251	0,000672735
K10841_ko03420_NucleotideexcisionrepairGeneticinformationProcessing_ReplicationandRepair_ERCC6,CSB,RAD26,DNAexcisionrepairproteinERCC-6	0,000357854	0,000183432	0,000132886
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K14326_ko03015_mRNAsurveillancepathwayGeneticinformationProcessing_Transcription_UPF1,RENT1,regulatorofnonsensetranscripts1[EC:3.6.4.-];K14326_ko03013_RNAtransportGeneticinformationProcessing_Transcription_UPF1,RENT1,regulatorofnonsense	0,000223011	0,000321006	0,000780705
K03657_ko03430_MismatchrepairGeneticinformationProcessing_ReplicationandRepair_uvrD,pcrA,DNAhelicaseII/ATP-dependentDNAhelicasePcrA[EC:3.6.4.12];K03657_ko03420_NucleotideexcisionrepairGeneticinformationProcessing_ReplicationandRepair_uv	0,004854369	0,005742441	0,005954952
K01119_ko00230_PurinemetabolismMetabolism_Nucleotidemetabolism_cpdB,2',3'-cyclic-nucleotide2'-phosphodiesterase/3'-nucleotidase[EC:3.1.4.163.1.3.6];K01119_ko00240_PyrimidinemetabolismMetabolism_Nucleotidemetabolism_cpdB,2',3'-cyclic-nuclec	0,000554933	0,000942637	0,000780705
K00688_ko00500_StarchandsucrosemetabolismMetabolism_Carbohydratemetabolism_E2.4.1.1,glgP,PYG,starchphosphorylase[EC:2.4.1.1];K00688_ko04910_Insulinsignalingpathway_Organismalsystem_Endocrinsystem_E2.4.1.1,glgP,PYG,starchphosphorylase[EC:	0,004289063	0,0038215	0,003546394
K01955_ko00250_Alanine,aspartateandglutamatemetabolismMetabolism_Aminoacidmetabolism_carB,CPA2,carbamoyl-phosphatesynthaselargesubunit[EC:6.3.5.5];K01955_ko00240_PyrimidinemetabolismMetabolism_Nucleotidemetabolism_carB,CPA2,carbar	0,005694548	0,004748851	0,004551344
K00969_ko00760_NicotinateandnicotinamidemetabolismMetabolism_Metabolismofcofactorsandvitamins_nadD,nicotinate-nucleotideadenylyltransferase[EC:2.7.7.18]	0,00050307	0,000642012	0,000747483
K03043_ko03020_RNApolymeraseGeneticinformationProcessing_Transcription_rpoB,DNA-directedRNApolymerasesubunitbeta[EC:2.7.7.6];K03043_ko00230_PurinemetabolismMetabolism_Nucleotidemetabolism_rpoB,DNA-directedRNApolymerasesubunitbeta	0,006239109	0,005329719	0,004136075
K02337_ko03030_DNAreplicationGeneticinformationProcessing_ReplicationandRepair_DPO3A1,dnaE,DNApolymeraseIIIsubunitalpha[EC:2.7.7.7];K02337_ko03440_HomologousrecombinationGeneticinformationProcessing_ReplicationandRepair_DPO3A1,dnaE,I	0,004745457	0,005941159	0,006054616
K11892_ko02010_CtransportersEnvironmentalinformationprocessing_Membranetransport_impK,ompA,vasF,dotU,typeVIsecretionsystemproteinImpK	1,55589E-05	1,01907E-05	8,30537E-06
K00754_ko00051_FructoseandmannosemetabolismMetabolism_Carbohydratemetabolism_E2.4.1.-,[EC:2.4.1.-]	0,019339681	0,021349448	0,028146905
K07636_ko02020_Two-componentsystemEnvironmentalinformationprocessing_Signaltrasduction_phoR,two-componentsystem,OmpRfamily,phosphateregulonsensorhistidinekinasePhoR[EC:2.7.13.3]	0,00313252	0,002797338	0,002524833
K01213_ko00040_PentoseandglucuronateinterconversionsMetabolism_Carbohydratemetabolism_E3.2.1.67,galacturan1,4-alpha-galacturonidase[EC:3.2.1.67];K01213_ko00500_StarchandsucrosemetabolismMetabolism_Carbohydratemetabolism_E3.2.1.67,gala	0,004449838	0,002384616	0,004734062
K01731_ko00040_PentoseandglucuronateinterconversionsMetabolism_Carbohydratemetabolism_E4.2.2.9,pectatedisaccharide-lyase[EC:4.2.2.9]	9,85395E-05	5,09533E-05	8,30537E-05

K10595_ko04120_Ubiquitinmediatedproteolysis_GeneticInformationProcessing_Folding,sortinganddegradation_HERC2,E3ubiquitin-proteinligaseHERC2[EC:6.3.2.19]	1,03726E-05	1,01907E-05	4,15269E-05
K02230_ko00830_Retinolmetabolism_Metabolism_Metabolismofcofactorsandvitamins_cobN,cobaltochelataseCobN[EC:6.6.1.2]	0,000440835	0,000224195	0,000265772
K01728_ko00040_PentoseandglucuronateinterconversionsMetabolism_Carbohydratemetabolism_E4.2.2.2,pel,pectatelyase[EC:4.2.2.2]	0,00046158	0,000468771	0,000473406
K01192_ko04142_Lysosome_CellularProcesses_Transportandcatabolism_E3.2.1.25,MANBA,manB,beta-mannosidase[EC:3.2.1.25];K01192_ko00511_Otherglycandegradation_Metabolism_Glycanbiosynthesisandmetabolism_E3.2.1.25,MANBA,manB,beta-mannosid	0,001296573	0,00267505	0,003064682
K07679_ko02020_Two-componentsystem_Environmentalinformationprocessing_Signaltrasduction_evgS,bvgS,two-componentsystem,NarLfamily,sensorhistidinekinaseEvgS[EC:2.7.13.3];K07679_ko05133_Pertussis_HumanDiseases_Infectiousdiseases_evgS,bvgS,tw	0,000191893	0,000178337	0,00010797
K02945_ko03010_Ribosome_GeneticinformationProcessing_Transcription_RP-S1,rpsA,smallsubunitribosomalproteinS1	0,00341258	0,00274129	0,002491612
K03723_ko03420_Nucleotideexcisionrepair_GeneticinformationProcessing_ReplicationandRepair_mfd,transcription-repaircouplingfactor(superfamilyIIhelicase)[EC:3.6.4.-]	0,003308854	0,003118344	0,002881964
K03701_ko03420_Nucleotideexcisionrepair_GeneticinformationProcessing_ReplicationandRepair_uvrA,excinucleaseABCsubunitA	0,004423907	0,004213841	0,0032474
K13924_ko02020_Two-componentsystem_Environmentalinformationprocessing_Signaltrasduction_cheBR,two-componentsystem,chemotaxisfamily,CheB/CheRfusionprotein[EC:2.1.1.803.1.1.61];K13924_ko02030_Bacterialchemotaxis_Organismalsystem_Cellmob	0,001166916	0,00191075	0,00245839
K00526_ko00230_Purinemetabolism_Metabolism_Nucleotidemetabolism_E1.17.4.1B,nrdB,nrdF,ribonucleoside-diphosphatereductasebetachain[EC:1.17.4.1];K00526_ko00240_Pyrimidinemetabolism_Metabolism_Nucleotidemetabolism_E1.17.4.1B,nrdB,nrdF,ribo	0,000228197	0,000331197	0,000282383
K01236_ko00500_Starchandsucrosemetabolism_Metabolism_Carbohydratemetabolism_treZ,glgZ,maltooligosyltrehalosetrehalohydrolase[EC:3.2.1.141]	1,55589E-05	2,03813E-05	2,49161E-05
K12823_ko03040_SpliceosomeGeneticinformationProcessing_Transcription_DDX5,DBP2,ATP-dependentRNAhelicaseDDX5/DBP2[EC:3.6.4.13];K12823_ko05230_CentralcarbonmetabolisminCancer_HumanDiseases_Cancers_DDX5,DBP2,ATP-dependentRNAhelicase	5,18629E-06	5,09533E-06	1,66107E-05
K03737_ko01200_Carbonmetabolism_Metabolism_Overview_nifJ,putativepyruvate-flavodoxinoxidoreductase[EC:1.2.7.-];K03737_ko00194_Photosynthesisproteins_Metabolism_Energymetabolism_nifJ,putativepyruvate-flavodoxinoxidoreductase[EC:1.2.7.-]	0,004470583	0,004998522	0,004102854
K02364_ko01053_Biosynthesisofsiderophoregroupnonribosomalpeptides_Metabolism_MetabolismofterpenoidsandpolyketidesentF,enterobactinsynthetasecomponentF[EC:2.7.7.-]	5,70492E-05	5,60487E-05	8,30537E-05
K01870_ko00970_Aminoacyl-tRNAbiosynthesis_Geneticinformationandprocessing_Transcription_IARS,ileS,isoleucyl-tRNAsynthetase[EC:6.1.1.5]	0,003811924	0,003689022	0,003845387
K01199_ko00500_Starchandsucrosemetabolism_Metabolism_Carbohydratemetabolism_E3.2.1.39,glucanendo-1,3-beta-D-glucosidase[EC:3.2.1.39]	0,000119285	0,000127383	9,96645E-05
K03110_ko02010_Ctransporters_Environmentalinformationprocessing_Membranetransport_ftsY,fusedsignalrecognitionparticlereceptor;K03110_ko04120_UbiquitinmediatedproteolysisGeneticInformationProcessing_Folding,sortinganddegradation_ftsY,fusedsig	0,001161729	0,001238166	0,0012375
K03582_ko03440_Homologousrecombination_GeneticinformationProcessing_ReplicationandRepair_recB,exodeoxyribonucleaseVbetasubunit[EC:3.1.11.5]	0,000414903	0,000402531	0,000348826
K00705_ko00500_Starchandsucrosemetabolism_Metabolism_Carbohydratemetabolism_malQ,4-alpha-glucanotransferase[EC:2.4.1.25]	0,003983072	0,004504275	0,003770639
K07678_ko02020_Two-componentsystem_Environmentalinformationprocessing_Signaltrasduction_barA,two-componentsystem,NarLfamily,sensorhistidinekinaseBarA[EC:2.7.13.3]	0,000191893	0,000168146	0,000473406
K00615_ko00030_Pentosephosphatepathway_Metabolism_Carbohydratemetabolism_E2.2.1.1,tktA,tktB,transketolase[EC:2.2.1.1];K00615_ko01051_BiosynthesisofansamycinsMetabolism_Metabolismofterpenoidsandpolyketides_E2.2.1.1,tktA,tktB,transketolase[	0,002764293	0,002705622	0,002425169
K01958_ko00020_Citratecycle(TCAcycle)_Metabolism_Carbohydratemetabolism_PC,pyc,pyruvatecarboxylase[EC:6.4.1.1];K01958_ko00620_Pyruvatemetabolism_Metabolism_Carbohydratemetabolism_PC,pyc,pyruvatecarboxylase[EC:6.4.1.1];K01958_ko01230_Bi	0,000207452	0,00015286	0,000116275
K01191_ko00511_Otherglycandegradation_Metabolism_Glycanbiosynthesisandmetabolism_E3.2.1.24,alpha-mannosidase[EC:3.2.1.24]	0,001094308	0,002603716	0,001835487
K07178_ko03008_Ribosomebiogenesisineukaryotes_GeneticinformationProcessing_Transcription_RIOK1,RIOkinase1[EC:2.7.11.1]	2,59315E-05	1,01907E-05	8,30537E-06
K07646_ko02020_Two-componentsystem_Environmentalinformationprocessing_Signaltrasduction_kdpD,two-componentsystem,OmpRfamily,sensorhistidinekinaseKdpD[EC:2.7.13.3]	0,000777944	0,000550296	0,000747483
K13821_ko00250_Alanine,aspartateandglutamatemetabolism_Metabolism_Aminoacidmetabolism_putA,prolinedehydrogenase/delta1-pyrroline-5-carboxylatedehydrogenase[EC:1.5.5.21.2.1.88];K13821_ko00330_Argnineandprolinemetabolism_Metabolism_Ami	3,11177E-05	1,5286E-05	3,32215E-05
K01176_ko00500_Starchandsucrosemetabolism_Metabolism_Carbohydratemetabolism_E3.2.1.1,amyA,malS,alpha-amylase[EC:3.2.1.1];K01176_ko04973_Carbohydratedigestionandabsorption_Organismalsystem_Digestivesystem_E3.2.1.1,amyA,malS,alpha-amyla	0,000897228	0,000647107	0,001154447
K12600_ko03018_RNAdegradation_GeneticInformationProcessing_Folding,sortinganddegradation_SKI3,TTC37,superkillerprotein3	0,001358808	0,002323472	0,0020099
K03070_ko02010_Ctransporters_Environmentalinformationprocessing_Membranetransport_secA,preproteintranslocasesubunitSecA;K03070_ko04120_UbiquitinmediatedproteolysisGeneticInformationProcessing_Folding,sortinganddegradation_secA,preprotein	0,004226828	0,004025314	0,003446729
K02314_ko04112_Cellcycle-Caulobacter_CellularProcesses_Cellgrowthanddeath_dnaB,replicativeDNAhelicase[EC:3.6.4.12];K02314_ko03030_DNAreplication_GeneticinformationProcessing_ReplicationandRepair_dnaB,replicativeDNAhelicase[EC:3.6.4.12]	0,002198988	0,00274129	0,002790605
K02488_ko04112_Cellcycle-Caulobacter_CellularProcesses_Cellgrowthanddeath_pleD,two-componentsystem,cellcycleresponseregulator;K02488_ko02020_Two-componentsystem_Environmentalinformationprocessing_Signaltrasduction_pleD,two-componentsyst	0,001338063	0,000912065	0,00156141
K03205_ko02010_Ctransporters_Environmentalinformationprocessing_Membranetransport_virD4,lvhD4,typeIVsecretionsystemproteinVirD4	0,014599411	0,013905166	0,014891532
K10875_ko03440_Homologousrecombination_GeneticinformationProcessing_ReplicationandRepair_RAD54L,RAD54,DNArepairandrecombinationproteinRAD54andRAD54-likeprotein[EC:3.6.4.-]	0,000114098	0,000117193	0,000240856
K01439_ko00300_Lysinebiosynthesis_Metabolism_Aminoacidmetabolism_dapE,succinyl-diaminopimelatedesuccinylase[EC:3.5.1.18];K01439_ko01230_BiosynthesisofaminoacidsMetabolism_Overview_dapE,succinyl-diaminopimelatedesuccinylase[EC:3.5.1.18]	0,000669032	0,000692965	0,000672735
K00820_ko00250_Alanine,aspartateandglutamatemetabolism_Metabolism_Aminoacidmetabolism_glmS,GFPT,glucosamine--fructose-6-phosphateaminotransferase(isomerizing)[EC:2.6.1.16];K00820_ko00520_AminosugarandnucleotidesugarmetabolismMetaboli	0,001602564	0,001523505	0,001403608
K00525_ko00230_Purinemetabolism_Metabolism_Nucleotidemetabolism_E1.17.4.1A,nrdA,nrdE,ribonucleoside-diphosphatereductasealphachain[EC:1.17.4.1];K00525_ko00240_Pyrimidinemetabolism_Metabolism_Nucleotidemetabolism_E1.17.4.1A,nrdA,nrdE,rib	0,001784084	0,001920941	0,002059732
K05939_ko00071_Fattyaciddegradation_Metabolism_Lipidmetabolism_aas,acyl-[acyl-carrier-protein]-phospholipidO-acyltransferase/long-chain-fatty-acid--[acyl-carrier-protein]ligase[EC:2.3.1.406.2.1.20];K05939_ko00564_Glycerophospholipidmetabolism_Metab	0,000207452	5,09533E-05	0,00010797
K00548_ko00270_CysteineandmethionineMetabolism_Metabolism_Aminoacidmetabolism_metH,MTR,5-methyltetrahydrofolate--homocysteinemethyltransferase[EC:2.1.1.13];K00548_ko00670_Onecarbonpoolbyfolate_Metabolism_Metabolismofcofactorsandvita	0,001281014	0,001890369	0,001420219
K05903_ko00190_Oxidativephosphorylation_Metabolism_Energymetabolism_E1.6.99.5,NADHdehydrogenase(quinone)[EC:1.6.99.5]	0,000103726	1,5286E-05	4,15269E-05
K01971_ko03410_Baseexcisionrepair_GeneticinformationProcessing_ReplicationandRepair_E6.5.1.1,lig,DNAligase(ATP)[EC:6.5.1.1];K01971_ko03430_Mismatchrepair_GeneticinformationProcessing_ReplicationandRepair_E6.5.1.1,lig,DNAligase(ATP)[EC:6.5.1.1];K(	0,000269687	0,000214004	0,000382047
K01710_ko00521_Streptomycinbiosynthesis_Metabolism_Biosynthesisofothersecondarymetabolites_E4.2.1.46,rfbB,rffG,dTDP-glucose4,6-dehydratase[EC:4.2.1.46];K01710_ko01055_BiosynthesisofvancomycingroupantibioticsMetabolism_Metabolismofterpenoi	0,002411626	0,001900559	0,001993289
K13590_ko04112_Cellcycle-Caulobacter_CellularProcesses_Cellgrowthanddeath_dgcB,diguanylatecyclase	0,000565306	0,000371959	0,000705957
K04486_ko00340_Histidinemetabolism_Metabolism_Aminoacidmetabolism_E3.1.3.15B,histidinol-phosphatase(PHPfamily)[EC:3.1.3.15];K04486_ko01230_Biosynthesisofaminoacids_Metabolism_Overview_E3.1.3.15B,histidinol-phosphatase(PHPfamily)[EC:3.1.3.15	0,000456394	0,000942637	0,000606292
K05515_ko00312_beta-Lactamresistance_HumanDiseases_Drugresistance_mrdA,penicillin-bindingprotein2;K05515_ko01005_Lipopolysaccharidebiosynthesisproteins_Metabolism_GlycanbiosynthesisandmetabolismmrdA,penicillin-bindingprotein2	0,001561074	0,001778271	0,001403608
K00527_ko00230_Purinemetabolism_Metabolism_Nucleotidemetabolism_nrdD,ribonucleoside-triphosphatereductase[EC:1.17.4.2];K00527_ko00240_Pyrimidinemetabolism_Metabolism_Nucleotidemetabolism_nrdD,ribonucleoside-triphosphatereductase[EC:1.1	0,00483881	0,003908121	0,004169297
K01941_ko00330_Argnineandprolinemetabolism_Metabolism_Aminoacidmetabolism_E6.3.4.6,ureacarboxylase[EC:6.3.4.6]	6,22355E-05	2,54767E-05	3,32215E-05
K03581_ko03440_Homologousrecombination_GeneticinformationProcessing_ReplicationandRepair_recD,exodeoxyribonucleaseValphasubunit[EC:3.1.11.5]	0,00244793	0,002878864	0,00323079
K12308_ko00052_Galactosemetabolism_Metabolism_Carbohydratemetabolism_bgaB,lacA,beta-galactosidase[EC:3.2.1.23]	0,00134325	0,002374426	0,002092954
K10877_ko03440_Homologousrecombination_GeneticinformationProcessing_ReplicationandRepair_RAD54B,DNArepairandrecombinationproteinRAD54B[EC:3.6.4.-]	0,000342295	0,000264957	0,000207634
K00143_ko00300_Lysinebiosynthesis_Metabolism_Aminoacidmetabolism_LYS2,L-aminoadipate-semialdehydedehydrogenase[EC:1.2.1.31];K00143_ko00310_Lysinedegradation_Metabolism_Aminoacidmetabolism_LYS2,L-aminoadipate-semialdehydedehydrogena	1,03726E-05	5,09533E-06	8,30537E-06
K01338_ko04112_Cellcycle-Caulobacter_CellularProcesses_Cellgrowthanddeath_lon,ATP-dependentLonprotease[EC:3.4.21.53]	0,003894905	0,00374507	0,003870303
K01007_ko00620_Pyruvatemetabolism_Metabolism_Carbohydratemetabolism_pps,ppsA,pyruvate,waterdikinase[EC:2.7.9.2];K01007_ko01200_Carbonmetabolism_Metabolism_Overview_pps,ppsA,pyruvate,waterdikinase[EC:2.7.9.2];K01007_ko00194_Photosynth	0,001099494	0,001406312	0,000905286
K10804_ko01040_BiosynthesisofunsaturatedfattyacidsMetabolism_Lipidmetabolism_tesA,acyl-CoAthioesteraseI[EC:3.1.2.-3.1.1.5]	2,59315E-05	1,5286E-05	6,6443E-05
K08300_ko03018_RNAdegradation_GeneticInformationProcessing_Folding,sortinganddegradation_rne,ribonucleaseE[EC:3.1.26.12]	0,000119285	0,000101907	0,000191024
K07787_ko02020_Two-componentsystem_Environmentalinformationprocessing_Signaltrasduction_cusA,silA,Cu(I)/Ag(I)effluxsystemmembraneproteinCusA/SilA	0,000523815	0,000728633	0,00055646
K12527_ko00450_SelenocompoundmetabolismMetabolism_Metabolismofotheraminoacids_ygfK,putativeselenatereductase[EC:1.97.1.9]	0,000119285	0,000127383	0,00010797
K02335_ko03410_Baseexcisionrepair_GeneticinformationProcessing_ReplicationandRepair_DPO1,polA,DNApolymeraseI[EC:2.7.7.7];K02335_ko03030_DNAreplication_GeneticinformationProcessing_ReplicationandRepair_DPO1,polA,DNApolymeraseI[EC:2.7.7.7];I	0,003008049	0,003933598	0,003770639
K01278_ko04974_Proteindigestionandabsorption_Organismalsystem_Digestivesystem_DPP4,dipeptidyl-peptidase4[EC:3.4.14.5]	0,000876483	0,0015286	0,00089698
K10188_ko02010_Ctransporters_Environmentalinformationprocessing_Membranetransport_lacE,araN,lactose/L-arabinosetransportsystemsubstrate-bindingprotein	0,000492698	0,000448389	0,000440185
K12257_ko02010_Ctransporters_Environmentalinformationprocessing_Membranetransport_secDF,SecD/SecFfusionprotein;K12257_ko04120_UbiquitinmediatedproteolysisGeneticInformationProcessing_Folding,sortinganddegradation_secDF,SecD/SecFfusionpr	0,002012281	0,001752795	0,001486662
K00102_ko00620_Pyruvatemetabolism_Metabolism_Carbohydratemetabolism_E1.1.2.4,dld,D-lactatedehydrogenase(cytochrome)[EC:1.1.2.4]	0,000176334	0,00030572	0,000124581
K01885_ko00970_Aminoacyl-tRNAbiosynthesis_Geneticinformationandprocessing_Transcription_EARS,gltX,glutamyl-tRNAsynthetase[EC:6.1.1.17];K01885_ko00830_RetinolmetabolismMetabolism_Metabolismofcofactorsandvitamins_EARS,gltX,glutamyl-tRNAsyr	0,001597378	0,001813939	0,001586326
K06160_ko02010_Ctransporters_Environmentalinformationprocessing_Membranetransport_pvdE,putativeATP-bindingcassettetransporter	0	5,09533E-06	0
K05305_ko00520_Aminosugarandnucleotidesugarmetabolism_Metabolism_Carbohydratemetabolism_FUK,fucokinase[EC:2.7.1.52];K05305_ko00051_FructoseandmannosemetabolismMetabolism_Carbohydratemetabolism_FUK,fucokinase[EC:2.7.1.52]	0,000202265	0,000392341	0,000431879
K11891_ko02010_Ctransporters_Environmentalinformationprocessing_Membranetransport_impL,vasK,icmF,typeVIsecretionsystemproteinImpL	0,000114098	4,07627E-05	5,81376E-05
K05366_ko00312_beta-Lactamresistance_HumanDiseases_Drugresistance_mrcA,penicillin-bindingprotein1A[EC:2.4.1.-3.4.-.-];K05366_ko01005_Lipopolysaccharidebiosynthesisproteins_Metabolism_Glycanbiosynthesisandmetabolism_mrcA,penicillin-bindingprote	0,002655381	0,003143821	0,003546394
K12111_ko00052_Galactosemetabolism_Metabolism_Carbohydratemetabolism_ebgA,evolvedbeta-galactosidasesubunitalpha[EC:3.2.1.23];K12111_ko00511_Otherglycandegradation_Metabolism_Glycanbiosynthesisandmetabolism_ebgA,evolvedbeta-galactosida	0,000103726	0,000122288	0,000141191
K01006_ko00620_Pyruvatemetabolism_Metabolism_Carbohydratemetabolism_ppdK,pyruvate,orthophosphatedikinase[EC:2.7.9.1];K01006_ko01200_Carbonmetabolism_Metabolism_Overview_ppdK,pyruvate,orthophosphatedikinase[EC:2.7.9.1];K01006_ko0019	0,003609659	0,002797338	0,002757383
K01869_ko00970_Aminoacyl-tRNAbiosynthesis_Geneticinformationandprocessing_Transcription_LARS,leuS,leucyl-tRNAsynthetase[EC:6.1.1.4]	0,003837856	0,003551448	0,002690941
K04066_ko03440_Homologousrecombination_GeneticinformationProcessing_ReplicationandRepair_priA,primosomalproteinN'(replicationfactorY)(superfamilyIIhelicase)[EC:3.6.4.-]	0,001628496	0,002190993	0,002059732

K04079_ko04151_PI3K-Aktsignalingpathway_Environmentalinformationprocessing_Signaltrasduction_htpG,HSP90A,molecularchaperoneHtpG;K04079_ko04141_Proteinprocessinginendoplasmicreticulum_GeneticInformationProcessing_Folding,sortinganddegrada	0,003028794	0,002568048	0,002591276
K02547_ko00312_beta-Lactamresistance_HumanDiseases_Drugresistance_mecR1,methicillinresistanceprotein	0,000814248	0,000606345	0,000564765
K01873_ko00970_Aminoacyl-tRNAbiosynthesis_Geneticinformationandprocessing_Transcription_VARS,valS,valyl-tRNAsynthetase[EC:6.1.1.9]	0,003604473	0,00267505	0,002558055
K01195_ko04142_Lysosome_CellularProcesses_Transportandcatabolism_uidA,GUSB,beta-glucuronidase[EC:3.2.1.31];K01195_ko00944_Flavoneandflavonolbiosynthesis_Metabolism_Biosynthesisofothersecondarymetabolites_uidA,GUSB,beta-glucuronidase[EC:3.2	0,000679404	0,000672584	0,001063088
K02667_ko02020_Two-componentsystem_Environmentalinformationprocessing_Signaltrasduction_pilR,two-componentsystem,NtrCfamily,responseregulatorPilR	0,000394158	0,000157955	0,000207634
K00656_ko00630_Glyoxylateanddicarboxylatemetabolism_Metabolism_Carbohydratemetabolism_E2.3.1.54,pflD,formateC-acetyltransferase[EC:2.3.1.54];K00656_ko00630_Glyoxylateanddicarboxylatemetabolism_Metabolism_Carbohydratemetabolism_E2.3.1.54	0,002686499	0,002252137	0,002043121
K00123_ko00630_Glyoxylateanddicarboxylatemetabolism_Metabolism_Carbohydratemetabolism_fdoG,fdfH,formatedehydrogenasemajorsubunit[EC:1.2.1.2];K00123_ko01200_Carbonmetabolism_Metabolism_Overview_fdoG,fdfH,formatedehydrogenasemajorsu	0,000570492	0,000392341	0,000498322
K04043_ko03018_RNAdegradation_GeneticInformationProcessing_Folding,sortinganddegradation_dnaK,molecularchaperoneDnaK;K04043_ko05152_Tuberculosis_HumanDiseases_Infectiousdiseases_dnaK,molecularchaperoneDnaK	0,003832669	0,002950198	0,002690941
K01681_ko00020_Citratecycle(TCAcycle)_Metabolism_Carbohydratemetabolism_ACO,acnA,aconitatehydratase[EC:4.2.1.3];K01681_ko00630_Glyoxylateanddicarboxylatemetabolism_Metabolism_Carbohydratemetabolism_ACO,acnA,aconitatehydratase[EC:4.2.1.3	0,001156543	0,000830539	0,001054782
K00702_ko00500_Starchandsucrosemetabolism_Metabolism_Carbohydratemetabolism_E2.4.1.20,cellobiosephosphorylase[EC:2.4.1.20]	0,000855738	0,000963018	0,000465101
K01872_ko00970_Aminoacyl-tRNAbiosynthesis_Geneticinformationandprocessing_Transcription_AARS,alaS,alanyl-tRNAsynthetase[EC:6.1.1.7]	0,002914696	0,002746385	0,002433474
K00244_ko02020_Two-componentsystem_Environmentalinformationprocessing_Signaltrasduction_frdA,fumaratereductaseflavoproteinsubunit[EC:1.3.5.4];K00244_ko00020_Citratecycle(TCAcycle)_Metabolism_Carbohydratemetabolism_frdA,fumaratereductasef	0,001270641	0,000835635	0,000988339
K03041_ko03020_RNApolymerase_GeneticinformationProcessing_Transcription_rpoA1,DNA-directedRNApolymerasesubunitA'[EC:2.7.7.6];K03041_ko00230_Purinemetabolism_Metabolism_Nucleotidemetabolism_rpoA1,DNA-directedRNApolymerasesubunitA'[E	0	0	1,66107E-05
K01081_ko00760_Nicotinateandnicotinamidemetabolism_Metabolism_Metabolismofcofactorsandvitamins_E3.1.3.5,5'-nucleotidase[EC:3.1.3.5];K01081_ko00230_Purinemetabolism_Metabolism_Nucleotidemetabolism_E3.1.3.5,5'-nucleotidase[EC:3.1.3.5];K0108	0,000928346	0,000672584	0,00044849
K01488_ko05340_Primaryimmunodeficiency_Humandiseases_Immunediseases_add,ADA,adenosinedeaminase[EC:3.5.4.4];K01488_ko00230_Purinemetabolism_Metabolism_Nucleotidemetabolism_add,ADA,adenosinedeaminase[EC:3.5.4.4]	0,000274873	0,000514629	0,000506628
K07456_ko03430_Mismatchrepair_GeneticinformationProcessing_ReplicationandRepair_mutS2,DNAmismatchrepairproteinMutS2	0,002058958	0,002552762	0,002549749
K04072_ko00350_Tyrosinemetabolism_Metabolism_Aminoacidmetabolism_adhE,acetaldehydedehydrogenase/alcoholdehydrogenase[EC:1.2.1.101.1.1.1];K04072_ko00010_Glycolysis/Gluconeogenesis_Metabolism_Carbohydratemetabolism_adhE,acetaldehydede	0,000876483	0,001054734	0,000996645
K00700_ko00500_Starchandsucrosemetabolism_Metabolism_Carbohydratemetabolism_glgB,1,4-alpha-glucanbranchingenzyme[EC:2.4.1.18]	0,002442743	0,00259862	0,00233381
K04085_ko04122_Sulfurrelaysystem_GeneticInformationProcessing_Folding,sortinganddegradation_tusA,sirA,tRNA2-thiouridinesynthesizingproteinA[EC:2.8.1.-]	0,000259315	0,000626726	0,000357131
K00087_ko00230_Purinemetabolism_Metabolism_Nucleotidemetabolism_ygeS,xdhA,xanthinedehydrogenasemolybdenum-bindingsubunit[EC:1.17.1.4]	0,00028006	0,00030572	0,00021594
K07306_ko00920_Sulfurmetabolism_Metabolism_Energymetabolism_dmsA,anaerobicdimethylsulfoxidereductasesubunitA[EC:1.8.5.3]	0,00018152	9,1716E-05	0,000174413
K01890_ko00970_Aminoacyl-tRNAbiosynthesis_Geneticinformationandprocessing_Transcription_FARSB,pheT,phenylalanyl-tRNAsynthetasebetachain[EC:6.1.1.20]	0,0023079	0,00258843	0,002400252
K08303_ko05120_EpithelialcellsignalinginHelicobacterpyloriinfection_HumanDiseases_Infectiousdiseases_K08303,putativeprotease[EC:3.4.-.-]	0,002416812	0,003332348	0,003023155
K01768_ko04113_Meiosis-yeast_CellularProcesses_Cellgrowthanddeath_E4.6.1.1,adenylatecyclase[EC:4.6.1.1];K01768_ko00230_Purinemetabolism_Metabolism_Nucleotidemetabolism_E4.6.1.1,adenylatecyclase[EC:4.6.1.1]	0,000648286	0,00091716	0,000855453
K01824_ko00100_Steroidbiosynthesis_Metabolism_Lipidmetabolism_EBP,cholestenoldelta-isomerase[EC:5.3.3.5]	6,22355E-05	0,000117193	8,30537E-05
K14439_ko04550_Signalingpathwaysregulatingpluripotencyofstemcells_Cellgrowthanddeath_Cellularcommunity_SMARCAD1,SWI/SNF-relatedmatrix-associatedactin-dependentregulatorofchromatinsubfamilyAcontainingDEAD/Hbox1[EC:3.6.4.12]	6,74218E-05	4,5858E-05	4,15269E-05
K12573_ko03018_RNAdegradation_GeneticInformationProcessing_Folding,sortinganddegradation_rnr,vacB,ribonucleaseR[EC:3.1.-.-]	0,002510165	0,002287805	0,002400252
K00937_ko03018_RNAdegradation_GeneticInformationProcessing_Folding,sortinganddegradation_ppk,polyphosphatekinase[EC:2.7.4.1];K00937_ko00190_Oxidativephosphorylation_Metabolism_Energymetabolism_ppk,polyphosphatekinase[EC:2.7.4.1]	0,001047631	0,001253452	0,000855453
K12524_ko00270_Cysteineandmethioninemetabolism_Metabolism_Aminoacidmetabolism_thrA,bifunctionalaspartokinase/homoserinedehydrogenase1[EC:2.7.2.41.1.1.3];K12524_ko00260_Glycine,serineandthreoninemetabolism_Metabolism_Aminoacidmetabol	0,000357854	0,000570677	0,00023255
K10844_ko03420_Nucleotideexcisionrepair_GeneticinformationProcessing_ReplicationandRepair_ERCC2,XPD,DNAexcisionrepairproteinERCC-2[EC:3.6.4.12];K10844_ko03022_Basaltranscriptionfactors_GeneticinformationProcessing_Transcription_ERCC2,XPD,DNA	0,000451207	0,000371959	0,000332215
K01256_ko00480_Glutathionemetabolism_Metabolism_Metabolismofotheraminoacids_pepN,aminopeptidaseN[EC:3.4.11.2]	0,000171148	0,000173241	0,000240856
K01775_ko00473_D-Alaninemetabolism_Metabolism_Metabolismofotheraminoacids_alr,alanineracemase[EC:5.1.1.1]	0,001389926	0,001691651	0,001212584
K12683_ko05133_Pertussis_HumanDiseases_Infectiousdiseases_brkA,serumresistanceprotein	0,000150402	0,00015286	0,000332215
K00281_ko00260_Glycine,serineandthreoninemetabolism_Metabolism_Aminoacidmetabolism_GLDC,gcvP,glycinedehydrogenase[EC:1.4.4.2];K00281_ko01200_Carbonmetabolism_Metabolism_Overview_GLDC,gcvP,glycinedehydrogenase[EC:1.4.4.2]	0,000176334	0,000264957	0,00023255
K02195_ko02010_Ctransporters_Environmentalinformationprocessing_MembranetransporT_ccmC,hemeexporterproteinC	0,000223011	0,000433103	0,000348826
K09458_ko00061_Fattyacidbiosynthesis_Metabolism_Lipidmetabolism_fabF,3-oxoacyl-[acyl-carrier-protein]synthaseII[EC:2.3.1.179];K09458_ko01212_Fattyacidmetabolism_Metabolism_Overview_fabF,3-oxoacyl-[acyl-carrier-protein]synthaseII[EC:2.3.1.179];K094	0,001462534	0,001202499	0,001071393
K01210_ko00500_Starchandsucrosemetabolism_Metabolism_Carbohydratemetabolism_E3.2.1.58,glucan1,3-beta-glucosidase[EC:3.2.1.58]	0,000134844	7,643E-05	4,98322E-05
K00370_ko02020_Two-componentsystem_Environmentalinformationprocessing_Signaltrasduction_narG,nitratereductasealphasubunit[EC:1.7.99.4];K00370_ko00910_Nitrogenmetabolism_Metabolism_Energymetabolism_narG,nitratereductasealphasubunit[EC:1.	2,07452E-05	1,5286E-05	4,98322E-05
K10843_ko03420_Nucleotideexcisionrepair_GeneticinformationProcessing_ReplicationandRepair_ERCC3,XPB,DNAexcisionrepairproteinERCC-3[EC:3.6.4.12];K10843_ko03022_Basaltranscriptionfactors_GeneticinformationProcessing_Transcription_ERCC3,XPB,DNA	0,002090076	0,001273833	0,000863759
K01198_ko00520_Aminosugarandnucleotidesugarmetabolism_Metabolism_Carbohydratemetabolism_xynB,xylan1,4-beta-xylosidase[EC:3.2.1.37];K01198_ko00500_Starchandsucrosemetabolism_Metabolism_Carbohydratemetabolism_xynB,xylan1,4-beta-xylosida	0,001042445	0,001187213	0,001079698
K03406_ko02020_Two-componentsystem_Environmentalinformationprocessing_Signaltrasduction_mcp,methyl-acceptingchemotaxisprotein;K03406_ko02030_Bacterialchemotaxis_Organismalsystem_Cellmobility_mcp,methyl-acceptingchemotaxisprotein	0,002256037	0,002399902	0,002383642
K01442_ko00120_Primarybileacidbiosynthesis_Metabolism_Lipidmetabolism_E3.5.1.24,cholylglycinehydrolase[EC:3.5.1.24];K01442_ko00121_Secondarybileacidbiosynthesis_Metabolism_Lipidmetabolism_E3.5.1.24,cholylglycinehydrolase[EC:3.5.1.24]	0,000539374	0,000626726	0,000631208
K01507_ko00190_Oxidativephosphorylation_Metabolism_Energymetabolism_ppa,inorganicpyrophosphatase[EC:3.6.1.1]	0,001561074	0,001538791	0,001586326
K00962_ko03018_RNAdegradation_GeneticInformationProcessing_Folding,sortinganddegradation_pnp,PNPT1,polyribonucleotidenucleotidyltransferase[EC:2.7.7.8];K00962_ko00230_Purinemetabolism_Metabolism_Nucleotidemetabolism_pnp,PNPT1,polyribonu	0,002805784	0,00319987	0,002699246
K02567_ko00910_Nitrogenmetabolism_Metabolism_Energymetabolism_napA,periplasmicnitratereductaseNapA[EC:1.7.99.4]	5,18629E-06	4,07627E-05	2,49161E-05
K01126_ko00564_Glycerophospholipidmetabolism_Metabolism_Lipidmetabolism_E3.1.4.46,glpQ,ugpQ,glycerophosphoryldiesterphosphodiesterase[EC:3.1.4.46]	0,000886856	0,000779586	0,001104614
K05813_ko02010_Ctransporters_Environmentalinformationprocessing_Membranetransport_ugpB,sn-glycerol3-phosphatetransportsystemsubstrate-bindingprotein	0,000876483	0,000478961	0,000564765
K10407_ko05132_Salmonellainfection_HumanDiseases_Infectiousdiseases_KLC,kinesinlightchain	3,6304E-05	6,62393E-05	9,13591E-05
K13745_ko00260_Glycine,serineandthreoninemetabolism_Metabolism_Aminoacidmetabolism_ddc,L-2,4-diaminobutyratedecarboxylase[EC:4.1.1.86]	3,6304E-05	3,56673E-05	5,81376E-05
K00691_ko00500_Starchandsucrosemetabolism_Metabolism_Carbohydratemetabolism_E2.4.1.8,mapA,maltosephosphorylase[EC:2.4.1.8]	0,000326736	0,000560487	0,000149497
K07720_ko02020_Two-componentsystem_Environmentalinformationprocessing_Signaltrasduction_yesN,two-componentsystem,responseregulatorYesN	0,004885487	0,004621468	0,005564599
K12528_ko00450_Selenocompoundmetabolism_Metabolism_Metabolismofotheraminoacids_xdhD,putativeselenatereductasemolybdopterin-bindingsubunit	7,26081E-05	1,5286E-05	0
K13542_ko00830_Retinolmetabolism_Metabolismofcofactorsandvitamins_cobA-hemD,uroporphyrinogenIIImethyltransferase/synthase[EC:2.1.1.1074.2.1.75]	0,000233383	0,000422913	0,000473406
K01771_ko00630_Glyoxylateanddicarboxylatemetabolism_Metabolism_Carbohydratemetabolism_E4.6.1.13,plc,1-phosphatidylinositolphosphodiesterase[EC:4.6.1.13]	0,000129657	5,60487E-05	9,96645E-05
K08352_ko00920_Sulfurmetabolism_Metabolism_Energymetabolism_phsA,psrA,thiosulfatereductase/polysulfidereductasechainA	9,85395E-05	5,09533E-05	4,15269E-05
K05851_ko05111_Vibriocholeraepathogeniccycle_HumanDiseases_Infectiousdiseases_E4.6.1.1A,cyaA,adenylatecyclase,class1[EC:4.6.1.1];K05851_ko00230_Purinemetabolism_Metabolism_Nucleotidemetabolism_E4.6.1.1A,cyaA,adenylatecyclase,class1[EC:4.6.1.1	2,07452E-05	6,62393E-05	7,47483E-05
K01053_ko00052_Galactosemetabolism_Metabolism_Carbohydratemetabolism_E3.1.1.17,gnl,RGN,gluconolactonase[EC:3.1.1.17];K01053_ko00030_Pentosephosphatepathway_Metabolism_Carbohydratemetabolism_E3.1.1.17,gnl,RGN,gluconolactonase[EC:3.1.1.	3,11177E-05	3,56673E-05	4,98322E-05
K12854_ko03040_Spliceosome_GeneticinformationProcessing_Transcription_SNRNP200,BRR2,pre-mRNA-splicinghelicaseBRR2[EC:3.6.4.13]	7,26081E-05	8,66207E-05	8,30537E-05
K00951_ko00230_Purinemetabolism_Metabolism_Nucleotidemetabolism_relA,GTPpyrophosphokinase[EC:2.7.6.5]	0,003604473	0,00365845	0,003612837
K01193_ko00052_Galactosemetabolism_Metabolism_Carbohydratemetabolism_E3.2.1.26,sacA,beta-fructofuranosidase[EC:3.2.1.26];K01193_ko00500_Starchandsucrosemetabolism_Metabolism_Carbohydratemetabolism_E3.2.1.26,sacA,beta-fructofuranosidase[	0,000674218	0,000799967	0,001021561
K00864_ko00561_Glycerolipidmetabolism_Metabolism_Lipidmetabolism_glpK,GK,glycerolkinase[EC:2.7.1.30];K00864_ko04920_Adipocytokinesignalingpathway_Organismalsystem_Endocrinsystem_glpK,GK,glycerolkinase[EC:2.7.1.30];K00864_ko04626_Plant-path	0,002785039	0,001554077	0,002200924
K00990_ko02020_Two-componentsystem_Environmentalinformationprocessing_Signaltrasduction_glnD,[protein-PII]uridylyltransferase[EC:2.7.7.59]	5,70492E-05	3,56673E-05	7,47483E-05
K00703_ko00500_Starchandsucrosemetabolism_Metabolism_Carbohydratemetabolism_E2.4.1.21,glgA,starchsynthase[EC:2.4.1.21]	0,000876483	0,001227975	0,000930202
K07677_ko02020_Two-componentsystem_Environmentalinformationprocessing_Signaltrasduction_rcsC,two-componentsystem,NarLfamily,capsularsynthesissensorhistidinekinaseRcsC[EC:2.7.13.3]	7,26081E-05	2,03813E-05	4,98322E-05
K01897_ko04146_Peroxisome_CellularProcesses_Transportandcatabolism_ACSL,fadD,long-chainacyl-CoAsynthetase[EC:6.2.1.3];K01897_ko00061_Fattyacidbiosynthesis_Metabolism_Lipidmetabolism_ACSL,fadD,long-chainacyl-CoAsynthetase[EC:6.2.1.3];K01897_k	0,003443698	0,003296681	0,003812166
K01423_ko00310_Lysinedegradation_Metabolism_Aminoacidmetabolism_E3.4.-.-,[EC:3.4.-.-];K01423_ko00780_Biotinmetabolism_Metabolism_Metabolismofcofactorsandvitamins_E3.4.-.-,[EC:3.4.-.-]	0,001799643	0,001599935	0,001926846
K01886_ko00970_Aminoacyl-tRNAbiosynthesis_Geneticinformationandprocessing_Transcription_QARS,glnS,glutaminyl-tRNAsynthetase[EC:6.1.1.18]	0,002375322	0,002624097	0,002682635
K05367_ko01005_Lipopolysaccharidebiosynthesisproteins_Metabolism_Glycanbiosynthesisandmetabolism_pbpC,penicillin-bindingprotein1C[EC:2.4.1.-]	6,22355E-05	0,000112097	0,000224245
K07407_ko00052_Galactosemetabolism_Metabolism_Carbohydratemetabolism_E3.2.1.22B,galA,rafA,alpha-galactosidase[EC:3.2.1.22];K07407_ko00603_Glycosphingolipidbiosynthesis-globoseries_Metabolism_Glycanbiosynthesisandmetabolism_E3.2.1.22B,galA,r	0,002779852	0,00297058	0,003446729
K13500_ko00532_Glycosaminoglycanbiosynthesis-chondroitinsulfate/dermatansulfate_Metabolism_Glycanbiosynthesisandmetabolism_fcbD,chondroitinsynthase[EC:2.4.1.1752.4.1.226]	0,000207452	0,000122288	0,00023255

K13525_ko04141_Proteinprocessinginendoplasmicreticulum_GeneticInformationProcessing_Folding,sortinganddegradation_VCP,CDC48,transitionalendoplasmicreticulumATPase;K13525_ko05134_Legionellosis_HumanDiseases_Infectiousdiseases_VCP,CDC48,trar	0,000471953	0,000647107	0,000855453
K03572_ko03430_Mismatchrepair_GeneticinformationProcessing_ReplicationandRepair_mutL,DNAmismatchrepairproteinMutL	0,001498838	0,001946417	0,001918541
K07648_ko02020_Two-componentsystem_Environmentalinformationprocessing_Signaltrasduction_arcB,two-componentsystem,OmpRfamily,aerobicrespirationcontrolsensorhistidinekinaseArcB[EC:2.7.13.3]	5,18629E-06	4,07627E-05	2,49161E-05
K00549_ko00270_Cysteineandmethioninemetabolism_Metabolism_Aminoacidmetabolism_metE,5-methyltetrahydropteroyltriglutamate--homocysteinemethyltransferase[EC:2.1.1.14];K00549_ko00450_Selenocompoundmetabolism_Metabolism_Metabolismofot	0,00036304	0,000351578	0,000249161
K00266_ko00250_Alanine,aspartateandglutamatemetabolism_Metabolism_Aminoacidmetabolism_gltD,glutamatesynthase(NADPH/NADH)smallchain[EC:1.4.1.131.4.1.14];K00266_ko00910_Nitrogenmetabolism_Metabolism_Energymetabolism_gltD,glutamatesyr	0,002074517	0,001768081	0,001627853
K00390_ko00920_Sulfurmetabolism_Metabolism_Energymetabolism_cysH,phosphoadenosinephosphosulfatereductase[EC:1.8.4.8]	0,00106319	0,000906969	0,001063088
K00441_ko00194_Photosynthesisproteins_Metabolism_Energymetabolism_frhB,coenzymeF420hydrogenasesubunitbeta[EC:1.12.98.1]	0,001032072	0,001783367	0,002773994
K10797_ko00360_Phenylalaninemetabolism_Metabolism_Aminoacidmetabolism_enr,2-enoatereductase[EC:1.3.1.31]	0,00036304	0,000249671	0,000298993
K01912_ko00360_Phenylalaninemetabolism_Metabolism_Aminoacidmetabolism_paaK,phenylacetate-CoAligase[EC:6.2.1.30]	0,000980209	0,000866207	0,001038171
K00833_ko00780_Biotinmetabolism_Metabolism_Metabolismofcofactorsandvitamins_bioA,adenosylmethionine-8-amino-7-oxononanoateaminotransferase[EC:2.6.1.62]	0,000819434	0,000642012	0,0007724
K03199_ko02010_Ctransporters_Environmentalinformationprocessing_Membranetransport_virB4,lvhB4,typeIVsecretionsystemproteinVirB4	0,000129657	0,000132479	0,000207634
K04042_ko00520_Aminosugarandnucleotidesugarmetabolism_Metabolism_Carbohydratemetabolism_glmU,bifunctionalUDP-N-acetylglucosaminepyrophosphorylase/Glucosamine-1-phosphateN-acetyltransferase[EC:2.7.7.232.3.1.157]	0,000726081	0,000815253	0,000872064
K03628_ko03018_RNAdegradation_GeneticInformationProcessing_Folding,sortinganddegradation_rho,transcriptionterminationfactorRho	0,001504025	0,001574458	0,000963423
K07347_ko05133_Pertussis_HumanDiseases_Infectiousdiseases_fimD,fimC,mrkC,htrE,cssD,outermembraneusherprotein	0,000145216	0,000132479	0,00034052
K13731_ko05100_Bacterialinvasionofepithelialcells_Humandiseases_Infectiousdiseases_inlB,internalinB	5,18629E-06	5,09533E-06	8,30537E-06
K13788_ko00630_Glyoxylateanddicarboxylatemetabolism_Metabolism_Carbohydratemetabolism_pta,phosphateacetyltransferase[EC:2.3.1.8];K13788_ko00620_Pyruvatemetabolism_Metabolism_Carbohydratemetabolism_pta,phosphateacetyltransferase[EC:2.3.	3,11177E-05	2,03813E-05	8,30537E-05
K01915_ko02020_Two-componentsystem_Environmentalinformationprocessing_Signaltrasduction_glnA,GLUL,glutaminesynthetase[EC:6.3.1.2];K01915_ko00250_Alanine,aspartateandglutamatemetabolism_Metabolism_Aminoacidmetabolism_glnA,GLUL,glutamii	0,003049539	0,003291586	0,002898575
K03589_ko04112_Cellcycle-Caulobacter_CellularProcesses_Cellgrowthanddeath_ftsQ,celldivisionproteinFtsQ	0,000762385	0,000876397	0,001187668
K02438_ko00500_Starchandsucrosemetabolism_Metabolism_Carbohydratemetabolism_treX,glgX,glycogenoperonprotein[EC:3.2.1.-]	0,000482325	0,000315911	0,000398658
K02977_ko03010_Ribosome_GeneticinformationProcessing_Transcription_RP-S27Ae,RPS27A,smallsubunitribosomalproteinS27Ae	1,55589E-05	0	0
K01847_ko00280_Valine,leucineandisoleucinedegradation_Metabolism_Aminoacidmetabolism_MUT,methylmalonyl-CoAmutase[EC:5.4.99.2];K01847_ko00630_Glyoxylateanddicarboxylatemetabolism_Metabolism_Carbohydratemetabolism_MUT,methylmalonyl-	0,002224919	0,001982085	0,001411913
K00849_ko00520_Aminosugarandnucleotidesugarmetabolism_Metabolism_Carbohydratemetabolism_galK,galactokinase[EC:2.7.1.6];K00849_ko00052_Galactosemetabolism_Metabolism_Carbohydratemetabolism_galK,galactokinase[EC:2.7.1.6]	0,001545515	0,001284024	0,000938507
K00966_ko00520_Aminosugarandnucleotidesugarmetabolism_Metabolism_Carbohydratemetabolism_GMPP,mannose-1-phosphateguanylyltransferase[EC:2.7.7.13];K00966_ko00051_Fructoseandmannosemetabolism_Metabolism_Carbohydratemetabolism_GMF	0,000534188	0,000397436	0,00044849
K10117_ko02010_Ctransporters_Environmentalinformationprocessing_Membranetransport_msmE,raffinose/stachyose/melibiosetransportsystemsubstrate-bindingprotein	0,000917974	0,001044543	0,000830537
K01840_ko00520_Aminosugarandnucleotidesugarmetabolism_Metabolism_Carbohydratemetabolism_manB,phosphomannomutase[EC:5.4.2.8];K01840_ko00051_Fructoseandmannosemetabolism_Metabolism_Carbohydratemetabolism_manB,phosphomannomu	0,00253091	0,002185898	0,002184313
K00697_ko00500_Starchandsucrosemetabolism_Metabolism_Carbohydratemetabolism_otsA,trehalose6-phosphatesynthase[EC:2.4.1.15]	5,70492E-05	2,54767E-05	6,6443E-05
K02006_ko02010_Ctransporters_Environmentalinformationprocessing_Membranetransport_cbiO,cobalt/nickeltransportsystemATP-bindingprotein	0,002058958	0,002496714	0,002740773
K03217_ko02010_Ctransporters_Environmentalinformationprocessing_Membranetransport_yidC,spoIIIJ,OXA1,YidC/Oxa1familymembraneproteininsertase;K03217_ko04120_Ubiquitinmediatedproteolysis_GeneticInformationProcessing_Folding,sortinganddegrad	0,00198635	0,001661079	0,001486662
K01809_ko00520_Aminosugarandnucleotidesugarmetabolism_Metabolism_Carbohydratemetabolism_manA,MPI,mannose-6-phosphateisomerase[EC:5.3.1.8];K01809_ko00051_Fructoseandmannosemetabolism_Metabolism_Carbohydratemetabolism_manA,MPI,	0,000746826	0,000983399	0,000913591
K11907_ko02010_Ctransporters_Environmentalinformationprocessing_Membranetransport_vasG,clpV,typeVIsecretionsystemproteinVasG	6,74218E-05	4,07627E-05	0
K11381_ko00280_Valine,leucineandisoleucinedegradation_Metabolism_Aminoacidmetabolism_bkdA,2-oxoisovaleratedehydrogenaseE1component[EC:1.2.4.4]	5,70492E-05	6,1144E-05	0,000149497
K04108_ko01220_Degradationofaromaticcompounds_Metabolism_Overview_hcrA,hbaC,4-hydroxybenzoyl-CoAreductasesubunitalpha[EC:1.3.7.9];K04108_ko00627_Aminobenzoatedegradation_Metabolism_Xenobioticsbiodegradationandmetabolism_hcrA,hbaC,4	5,18629E-06	1,01907E-05	0
K07713_ko02020_Two-componentsystem_Environmentalinformationprocessing_Signaltrasduction_zraR,hydG,two-componentsystem,NtrCfamily,responseregulatorHydG	0,001535142	0,00198718	0,001494967
K01712_ko00340_Histidinemetabolism_Metabolism_Aminoacidmetabolism_hutU,UROC1,urocanatehydratase[EC:4.2.1.49]	0,00060161	0,000555391	0,000506628
K05364_ko01005_Lipopolysaccharidebiosynthesisproteins_Metabolism_Glycanbiosynthesisandmetabolism_E2.4.1.129,peptidoglycanglycosyltransferase[EC:2.4.1.129]	0,002681313	0,002807529	0,00502475
K03702_ko03420_Nucleotideexcisionrepair_GeneticinformationProcessing_ReplicationandRepair_uvrB,excinucleaseABCsubunitB	0,003526678	0,002619002	0,002940102
K03781_ko04146_Peroxisome_CellularProcesses_Transportandcatabolism_katE,CAT,catB,srpA,catalase[EC:1.11.1.6];K03781_ko04066_HIF-1signalingpathway_Environmentalinformationprocessing_Signaltrasduction_katE,CAT,catB,srpA,catalase[EC:1.11.1.6];K0378	0,000186706	0,000122288	0,000166107
K02564_ko00520_Aminosugarandnucleotidesugarmetabolism_Metabolism_Carbohydratemetabolism_nagB,GNPDA,glucosamine-6-phosphatedeaminase[EC:3.5.99.6]	0,001135798	0,001304405	0,000988339
K01139_ko00230_Purinemetabolism_Metabolism_Nucleotidemetabolism_spoT,HDDC3,guanosine-3',5'-bis(diphosphate)3'-pyrophosphohydrolase[EC:3.1.7.2]	0,000129657	3,0572E-05	0,00010797
K00054_ko00900_Terpenoidbackbonebiosynthesis_Metabolism_Metabolismofterpenoidsandpolyketides_mvaA,hydroxymethylglutaryl-CoAreductase[EC:1.1.1.88]	2,07452E-05	3,0572E-05	6,6443E-05
K01369_ko04142_Lysosome_CellularProcesses_Transportandcatabolism_LGMN,legumain[EC:3.4.22.34];K01369_ko04612_Antigenprocessingandpresentation_Organismalsystem_Immunesystem_LGMN,legumain[EC:3.4.22.34]	0,000103726	7,13347E-05	0,000116275
K03407_ko02020_Two-componentsystem_Environmentalinformationprocessing_Signaltrasduction_cheA,two-componentsystem,chemotaxisfamily,sensorkinaseCheA[EC:2.7.13.3];K03407_ko02030_Bacterialchemotaxis_Organismalsystem_Cellmobility_cheA,two-c	0,000430462	0,00038215	0,000365436
K12553_ko00312_beta-Lactamresistance_HumanDiseases_Drugresistance_pbp3,penicillin-bindingprotein3[EC:3.4.-.-];K12553_ko01005_Lipopolysaccharidebiosynthesisproteins_Metabolism_Glycanbiosynthesisandmetabolism_pbp3,penicillin-bindingprotein3[EC:3	1,55589E-05	6,1144E-05	4,15269E-05
K02343_ko03030_DNAreplication_GeneticinformationProcessing_ReplicationandRepair_DPO3G,dnaX,DNApolymeraseIIIsubunitgamma/tau[EC:2.7.7.7];K02343_ko03440_HomologousrecombinationGeneticinformationProcessing_ReplicationandRepair_DPO3G,dr	0,001545515	0,001625411	0,00166938
K05290_ko00563_Glycosylphosphatidylinositol(GPI)-anchorbiosynthesis_Metabolism_Glycanbiosynthesisandmetabolism_PIGK,phosphatidylinositolglycan,classK[EC:2.6.-.-]	5,18629E-06	1,01907E-05	3,32215E-05
K01874_ko00970_Aminoacyl-tRNAbiosynthesis_Geneticinformationandprocessing_Transcription_MARS,metG,methionyl-tRNAsynthetase[EC:6.1.1.10];K01874_ko00450_Selenocompoundmetabolism_Metabolism_Metabolismofotheraminoacids_MARS,metG,meth	0,00309103	0,002440665	0,002641108
K10112_ko02010_Ctransporters_Environmentalinformationprocessing_Membranetransport_msmX,msmK,malK,sugC,ggtA,msiK,multiplesugartransportsystemATP-bindingprotein	0,000938719	0,000978304	0,000830537
K01892_ko00970_Aminoacyl-tRNAbiosynthesis_Geneticinformationandprocessing_Transcription_HARS,hisS,histidyl-tRNAsynthetase[EC:6.1.1.21]	0,001446975	0,001666174	0,001195974
K13990_ko00340_Histidinemetabolism_Metabolism_Aminoacidmetabolism_FTCD,glutamateformiminotransferase/formiminotetrahydrofolatecyclodeaminase[EC:2.1.2.54.3.1.4];K13990_ko00670_Onecarbonpoolbyfolate_Metabolism_Metabolismofcofactorsandv	0,000207452	0,000183432	0,00021594
K07462_ko03410_Baseexcisionrepair_GeneticinformationProcessing_ReplicationandRepair_recJ,single-stranded-DNA-specificexonuclease[EC:3.1.-.-];K07462_ko03440_HomologousrecombinationGeneticinformationProcessing_ReplicationandRepair_recJ,single-s	0,001830761	0,001915845	0,001752433
K01843_ko00310_Lysinedegradation_Metabolism_Aminoacidmetabolism_kamA,lysine2,3-aminomutase[EC:5.4.3.2]	7,77944E-05	0,000183432	0,000166107
K01972_ko03410_Baseexcisionrepair_GeneticinformationProcessing_ReplicationandRepair_E6.5.1.2,ligA,ligB,DNAligase(NAD+)[EC:6.5.1.2];K01972_ko03030_DNAreplication_GeneticinformationProcessing_ReplicationandRepair_E6.5.1.2,ligA,ligB,DNAligase(NAD+)	0,00202784	0,002124754	0,002084648
K03703_ko03420_Nucleotideexcisionrepair_GeneticinformationProcessing_ReplicationandRepair_uvrC,excinucleaseABCsubunitC	0,001799643	0,002094182	0,001960068
K01159_ko03440_Homologousrecombination_GeneticinformationProcessing_ReplicationandRepair_ruvC,crossoverjunctionendodeoxyribonucleaseRuvC[EC:3.1.22.4]	0,000414903	0,000264957	0,000174413
K02303_ko00830_Retinolmetabolism_Metabolism_Metabolismofcofactorsandvitamins_cobA,uroporphyrin-IIIC-methyltransferase[EC:2.1.1.107]	1,03726E-05	1,5286E-05	0
K09667_ko00514_OthertypesofO-glycanbiosynthesis_Metabolism_Glycanbiosynthesisandmetabolism_OGT,proteinO-GlcNActransferase[EC:2.4.1.255]	2,59315E-05	1,01907E-05	3,32215E-05
K07260_ko02020_Two-componentsystem_Environmentalinformationprocessing_Signaltrasduction_vanY,D-alanyl-D-alaninecarboxypeptidase[EC:3.4.16.4];K07260_ko01005_Lipopolysaccharidebiosynthesisproteins_Metabolism_Glycanbiosynthesisandmetabolism_	0,00036304	0,000132479	0,00032391
K10852_ko00311_Penicillinandcephalosporinbiosynthesis_Metabolism_Biosynthesisofothersecondarymetabolites_E2.3.1.164,isopenicillin-NN-acyltransferase[EC:2.3.1.164]	0,000103726	4,5858E-05	2,49161E-05
K01662_ko00730_Thiaminemetabolism_Metabolism_Metabolismofcofactorsandvitamins_dxs,1-deoxy-D-xylulose-5-phosphatesynthase[EC:2.2.1.7];K01662_ko00900_Terpenoidbackbonebiosynthesis_Metabolism_Metabolismofterpenoidsandpolyketides_dxs,1-de	0,001732221	0,001875083	0,001960068
K02400_ko02040_Flagellarassembly_Organismalsystem_Cellmobility_flhA,flagellarbiosynthesisproteinFlhA	0,000570492	0,000387245	0,000290688
K06148_ko02010_Ctransporters_Environmentalinformationprocessing_Membranetransport_ABCC-BAC,ATP-bindingcassette,subfamilyC,bacterial	0,002396067	0,002639383	0,003596226
K01621_ko00030_Pentosephosphatepathway_Metabolism_Carbohydratemetabolism_E4.1.2.9,phosphoketolase[EC:4.1.2.9];K01621_ko00194_Photosynthesisproteins_Metabolism_Energymetabolism_E4.1.2.9,phosphoketolase[EC:4.1.2.9]	0,000269687	8,66207E-05	0,000157802
K01541_ko00190_Oxidativephosphorylation_Metabolism_Energymetabolism_E3.6.3.10,H+/K+-exchangingATPase[EC:3.6.3.10]	0	5,09533E-06	0
K11824_ko04144_Endocytosis_CellularProcesses_Transportandcatabolism_AP2A,AP-2complexsubunitalpha;K11824_ko04721_Synapticvesiclecycle_Environmentalinformationprocessing_Signaltransduction_AP2A,AP-2complexsubunitalpha;K11824_ko05016_Hunti	1,03726E-05	2,03813E-05	3,32215E-05
K01002_ko00561_Glycerolipidmetabolism_Metabolism_Lipidmetabolism_mdoB,phosphoglyceroltransferase[EC:2.7.8.20]	0,000627541	0,000662393	0,000905286
K01810_ko00520_Aminosugarandnucleotidesugarmetabolism_Metabolism_Carbohydratemetabolism_GPI,pgi,glucose-6-phosphateisomerase[EC:5.3.1.9];K01810_ko00010_Glycolysis/Gluconeogenesis_Metabolism_Carbohydratemetabolism_GPI,pgi,glucose-6-phc	0,002053771	0,001813939	0,001279027
K01218_ko00051_Fructoseandmannosemetabolism_Metabolism_Carbohydratemetabolism_E3.2.1.78,mannanendo-1,4-beta-mannosidase[EC:3.2.1.78]	0,000357854	0,000570677	0,000274077
K06896_ko00500_Starchandsucrosemetabolism_Metabolism_Carbohydratemetabolism_mapP,maltose6'-phosphatephosphatase[EC:3.1.3.90]	0,000653473	0,001095497	0,001038171
K01784_ko00520_Aminosugarandnucleotidesugarmetabolism_Metabolism_Carbohydratemetabolism_galE,GALE,UDP-glucose4-epimerase[EC:5.1.3.2];K01784_ko00052_Galactosemetabolism_Metabolism_Carbohydratemetabolism_galE,GALE,UDP-glucose4-epim	0,003656336	0,003704308	0,003189263
K08724_ko01005_Lipopolysaccharidebiosynthesisproteins_Metabolism_Glycanbiosynthesisandmetabolism_pbpB,penicillin-bindingprotein2B	0,000202265	0,000112097	0,000224245

K01950_ko00760_Nicotinateandnicotinamidemetabolism_Metabolism_Metabolismofcofactorsandvitamins_E6.3.5.1,NADSYN1,QNS1,nadE,NAD+synthase(glutamine-hydrolysing)[EC:6.3.5.1]	0,001073562	0,001197403	0,00100495
K02763_ko02010_Ctransporters_Environmentalinformationprocessing_Membranetransport_PTS-Dgl-EIIA,gamP,PTSsystem,D-glucosamine-specificIIAcomponent[EC:2.7.1.69];K02763_ko00520_Aminosugarandnucleotidesugarmetabolism_Metabolism_Carbohydrat	0,000316364	0,000585963	0,000481712
K05341_ko00500_Starchandsucrosemetabolism_Metabolism_Carbohydratemetabolism_E2.4.1.4,amylosucrase[EC:2.4.1.4]	0,000285246	0,000321006	5,81376E-05
K04041_ko00051_Fructoseandmannosemetabolism_Metabolism_Carbohydratemetabolism_fbp3,fructose-1,6-bisphosphataseII[EC:3.1.3.11];K04041_ko00010_Glycolysis/Gluconeogenesis_Metabolism_Carbohydratemetabolism_fbp3,fructose-1,6-bisphosphataseI	0,001047631	0,001075115	0,000946812
K02123_ko00190_Oxidativephosphorylation_Metabolism_Energymetabolism_ATPVI,ntpI,atpI,V/A-typeH+-transportingATPasesubunitI	0,000632728	0,000866207	0,000697651
K04567_ko00970_Aminoacyl-tRNAbiosynthesis_Geneticinformationandprocessing_Transcription_KARS,lysS,lysyl-tRNAsynthetase,classII[EC:6.1.1.6]	0,002982118	0,002562953	0,002641108
K01868_ko00970_Aminoacyl-tRNAbiosynthesis_Geneticinformationandprocessing_Transcription_TARS,thrS,threonyl-tRNAsynthetase[EC:6.1.1.3]	0,002847274	0,002756576	0,002317199
K00100_ko00051_Fructoseandmannosemetabolism_Metabolism_Carbohydratemetabolism_E1.1.1.-,[EC:1.1.1.-];K00100_ko00630_Glyoxylateanddicarboxylatemetabolism_Metabolism_Carbohydratemetabolism_E1.1.1.-,[EC:1.1.1.-];K00100_ko00591_Linoleicacidr	0,004984026	0,00434632	0,004933391
K11690_ko02020_Two-componentsystem_Environmentalinformationprocessing_Signaltrasduction_dctM,C4-dicarboxylatetransporter,DctMsubunit	0,001483279	0,001064925	0,001054782
K01649_ko00290_Valine,leucineandisoleucinebiosynthesis_Metabolism_Aminoacidmetabolism_leuA,2-isopropylmalatesynthase[EC:2.3.3.13];K01649_ko00620_Pyruvatemetabolism_Metabolism_Carbohydratemetabolism_leuA,2-isopropylmalatesynthase[EC:2.3.3	0,001882624	0,003062296	0,003380286
K02798_ko02010_Ctransporters_Environmentalinformationprocessing_Membranetransport_PTS-Mtl-EIIA,mtlA,PTSsystem,mannitol-specificIIAcomponent[EC:2.7.1.69];K02798_ko00051_Fructoseandmannosemetabolism_Metabolism_Carbohydratemetabolism_PT	0,000191893	0,000101907	0,000149497
K07718_ko02020_Two-componentsystem_Environmentalinformationprocessing_Signaltrasduction_yesM,two-componentsystem,sensorhistidinekinaseYesM[EC:2.7.13.3]	0,003065098	0,003174393	0,003513172
K00687_ko00312_beta-Lactamresistance_HumanDiseases_Drugresistance_pbp2B,penA,penicillin-bindingprotein2B[EC:2.3.2.-];K00687_ko01005_Lipopolysaccharidebiosynthesisproteins_Metabolism_Glycanbiosynthesisandmetabolism_pbp2B,penA,penicillin-bindi	4,66766E-05	4,07627E-05	2,49161E-05
K00945_ko00240_Pyrimidinemetabolism_Metabolism_Nucleotidemetabolism_cmk,cytidylatekinase[EC:2.7.4.14]	0,002131566	0,001620316	0,002092954
K02016_ko02010_Ctransporters_Environmentalinformationprocessing_Membranetransport_ABC.FEV.S,ironcomplextransportsystemsubstrate-bindingprotein	0,001281014	0,00145217	0,001478356
K09883_ko00830_Retinolmetabolism_Metabolism_Metabolismofcofactorsandvitamins_cobT,cobaltochelataseCobT[EC:6.6.1.2]	0,000114098	0	4,15269E-05
K00600_ko00260_Glycine,serineandthreoninemetabolism_Metabolism_Aminoacidmetabolism_glyA,SHMT,glycinehydroxymethyltransferase[EC:2.1.2.1];K00600_ko00630_Glyoxylateanddicarboxylatemetabolism_Metabolism_Carbohydratemetabolism_glyA,SHMT	0,001675172	0,001350263	0,001262417
K00239_ko05134_Legionellosis_HumanDiseases_Infectiousdiseases_sdhA,succinatedehydrogenaseflavoproteinsubunit[EC:1.3.5.1];K00239_ko00020_Citratecycle(TCAcycle)_Metabolism_Carbohydratemetabolism_sdhA,succinatedehydrogenaseflavoproteinsubunit	0,001908555	0,001396121	0,001245806
K03883_ko05012_Parkinson'sdisease_HumanDiseases_Degenerativediseases_ND5,NADH-ubiquinoneoxidoreductasechain5[EC:1.6.5.3];K03883_ko00190_Oxidativephosphorylation_Metabolism_Energymetabolism_ND5,NADH-ubiquinoneoxidoreductasechain5[EC:	0	1,5286E-05	1,66107E-05
K11263_ko00280_Valine,leucineandisoleucinedegradation_Metabolism_Aminoacidmetabolism_bccA,acetyl-/propionyl-CoAcarboxylase,biotincarboxylase,biotincarboxylcarrierprotein[EC:6.4.1.2 6.4.1.3 6.3.4.14];K11263_ko00630_Glyoxylateanddicarboxylatemetab	2,07452E-05	1,5286E-05	1,66107E-05
K12574_ko03018_RNAdegradation_GeneticInformationProcessing_Folding,sortinganddegradation_rnj,ribonucleaseJ[EC:3.1.-.-]	0,001363995	0,00137574	0,001719212
K00971_ko00520_Aminosugarandnucleotidesugarmetabolism_Metabolism_Carbohydratemetabolism_manC,cpsB,mannose-1-phosphateguanylyltransferase[EC:2.7.7.13];K00971_ko00051_Fructoseandmannosemetabolism_Metabolism_Carbohydratemetabolism_	0,00060161	0,0006827775	0,00066443
K00797_ko00330_Arginineandprolinemetabolism_Metabolism_Aminoacidmetabolism_speE,SRM,spermidinesynthase[EC:2.5.1.16];K00797_ko00270_Cysteineandmethioninemetabolism_Metabolism_Aminoacidmetabolism_speE,SRM,spermidinesynthase[EC:2.5.1	0,000191893	0,000300625	0,000265772
K01919_ko00480_Glutathionemetabolism_Metabolism_Metabolismofotheraminoacids_gshA,glutamate--cysteineligase[EC:6.3.2.2]	7,77944E-05	3,0572E-05	6,6443E-05
K07712_ko02020_Two-componentsystem_Environmentalinformationprocessing_Signaltrasduction_glnG,ntrC,two-componentsystem,NtrCfamily,nitrogenregulationresponseregulatorGlnG	0,00050307	0,000331197	0,000398658
K02768_ko02010_Ctransporters_Environmentalinformationprocessing_Membranetransport_PTS-Fru-EIIA,fruB,PTSsystem,fructose-specificIIAcomponent[EC:2.7.1.69];K02768_ko00051_Fructoseandmannosemetabolism_Metabolism_Carbohydratemetabolism_PTS	0,0006431	0,000453485	0,000573071
K01173_ko04210_Apoptosis_Cellularprocesses_Cellgrowthanddeath_ENDOG,endonucleaseG,mitochondrial	0,000414903	0,000433103	0,000390352
K01178_ko00500_Starchandsucrosemetabolism_Metabolism_Carbohydratemetabolism_E3.2.1.3,glucoamylase[EC:3.2.1.3]	9,33532E-05	9,1716E-05	0,000132886
K01076_ko01040_Biosynthesisofunsaturatedfattyacids_Metabolism_Lipidmetabolism_E3.1.2.-,[EC:3.1.2.-];K01076_ko00903_Limoneneandpinenedegradation_Metabolism_Metabolismofterpenoidsandpolyketides_E3.1.2.-,[EC:3.1.2.-]	0,000129657	0,000163051	0,000282383
K12556_ko00312_beta-Lactamresistance_HumanDiseases_Drugresistance_pbp2X,penicillin-bindingprotein2X[EC:2.3.2.-];K12556_ko01005_Lipopolysaccharidebiosynthesisproteins_Metabolism_Glycanbiosynthesisandmetabolism_pbp2X,penicillin-bindingprotein2	3,6304E-05	1,01907E-05	5,81376E-05
K01652_ko00290_Valine,leucineandisoleucinebiosynthesis_Metabolism_Aminoacidmetabolism_E2.2.1.6L,ilvB,ilvG,ilvI,acetolactatesynthaseI/II/IIIlargesubunit[EC:2.2.1.6];K01652_ko00630_Glyoxylateanddicarboxylatemetabolism_Metabolism_Carbohydratemetab	0,001561074	0,001523505	0,001694296
K01960_ko00020_Citratecycle(TCAcycle)_Metabolism_Carbohydratemetabolism_pycB,pyruvatecarboxylasesubunitB[EC:6.4.1.1];K01960_ko00620_Pyruvatemetabolism_Metabolism_Carbohydratemetabolism_pycB,pyruvatecarboxylasesubunitB[EC:6.4.1.1];K0196(	0,000917974	0,001151545	0,000813926
K01464_ko00770_PantothenateandCoABiosynthesis_Metabolism_Metabolismofcofactorsandvitamins_DPYS,dht,hydA,dihydropyrimidinase[EC:3.5.2.2];K01464_ko00410_beta-Alaninemetabolism_Metabolism_Metabolismofotheraminoacids_DPYS,dht,hydA,dihydr	0,000259315	0,000163051	0,000199329
K08348_ko02020_Two-componentsystem_Environmentalinformationprocessing_Signaltrasduction_fdnG,formatedehydrogenase-N,alphasubunit[EC:1.1.5.6]	3,6304E-05	0	3,32215E-05
K01182_ko00052_Galactosemetabolism_Metabolism_Carbohydratemetabolism_E3.2.1.10,oligo-1,6-glucosidase[EC:3.2.1.10];K01182_ko00500_Starchandsucrosemetabolism_Metabolism_Carbohydratemetabolism_E3.2.1.10,oligo-1,6-glucosidase[EC:3.2.1.10]	0,000720895	0,000861111	0,000539849
K03590_ko04112_Cellcycle-Caulobacter_CellularProcesses_Cellgrowthanddeath_ftsA,celldivisionproteinFtsA	0,000565306	0,000723537	0,0007724
K07706_ko02020_Two-componentsystem_Environmentalinformationprocessing_Signaltrasduction_agrC,two-componentsystem,AgrAfamily,sensorhistidinekinaseAgrC[EC:2.7.13.-]	0,000860924	0,001034353	0,001353776
K05365_ko01005_Lipopolysaccharidebiosynthesisproteins_Metabolism_Glycanbiosynthesisandmetabolism_mrcB,penicillin-bindingprotein1B[EC:2.4.1.1293.4.-.-]	7,26081E-05	4,07627E-05	7,47483E-05
K01486_ko00230_Purinemetabolism_Metabolism_Nucleotidemetabolism_ade,adeninedeaminase[EC:3.5.4.2]	0,001255083	0,000810158	0,001395302
K03575_ko03410_Baseexcisionrepair_GeneticinformationProcessing_ReplicationandRepair_mutY,A/G-specificadenineglycosylase[EC:3.2.2.-]	0,000726081	0,000912065	0,001038171
K02761_ko02010_Ctransporters_Environmentalinformationprocessing_Membranetransport_PTS-Cel-EIIC,celB,PTSsystem,cellobiose-specificIICcomponent	0,000518629	0,000845825	0,000905286
K00198_ko01200_Carbonmetabolism_Metabolism_Overview_cooS,acsA,carbon-monoxidedehydrogenasecatalyticsubunit[EC:1.2.99.21.2.7.4];K00198_ko00633_Nitrotoluenedegradation_Metabolism_Xenobioticsbiodegradationandmetabolism_cooS,acsA,carbon-r	0,000171148	0,000402531	0,000174413
K01879_ko00970_Aminoacyl-tRNAbiosynthesis_Geneticinformationandprocessing_Transcription_glyS,glycyl-tRNAsynthetasebetachain[EC:6.1.1.14]	0,000243756	0,000453485	0,000382047
K01585_ko00330_Arginineandprolinemetabolism_Metabolism_Aminoacidmetabolism_E4.1.1.19S,speA,arginginedecarboxylase[EC:4.1.1.19]	0,001140984	0,001090401	0,000597987
K01814_ko00340_Histidinemetabolism_Metabolism_Aminoacidmetabolism_hisA,phosphoribosylformimino-5-aminoimidazolecarboxamideribotideisomerase[EC:5.3.1.16];K01814_ko01230_Biosynthesisofaminoacids_Metabolism_Overview_hisA,phosphoribosylfo	0,002442743	0,001284024	0,000963423
K10912_ko02020_Two-componentsystem_Environmentalinformationprocessing_Signaltrasduction_luxO,two-componentsystem,repressorproteinLuxO;K10912_ko05111_Vibriocholeraepathogeniccycle_HumanDiseases_Infectiousdiseases_luxO,two-componentsys	0	1,01907E-05	8,30537E-06
K02809_ko02010_Ctransporters_Environmentalinformationprocessing_Membranetransport_PTS-Scr-EIIB,scrA,PTSsystem,sucrose-specificIIBcomponent[EC:2.7.1.69];K02809_ko00500_Starchandsucrosemetabolism_Metabolism_Carbohydratemetabolism_PTS-Scr-	0,000191893	0,000346483	0,000357131
K11069_ko02010_Ctransporters_Environmentalinformationprocessing_Membranetransport_potD,spermidine/putrescinetransportsystemsubstrate-bindingprotein	0,000554933	0,000983399	0,000805621
K00955_ko00920_Sulfurmetabolism_Metabolism_Energymetabolism_cysNC,bifunctionalenzymeCysN/CysC[EC:2.7.7.42.7.1.25];K00955_ko00450_Selenocompoundmetabolism_Metabolism_Metabolismofotheraminoacids_cysNC,bifunctionalenzymeCysN/CysC[EC:	6,74218E-05	0	2,49161E-05
K07710_ko02020_Two-componentsystem_Environmentalinformationprocessing_Signaltrasduction_atoS,two-componentsystem,NtrCfamily,sensorhistidinekinaseAtoS[EC:2.7.13.3]	5,70492E-05	3,56673E-05	8,30537E-05
K10798_ko03410_Baseexcisionrepair_GeneticinformationProcessing_ReplicationandRepair_PARP,poly[ADP-ribose]polymerase[EC:2.4.2.30]	3,11177E-05	4,07627E-05	7,47483E-05
K00029_ko00620_Pyruvatemetabolism_Metabolism_Carbohydratemetabolism_E1.1.1.40,maeB,malatedehydrogenase(oxaloacetate-decarboxylating)(NADP+)[EC:1.1.1.40];K00029_ko01200_Carbonmetabolism_Metabolism_Overview_E1.1.1.40,maeB,malatedehy	0,000596424	0,000509533	0,000539849
K04034_ko00830_Retinolmetabolism_Metabolism_Metabolismofcofactorsandvitamins_bchE,anaerobicmagnesium-protoporphyrinIXmonomethylestercyclase[EC:4.-.-.-]	0,000793503	0,001543886	0,001760739
K02111_ko00190_Oxidativephosphorylation_Metabolism_Energymetabolism_ATPF1A,atpA,F-typeH+-transportingATPasesubunitalpha[EC:3.6.3.14];K02111_ko00195_Photosynthesis_Metabolism_Energymetabolism_ATPF1A,atpA,F-typeH+-transportingATPasesubu	0,002157497	0,001747699	0,001503272
K02453_ko02010_Ctransporters_Environmentalinformationprocessing_Membranetransport_gspD,generalsecretionpathwayproteinD	4,14903E-05	4,5858E-05	9,96645E-05
K10125_ko02020_Two-componentsystem_Environmentalinformationprocessing_Signaltrasduction_dctB,two-componentsystem,NtrCfamily,C4-dicarboxylatetransportsensorhistidinekinaseDctB[EC:2.7.13.3]	4,14903E-05	0,000112097	0,00021594
K02818_ko02010_Ctransporters_Environmentalinformationprocessing_Membranetransport_PTS-Tre-EIIB,treB,PTSsystem,trehalose-specificIIBcomponent[EC:2.7.1.69];K02818_ko00500_Starchandsucrosemetabolism_Metabolism_Carbohydratemetabolism_PTS-Tr	5,70492E-05	6,1144E-05	6,6443E-05
K12264_ko05132_Salmonellainfection_HumanDiseases_Infectiousdiseases_norV,anaerobicnitricoxidereductaseflavorubredoxin	0,001151357	0,000957923	0,001295638
K10615_ko04120_Ubiquitinmediatedproteolysis_GeneticInformationProcessing_Folding,sortinganddegradation_HERC4,E3ubiquitin-proteinligaseHERC4[EC:6.3.2.19]	1,55589E-05	4,07627E-05	8,30537E-06
K05592_ko03018_RNAdegradation_GeneticInformationProcessing_Folding,sortinganddegradation_deaD,cshA,ATP-dependentRNAhelicaseDeaD[EC:3.6.4.13]	0,001644054	0,002282709	0,001760739
K00817_ko00340_Histidinemetabolism_Metabolism_Aminoacidmetabolism_hisC,histidinol-phosphateaminotransferase[EC:2.6.1.9];K00817_ko00360_Phenylalaninemetabolism_Metabolism_Aminoacidmetabolism_hisC,histidinol-phosphateaminotransferase[EC:2	0,000674218	0,000799967	0,000739178
K01515_ko00230_Purinemetabolism_Metabolism_Nucleotidemetabolism_nudF,ADP-ribosepyrophosphatase[EC:3.6.1.13]	0,000860924	0,001905655	0,001362081
K08218_ko00312_beta-Lactamresistance_HumanDiseases_Drugresistance_ampG,MFStransporter,PATfamily,beta-lactamaseinductionsignaltransducerAmpG	0,000617169	0,000799967	0,000523238
K00852_ko00030_Pentosephosphatepathway_Metabolism_Carbohydratemetabolism_rbsK,RBKS,ribokinase[EC:2.7.1.15]	0,000586051	0,000754109	0,000880369
K00800_ko00400_Phenylalanine,tyrosineandtryptophanbiosynthesis_Metabolism_Aminoacidmetabolism_aroA,3-phosphoshikimate1-carboxyvinyltransferase[EC:2.5.1.19];K00800_ko01230_Biosynthesisofaminoacids_Metabolism_Overview_aroA,3-phosphoshikim	0,000606796	0,000896779	0,00055646
K00547_ko00270_Cysteineandmethioninemetabolism_Metabolism_Aminoacidmetabolism_mmuM,homocysteineS-methyltransferase[EC:2.1.1.10]	0,000108912	0,000122288	0,000132886
K05358_ko00400_Phenylalanine,tyrosineandtryptophanbiosynthesis_Metabolism_Aminoacidmetabolism_quiA,quinatedehydrogenase(quinone)[EC:1.1.5.8]	1,55589E-05	0	0
K00764_ko00250_Alanine,aspartateandglutamatemetabolism_Metabolism_Aminoacidmetabolism_purF,PPAT,amidophosphoribosyltransferase[EC:2.4.2.14];K00764_ko00230_Purinemetabolism_Metabolism_Nucleotidemetabolism_purF,PPAT,amidophosphoribos	0,002245664	0,00160503	0,001818876
K03596_ko05134_Legionellosis_HumanDiseases_Infectiousdiseases_lepA,GTP-bindingproteinLepA	0,002857647	0,002695432	0,002101259
K15022_ko01200_Carbonmetabolism_Metabolism_Overview_fdhB1,formatedehydrogenasebetasubunit[EC:1.2.1.43];K15022_ko00194_Photosynthesisproteins_Metabolism_Energymetabolism_fdhB1,formatedehydrogenasebetasubunit[EC:1.2.1.43];K15022_ko00	0,000103726	3,56673E-05	1,66107E-05

K01876_ko00970_Aminoacyl-tRNAbiosynthesis_Geneticinformationandprocessing_Transcription_DARS,aspS,aspartyl-tRNAsynthetase[EC:6.1.1.12]	0,002442743	0,002583334	0,002466695
K01596_ko04066_HIF-1signalingpathway_Environmentalinformationprocessing_Signaltrasduction_E4.1.1.32,pckA,PEPCK,phosphoenolpyruvatecarboxykinase(GTP)[EC:4.1.1.32];K01596_ko04151_PI3K-Aktsignalingpathway_Environmentalinformationprocessing_Sig	0,000238569	4,5858E-05	6,6443E-05
K00595_ko00830_Retinolmetabolism_Metabolism_Metabolismofcofactorsandvitamins_cobL,precorrin-6YC5,15-methyltransferase(decarboxylating)[EC:2.1.1.132]	0,000326736	0,00022929	0,000265772
K01077_ko02020_Two-componentsystem_Environmentalinformationprocessing_Signaltrasduction_E3.1.3.1,phoA,phoB,alkalinephosphatase[EC:3.1.3.1];K01077_ko00785_Lipoicacidmetabolism_Metabolism_Metabolismofcofactorsandvitamins_E3.1.3.1,phoA,pho	0,001006141	0,001013971	0,000880369
K01841_ko00440_Phosphonateandphosphinatemetabolism_Metabolism_Metabolismofotheraminoacids_pepM,phosphoenolpyruvatephosphomutase[EC:5.4.2.9]	0,000311177	0,000147765	0,000298993
K03583_ko03440_Homologousrecombination_GeneticinformationProcessing_ReplicationandRepair_recC,exodeoxyribonucleaseVgammasubunit[EC:3.1.11.5]	4,66766E-05	6,62393E-05	9,13591E-05
K01953_ko00250_Alanine,aspartateandglutamatemetabolism_Metabolism_Aminoacidmetabolism_asnB,ASNS,asparaginesynthase(glutamine-hydrolysing)[EC:6.3.5.4]	0,001415858	0,001722223	0,001827182
K00174_ko00020_Citratecycle(TCAcycle)_Metabolism_Carbohydratemetabolism;K00174_ko01200_Carbonmetabolism_Metabolism_Overview;K00174_ko00194_Photosynthesisproteins_Metabolism_Energymetabolism	0,0016648	0,001554077	0,001129531
K03367_ko05150_Staphylococcusaureusinfection_HumanDiseases_Infectiousdiseases_dltA,D-alanine--poly(phosphoribitol)ligasesubunit1[EC:6.1.1.13];K03367_ko00473_D-Alaninemetabolism_Metabolism_Metabolismofotheraminoacids_dltA,D-alanine--poly(phos	5,18629E-05	0,000147765	0,000132886
K00655_ko00561_Glycerolipidmetabolism_Metabolism_Lipidmetabolism_plsC,1-acyl-sn-glycerol-3-phosphateacyltransferase[EC:2.3.1.51];K00655_ko00564_Glycerophospholipidmetabolism_Metabolism_Lipidmetabolism_plsC,1-acyl-sn-glycerol-3-phosphateacyltr	0,001032072	0,001024162	0,001212584
K14155_ko00270_Cysteineandmethioninemetabolism_Metabolism_Aminoacidmetabolism_patB,malY,cystathionebeta-lyase[EC:4.4.1.8];K14155_ko00450_Selenocompoundmetabolism_Metabolism_Metabolismofotheraminoacids_patB,malY,cystathionebeta-lyase	0,000949091	0,001350263	0,000797316
K12598_ko03018_RNAdegradation_GeneticInformationProcessing_Folding,sortinganddegradation_MTR4,SKIV2L2,ATP-dependentRNAhelicaseDOB1[EC:3.6.4.13]	3,6304E-05	2,54767E-05	3,32215E-05
K12599_ko03018_RNAdegradation_GeneticInformationProcessing_Folding,sortinganddegradation_SKI2,SKIV2L,antiviralhelicaseSKI2[EC:3.6.4.-]	9,85395E-05	6,62393E-05	0,000124581
K00974_ko03013_RNAtransport_GeneticinformationProcessing_Transcription_cca,tRNAnucleotidyltransferase(CCA-addingenzyme)[EC:2.7.7.723.1.3.-3.1.4.-]	0,000767571	0,000932446	0,000946812
K00335_ko00190_Oxidativephosphorylation_Metabolism_Energymetabolism_nuoF,NADH-quinoneoxidoreductasesubunitF[EC:1.6.5.3]	0,000809061	0,000621631	0,000813926
K02545_ko00312_beta-Lactamresistance_HumanDiseases_Drugresistance_mecA,penicillin-bindingprotein2prime	0,000223011	0,000173241	0,000398658
K01818_ko00051_Fructoseandmannosemetabolism_Metabolism_Carbohydratemetabolism_fucI,L-fucoseisomerase[EC:5.3.1.25]	0,000990582	0,000947732	0,000440185
K11085_ko02010_Ctransporters_Environmentalinformationprocessing_Membranetransport_msbA,ATP-bindingcassette,subfamilyB,bacterialMsbA[EC:3.6.3.-]	0,001182474	0,001024162	0,0012375
K02755_ko02010_Ctransporters_Environmentalinformationprocessing_Membranetransport_PTS-Bgl-EIIA,bglF,PTSsystem,beta-glucosides-specificIIAcomponent[EC:2.7.1.69]	0,000731267	0,000514629	0,000573071
K09691_ko02010_Ctransporters_Environmentalinformationprocessing_Membranetransport_ABC-2.LPSE.A,lipopolysaccharidetransportsystemATP-bindingprotein	0,000871297	0,00068787	0,001171057
K10439_ko02010_Ctransporters_Environmentalinformationprocessing_Membranetransport_rbsB,ribosetransportsystemsubstrate-bindingprotein;K10439_ko02030_Bacterialchemotaxis_Organismalsystem_Cellmobility_rbsB,ribosetransportsystemsubstrate-bindir	0,000793503	0,000743919	0,000838843
K00341_ko00190_Oxidativephosphorylation_Metabolism_Energymetabolism_nuoL,NADH-quinoneoxidoreductasesubunitL[EC:1.6.5.3]	0,001182474	0,000886588	0,000913591
K01584_ko00330_Arginineandprolinemetabolism_Metabolism_Aminoacidmetabolism_E4.1.1.19A,adi,argininedecarboxylase[EC:4.1.1.19]	1,03726E-05	3,0572E-05	2,49161E-05
K01887_ko00970_Aminoacyl-tRNAbiosynthesis_Geneticinformationandprocessing_Transcription_RARS,argS,arginyl-tRNAsynthetase[EC:6.1.1.19]	0,002499793	0,00266486	0,002408558
K03685_ko03008_Ribosomebiogenesisineukaryotes_GeneticinformationProcessing_Transcription_rnc,DROSHA,RNT1,ribonucleaseIII[EC:3.1.26.3];K03685_ko05205_Proteoglycansincancer_HumanDiseases_Cancers_rnc,DROSHA,RNT1,ribonucleaseIII[EC:3.1.26.3]	0,000534188	0,000703156	0,000639514
K02927_ko03010_Ribosome_GeneticinformationProcessing_Transcription_RP-L40e,RPL40,largesubunitribosomalproteinL40e	1,03726E-05	0	0,000157802
K01667_ko00380_Tryptophanmetabolism_Metabolism_Aminoacidmetabolism_tnaA,tryptophanase[EC:4.1.99.1]	0,000471953	9,68113E-05	0,000224245
K01951_ko00230_Purinemetabolism_Metabolism_Nucleotidemetabolism_guaA,GMPS,GMPsynthase(glutamine-hydrolysing)[EC:6.3.5.2];K01951_ko00983_Drugmetabolism-otherenzymes_Metabolism_Xenobioticsbiodegradationandmetabolism_guaA,GMPS,GMP	0,002603518	0,001508219	0,001810571
K00895_ko00051_Fructoseandmannosemetabolism_Metabolism_Carbohydratemetabolism_E2.7.1.90,pfk,pyrophosphate--fructose-6-phosphate1-phosphotransferase[EC:2.7.1.90]	0,000969837	0,000871302	0,000606292
K01938_ko00670_Onecarbonpoolbyfolate_Metabolism_Metabolismofcofactorsandvitamins_fhs,formate--tetrahydrofolateligase[EC:6.3.4.3];K01938_ko01200_Carbonmetabolism_Metabolism_Overview_fhs,formate--tetrahydrofolateligase[EC:6.3.4.3];K01938_ko(	0,001172102	0,001523505	0,001229195
K07192_ko04910_Insulinsignalingpathway_Organismalsystem_Endocrinsystem_FLOT,flotillin	0,000342295	0,00038215	0,000423574
K13487_ko02020_Two-componentsystem_Environmentalinformationprocessing_Signaltrasduction_wspA,methyl-acceptingchemotaxisproteinWspA	2,07452E-05	0	0
K04720_ko00830_Retinolmetabolism_Metabolism_Metabolismofcofactorsandvitamins_cobD,threonine-phosphatedecarboxylase[EC:4.1.1.81]	0,00050307	0,0007643	0,000672735
K02117_ko00190_Oxidativephosphorylation_Metabolism_Energymetabolism_ATPVA,ntpA,atpA,V/A-typeH+-transportingATPasesubunitA[EC:3.6.3.14]	0,000767571	0,000616535	0,000647819
K00122_ko00630_Glyoxylateanddicarboxylatemetabolism_Metabolism_Carbohydratemetabolism_FDH,formatedehydrogenase[EC:1.2.1.2];K00122_ko01200_Carbonmetabolism_Metabolism_Overview_FDH,formatedehydrogenase[EC:1.2.1.2];K00122_ko00194_Ph	7,77944E-05	8,66207E-05	0,00010797
K02690_ko00195_Photosynthesis_Metabolism_Energymetabolism_psaB,photosystemIP700chlorophyllaapoproteinA2	0	1,01907E-05	0
K01687_ko00290_Valine,leucineandisoleucinebiosynthesis_Metabolism_Aminoacidmetabolism_ilvD,dihydroxy-aciddehydratase[EC:4.2.1.9];K01687_ko01210_Oxocarboxylicacidmetabolism_Metabolism_Overview_ilvD,dihydroxy-aciddehydratase[EC:4.2.1.9];K016	0,001353622	0,001319691	0,001478356
K01547_ko02020_Two-componentsystem_Environmentalinformationprocessing_Signaltrasduction_kdpB,K+-transportingATPaseATPaseBchain[EC:3.6.3.12]	0,000342295	0,000249671	0,000456795
K00631_ko00561_Glycerolipidmetabolism_Metabolism_Lipidmetabolism_plsB,glycerol-3-phosphateO-acyltransferase[EC:2.3.1.15];K00631_ko00564_Glycerophospholipidmetabolism_Metabolism_Lipidmetabolism_plsB,glycerol-3-phosphateO-acyltransferase[EC:2	1,03726E-05	1,01907E-05	2,49161E-05
K01654_ko00520_Aminosugarandnucleotidesugarmetabolism_Metabolism_Carbohydratemetabolism_E2.5.1.56,neuB,N-acetylneuraminatesynthase[EC:2.5.1.56]	0,000549747	0,000606345	0,000573071
K01546_ko02020_Two-componentsystem_Environmentalinformationprocessing_Signaltrasduction_kdpA,K+-transportingATPaseATPaseAchain[EC:3.6.3.12]	0,000228197	0,000117193	0,00021594
K03814_ko01005_Lipopolysaccharidebiosynthesisproteins_Metabolism_Glycanbiosynthesisandmetabolism_mtgA,monofunctionalbiosynthenticpeptidoglycantransglycosylase[EC:2.4.1.-]	8,8167E-05	6,62393E-05	9,13591E-05
K02011_ko02010_Ctransporters_Environmentalinformationprocessing_Membranetransport_afuB,fbpB,iron(III)transportsystempermeaseprotein	0,00088167	0,000799967	0,001370386
K03147_ko00730_Thiaminemetabolism_Metabolism_Metabolismofcofactorsandvitamins_thiC,phosphomethylpyrimidinesynthase[EC:4.1.99.17]	0,000975023	0,000698061	0,000705957
K03243_ko03013_RNAtransport_GeneticinformationProcessing_Transcription_EIF5B,translationinitiationfactor5B	5,18629E-06	0	1,66107E-05
K13893_ko02010_Ctransporters_Environmentalinformationprocessing_Membranetransport_yejA,microcinCtransportsystemsubstrate-bindingprotein	2,07452E-05	5,09533E-06	1,66107E-05
K06223_ko03430_Mismatchrepair_GeneticinformationProcessing_ReplicationandRepair_dam,DNAadeninemethylase[EC:2.1.1.72]	0,001239524	0,001095497	0,001760739
K00848_ko00051_Fructoseandmannosemetabolism_Metabolism_Carbohydratemetabolism_rhaB,rhamnulokinase[EC:2.7.1.5];K00848_ko00040_Pentoseandglucuronateinterconversions_Metabolism_Carbohydratemetabolism_rhaB,rhamnulokinase[EC:2.7.1.5]	0,00032155	0,000356673	0,000465101
K02551_ko00130_Ubiquinoneandotherterpenoid-quinonebiosynthesis_Metabolism_Metabolismofcofactorsandvitamins_menD,2-succinyl-5-enolpyruvyl-6-hydroxy-3-cyclohexene-1-carboxylatesynthase[EC:2.2.1.9]	0,000228197	0,000326101	0,000622903
K00803_ko04146_Peroxisome_CellularProcesses_Transportandcatabolism_AGPS,agpS,alkyldihydroxyacetonephosphatesynthase[EC:2.5.1.26];K00803_ko00564_Glycerophospholipidmetabolism_Metabolism_Lipidmetabolism_AGPS,agpS,alkyldihydroxyacetonepho	4,14903E-05	3,0572E-05	3,32215E-05
K02974_ko03010_Ribosome_GeneticinformationProcessing_Transcription_RP-S24e,RPS24,smallsubunitribosomalproteinS24e	0	1,01907E-05	0
K01881_ko00970_Aminoacyl-tRNAbiosynthesis_Geneticinformationandprocessing_Transcription_PARS,proS,prolyl-tRNAsynthetase[EC:6.1.1.15]	0,002339018	0,002170612	0,002200924
K03639_ko04122_Sulfurrelaysystem_GeneticInformationProcessing_Folding,sortinganddegradation_MOCS1,moaA,cyclicpyranopterinphosphatesynthase[EC:4.1.99.18];K03639_ko00785_Lipoicacidmetabolism_Metabolism_Metabolismofcofactorsandvitamins_MO	0,000534188	0,000835635	0,000988339
K01207_ko00312_beta-Lactamresistance_HumanDiseases_Drugresistance_nagZ,beta-N-acetylhexosaminidase[EC:3.2.1.52];K01207_ko00520_Aminosugarandnucleotidesugarmetabolism_Metabolism_Carbohydratemetabolism_nagZ,beta-N-acetylhexosaminidase[	0,000554933	0,001100592	0,000955118
K00863_ko00561_Glycerolipidmetabolism_Metabolism_Lipidmetabolism_E2.7.1.29,DAK1,DAK2,dihydroxyacetonekinase[EC:2.7.1.29];K00863_ko01200_Carbonmetabolism_Metabolism_Overview_E2.7.1.29,DAK1,DAK2,dihydroxyacetonekinase[EC:2.7.1.29];K0086	4,66766E-05	1,5286E-05	2,49161E-05
K07652_ko02020_Two-componentsystem_Environmentalinformationprocessing_Signaltrasduction_vicK,two-componentsystem,OmpRfamily,sensorhistidinekinaseVicK[EC:2.7.13.3]	0,000529002	0,000407627	0,000481712
K03587_ko00312_beta-Lactamresistance_HumanDiseases_Drugresistance_ftsI,celldivisionproteinFtsI(penicillin-bindingprotein3);K03587_ko01005_Lipopolysaccharidebiosynthesisproteins_Metabolism_Glycanbiosynthesisandmetabolism_ftsI,celldivisionproteinFts	0,00088167	0,000794872	0,000506628
K01208_ko00500_Starchandsucrosemetabolism_Metabolism_Carbohydratemetabolism_E3.2.1.54,cyclomaltodextrinase[EC:3.2.1.54]	0,000311177	0,000270053	0,000332215
K01493_ko00240_Pyrimidinemetabolism_Metabolism_Nucleotidemetabolism_comEB,dCMPdeaminase[EC:3.5.4.12]	0,000689777	0,000810158	0,00066443
K00362_ko00910_Nitrogenmetabolism_Metabolism_Energymetabolism_nirB,nitritereductase(NADH)largesubunit[EC:1.7.1.15]	0,000129657	0,000107002	0,000157802
K01729_ko00051_Fructoseandmannosemetabolism_Metabolism_Carbohydratemetabolism_algL,poly(beta-D-mannuronate)lyase[EC:4.2.2.3]	6,22355E-05	7,643E-05	8,30537E-05
K08483_ko02010_Ctransporters_Environmentalinformationprocessing_Membranetransport_PTS-EI.PTSI,ptsI,phosphotransferasesystem,enzymeI,PtsI[EC:2.7.3.9]	0,001239524	0,001350263	0,001370386
K03857_ko00563_Glycosylphosphatidylinositol(GPI)-anchorbiosynthesis_Metabolism_Glycanbiosynthesisandmetabolism_PIGA,GPI3,phosphatidylinositolglycan,classA[EC:2.4.1.198]	6,74218E-05	5,09533E-05	0,000124581
K12495_ko04144_Endocytosis_CellularProcesses_Transportandcatabolism_IQSEC,IQmotifandSEC7domain-containingprotein	5,18629E-06	1,01907E-05	0
K03588_ko04112_Cellcycle-Caulobacter_CellularProcesses_Cellgrowthanddeath_ftsW,spoVE,celldivisionproteinFtsW	0,001130612	0,00114645	0,001494967
K10109_ko02010_Ctransporters_Environmentalinformationprocessing_Membranetransport_malF,maltose/maltodextrintransportsystempermeaseprotein	0,000150402	0,000198718	0,00021594
K02777_ko02010_Ctransporters_Environmentalinformationprocessing_Membranetransport_PTS-Glc-EIIA,crr,PTSsystem,glucose-specificIIAcomponent[EC:2.7.1.69];K02777_ko00520_Aminosugarandnucleotidesugarmetabolism_Metabolism_Carbohydratemetabol	0,000191893	0,000147765	8,30537E-05
K02778_ko02010_Ctransporters_Environmentalinformationprocessing_Membranetransport_PTS-Glc-EIIB,ptsG,PTSsystem,glucose-specificIIBcomponent[EC:2.7.1.69];K02778_ko00520_Aminosugarandnucleotidesugarmetabolism_Metabolism_Carbohydratemetab	6,74218E-05	6,62393E-05	8,30537E-05
K10909_ko02020_Two-componentsystem_Environmentalinformationprocessing_Signaltrasduction_luxQ,two-componentsystem,autoinducer2sensorkinase/phosphataseLuxQ[EC:2.7.13.33.1.3.-];K10909_ko05111_Vibriocholeraepathogeniccycle_HumanDiseases_In	1,03726E-05	2,03813E-05	0,00023255
K02584_ko02020_Two-componentsystem_Environmentalinformationprocessing_Signaltrasduction_nifA,Nif-specificregulatoryprotein	0,000274873	0,000315911	0,000249161

K07704_ko02020_Two-componentsystem_Environmentalinformationprocessing_Signaltrasduction_lytS,two-componentsystem,LytTfamily,sensorhistidinekinaseLytS[EC:2.7.13.3]	0,000274873	0,000295529	0,00032391
K02396_ko02040_Flagellarassembly_Organismalsystem_Cellmobility_flgK,flagellarhook-associatedprotein1FlgK	0,000197079	0,000122288	8,30537E-05
K01129_ko00230_Purinemetabolism_Metabolism_Nucleotidemetabolism_dgt,dGTPase[EC:3.1.5.1]	0,001026886	0,000856016	0,000980034
K03429_ko00561_Glycerolipidmetabolism_Metabolism_Lipidmetabolism_ugtP,1,2-diacylglycerol3-glucosyltransferase[EC:2.4.1.157]	0,000798689	0,001110783	0,00122089
K01428_ko05120_EpithelialcellsignalinginHelicobacterpyloriinfection_HumanDiseases_Infectiousdiseases_ureC,ureasesubunitalpha[EC:3.5.1.5];K01428_ko00791_Atrazinedegradation_Humandiseases_Xenobioticsbiodegradationandmetabolism_ureC,ureasesubuni	0,000305991	0,000422913	0,000315604
K10441_ko02010_Ctransporters_Environmentalinformationprocessing_Membranetransport_rbsA,ribosetransportsystemATP-bindingprotein[EC:3.6.3.17]	0,001182474	0,001126069	0,0012375
K01835_ko00521_Streptomycinbiosynthesis_Metabolism_Biosynthesisofothersecondarymetabolites_pgm,phosphoglucomutase[EC:5.4.2.2];K01835_ko00520_Aminosugarandnucleotidesugarmetabolism_Metabolism_Carbohydratemetabolism_pgm,phosphogluco	0,000637914	0,000642012	0,000647819
K00690_ko00500_Starchandsucrosemetabolism_Metabolism_Carbohydratemetabolism_E2.4.1.7,sucrosephosphorylase[EC:2.4.1.7]	0,000171148	0,000300625	0,000157802
K01509_ko00230_Purinemetabolism_Metabolism_Nucleotidemetabolism_ENTPD2,adenosinetriphosphatase[EC:3.6.1.3]	6,74218E-05	6,62393E-05	0,00010797
K02390_ko02040_Flagellarassembly_Organismalsystem_Cellmobility_flgE,flagellarhookproteinFlgE	0,000108912	0,000157955	0,000207634
K02342_ko03030_DNAreplication_GeneticinformationProcessing_ReplicationandRepair_DPO3E,dnaQ,DNApolymeraseIIIsubunitepsilon[EC:2.7.7.7];K02342_ko03440_Homologousrecombination_GeneticinformationProcessing_ReplicationandRepair_DPO3E,dnaQ,[	0,001052817	0,001090401	0,001362081
K14138_ko01200_Carbonmetabolism_Metabolism_Overview_acsB,acetyl-CoAsynthase[EC:2.3.1.169];K14138_ko00194_Photosynthesisproteins_Metabolism_Energymetabolism_acsB,acetyl-CoAsynthase[EC:2.3.1.169]	0,000103726	0,000295529	9,96645E-05
K01754_ko00260_Glycine,serineandthreoninemetabolism_Metabolism_Aminoacidmetabolism_E4.3.1.19,ilvA,tdcB,threoninedehydratase[EC:4.3.1.19];K01754_ko00290_Valine,leucineandisoleucinebiosynthesis_Metabolism_Aminoacidmetabolism_E4.3.1.19,ilvA,t	0,000580865	0,00084073	0,00068104
K00927_ko00010_Glycolysis/Gluconeogenesis_Metabolism_Carbohydratemetabolism_PGK,pgk,phosphoglyceratekinase[EC:2.7.2.3];K00927_ko01230_Biosynthesisofaminoacids_Metabolism_Overview_PGK,pgk,phosphoglyceratekinase[EC:2.7.2.3];K00927_ko0120	0,001991536	0,001620316	0,001586326
K12856_ko03040_Spliceosome_GeneticinformationProcessing_Transcription_PRPF8,PRP8,pre-mRNA-processingfactor8	0	5,09533E-06	0
K11927_ko03018_RNAdegradation_GeneticInformationProcessing_Folding,sortinganddegradation_rhlE,ATP-dependentRNAhelicaseRhlE[EC:3.6.4.13]	0,000383786	0,000560487	0,000199329
K07326_ko05133_Pertussis_HumanDiseases_Infectiousdiseases_fhaC,hemolysinactivation/secretionprotein	0,000145216	0,000101907	0,000174413
K01937_ko00240_Pyrimidinemetabolism_Metabolism_Nucleotidemetabolism_pyrG,CTPS,CTPsynthase[EC:6.3.4.2]	0,001789271	0,001564267	0,001619548
K03526_ko00900_Terpenoidbackbonebiosynthesis_Metabolism_Metabolismofterpenoidsandpolyketides_E1.17.7.1,gcpE,ispG,(E)-4-hydroxy-3-methylbut-2-enyl-diphosphatesynthase[EC:1.17.7.1]	0,000943905	0,001049639	0,000938507
K00973_ko00521_Streptomycinbiosynthesis_Metabolism_Biosynthesisofothersecondarymetabolites_E2.7.7.24,rfbA,rffH,glucose-1-phosphatethymidylyltransferase[EC:2.7.7.24];K00973_ko00523_Polyketidesugarunitbiosynthesis_Metabolism_Metabolismofterpen	0,001306945	0,001197403	0,001187668
K00111_ko00564_Glycerophospholipidmetabolism_Metabolism_Lipidmetabolism_glpA,glpD,glycerol-3-phosphatedehydrogenase[EC:1.1.5.3]	0,000570492	0,000529915	0,000581376
K01962_ko00630_Glyoxylateanddicarboxylatemetabolism_Metabolism_Carbohydratemetabolism_accA,acetyl-CoAcarboxylasecarboxyltransferasesubunitalpha[EC:6.4.1.2];K01962_ko00620_Pyruvatemetabolism_Metabolism_Carbohydratemetabolism_accA,acety	0,000451207	0,000371959	0,00032391
K03385_ko05132_Salmonellainfection_HumanDiseases_Infectiousdiseases_nrfA,nitritereductase(cytochromec-552)[EC:1.7.2.2];K03385_ko00910_Nitrogenmetabolism_Metabolism_Energymetabolism_nrfA,nitritereductase(cytochromec-552)[EC:1.7.2.2]	6,74218E-05	0,000112097	0,000224245
K00169_ko00020_Citratecycle(TCAcycle)_Metabolism_Carbohydratemetabolism_porA,pyruvateferredoxinoxidoreductase,alphasubunit[EC:1.2.7.1];K00169_ko00010_Glycolysis/Gluconeogenesis_Metabolism_Carbohydratemetabolism_porA,pyruvateferredoxinoxi	0,000129657	7,643E-05	0,000182718
K03927_ko00983_Drugmetabolism-otherenzymes_Metabolism_Xenobioticsbiodegradationandmetabolism_CES2,carboxylesterase2[EC:3.1.1.13,1.1.843.1.1.56]	0,000290432	0,000636917	0,000298993
K00088_ko00230_Purinemetabolism_Metabolism_Nucleotidemetabolism_guaB,IMPdehydrogenase[EC:1.1.1.205];K00088_ko00983_Drugmetabolism-otherenzymes_Metabolism_Xenobioticsbiodegradationandmetabolism_guaB,IMPdehydrogenase[EC:1.1.1.205]	0,001856692	0,001655983	0,001411913
K03076_ko02010_Ctransporters_Environmentalinformationprocessing_Membranetransport_secY,preproteintranslocasesubunitSecY;K03076_ko04120_Ubiquitinmediatedproteolysis_GeneticInformationProcessing_Folding,sortinganddegradation_secY,preproteint	0,002385694	0,001946417	0,001594631
K01744_ko00250_Alanine,aspartateandglutamatemetabolism_Metabolism_Aminoacidmetabolism_aspA,aspartateammonia-lyase[EC:4.3.1.1]	0,00046158	0,000198718	0,00023255
K01130_ko00600_Sphingolipidmetabolism_Metabolism_Lipidmetabolism_E3.1.6.1,aslA,arylsulfatase[EC:3.1.6.1];K01130_ko00140_Steroidhormonebiosynthesis_Metabolism_Lipidmetabolism_E3.1.6.1,aslA,arylsulfatase[EC:3.1.6.1]	0,000497884	0,000672584	0,000880369
K02072_ko02010_Ctransporters_Environmentalinformationprocessing_Membranetransport_metI,D-methioninetransportsystempermeaseprotein	0,000165961	0,000193623	0,000182718
K01610_ko00020_Citratecycle(TCAcycle)_Metabolism_Carbohydratemetabolism_E4.1.1.49,pckA,phosphoenolpyruvatecarboxykinase(ATP)[EC:4.1.1.49];K01610_ko00010_Glycolysis/Gluconeogenesis_Metabolism_Carbohydratemetabolism_E4.1.1.49,pckA,phospho	0,002157497	0,001661079	0,001445135
K00336_ko00190_Oxidativephosphorylation_Metabolism_Energymetabolism_nuoG,NADH-quinoneoxidoreductasesubunitG[EC:1.6.5.3]	0,000866111	0,000759205	0,000705957
K01895_ko00010_Glycolysis/Gluconeogenesis_Metabolism_Carbohydratemetabolism_ACSS,acs,acetyl-CoAsynthetase[EC:6.2.1.1];K01895_ko00630_Glyoxylateanddicarboxylatemetabolism_Metabolism_Carbohydratemetabolism_ACSS,acs,acetyl-CoAsynthetase[EC	0,000788316	0,000356673	0,000431879
K01928_ko00300_Lysinebiosynthesis_Metabolism_Aminoacidmetabolism_murE,UDP-N-acetylmuramoyl-L-alanyl-D-glutamate--2,6-diaminopimelateligase[EC:6.3.2.13];K01928_ko01005_Lipopolysaccharidebiosynthesisproteins_Metabolism_Glycanbiosynthesisanc	0,001623309	0,001737509	0,002192618
K00647_ko00061_Fattyacidbiosynthesis_Metabolism_Lipidmetabolism_fabB,3-oxoacyl-[acyl-carrier-protein]synthaseI[EC:2.3.1.41];K00647_ko01212_Fattyacidmetabolism_Metabolism_Overview_fabB,3-oxoacyl-[acyl-carrier-protein]synthaseI[EC:2.3.1.41];K00647_	0,000145216	9,1716E-05	0,000116275
K04035_ko00830_Retinolmetabolism_Metabolismofcofactorsandvitamins_E1.14.13.81,acsF,chlE,magnesium-protoporphyrinIXmonomethylester(oxidative)cyclase[EC:1.14.13.81]	0,000233383	0,000295529	0,000315604
K06131_ko00564_Glycerophospholipidmetabolism_Metabolism_Lipidmetabolism_cls,cardiolipinsynthase[EC:2.7.8.-]	0,001032072	0,001416503	0,001187668
K01750_ko00330_Arginineandprolinemetabolism_Metabolism_Aminoacidmetabolism_E4.3.1.12,ocd,ornithinecyclodeaminase[EC:4.3.1.12];K01750_ko01230_Biosynthesisofaminoacids_Metabolism_Overview_E4.3.1.12,ocd,ornithinecyclodeaminase[EC:4.3.1.12]	0,000119285	0,000157955	0,000182718
K13541_ko00830_Retinolmetabolism_Metabolismofcofactorsandvitamins_cbiGH-cobJ,cobalt-precorrin5Ahydrolase/precorrin-3BC17-methyltransferase[EC:3.7.1.122.1.1.131]	1,03726E-05	0	8,30537E-06
K00853_ko00040_Pentoseandglucuronateinterconversions_Metabolism_Carbohydratemetabolism_araB,L-ribulokinase[EC:2.7.1.16]	0,000803875	0,001064925	0,000465101
K00651_ko00270_Cysteineandmethioninemetabolism_Metabolism_Aminoacidmetabolism_metA,homoserineO-succinyltransferase[EC:2.3.1.46];K00651_ko00920_Sulfurmetabolism_Metabolism_Energymetabolism_metA,homoserineO-succinyltransferase[EC:2.3.	0,000482325	0,000560487	0,000548155
K01676_ko00020_Citratecycle(TCAcycle)_Metabolism_Carbohydratemetabolism_E4.2.1.2A,fumA,fumB,fumaratehydratase,classI[EC:4.2.1.2];K01676_ko00620_Pyruvatemetabolism_Metabolism_Carbohydratemetabolism_E4.2.1.2A,fumA,fumB,fumaratehydratase,	0,001379554	0,000963018	0,000855453
K01201_ko04142_Lysosome_CellularProcesses_Transportandcatabolism_GBA,srfJ,glucosylceramidase[EC:3.2.1.45];K01201_ko00511_Otherglycandegradation_Metabolism_Glycanbiosynthesisandmetabolism_GBA,srfJ,glucosylceramidase[EC:3.2.1.45];K01201_ko0(	0,000451207	0,000407627	0,00032391
K04077_ko03018_RNAdegradation_GeneticInformationProcessing_Folding,sortinganddegradation_groEL,HSPD1,chaperoninGroEL;K04077_ko04940_Typeldiabetesmellitus_Humandiseases_EndocrineandmetabolicdiseasesgroEL,HSPD1,chaperoninGroEL;K04077_	0,002691685	0,002282709	0,001976679
K01858_ko00521_Streptomycinbiosynthesis_Metabolism_Biosynthesisofothersecondarymetabolites_E5.5.1.4,INO1,myo-inositol-1-phosphatesynthase[EC:5.5.1.4];K01858_ko00630_Glyoxylateanddicarboxylatemetabolism_Metabolism_Carbohydratemetabolism_E	0,001078749	0,000647107	0,000639514
K05685_ko02010_Ctransporters_Environmentalinformationprocessing_Membranetransport_macB,macrolidetransportsystemATP-binding/permeaseprotein[EC:3.6.3.-]	7,77944E-05	5,60487E-05	8,30537E-05
K13963_ko05146_Amoebiasis_HumanDiseases_Infectiousdiseases_SERPINB,serpinB	0,000269687	0,000254767	0,000390352
K03738_ko00030_Pentosephosphatepathway_Metabolism_Carbohydratemetabolism_aor,aldehyde:ferredoxinoxidoreductase[EC:1.2.7.5];K03738_ko01200_Carbonmetabolism_Metabolism_Overview_aor,aldehyde:ferredoxinoxidoreductase[EC:1.2.7.5]	8,8167E-05	4,5858E-05	0,000157802
K00876_ko00240_Pyrimidinemetabolism_Metabolism_Nucleotidemetabolism_udk,UCK,uridinekinase[EC:2.7.1.48];K00876_ko00983_Drugmetabolism-otherenzymes_Metabolism_Xenobioticsbiodegradationandmetabolism_udk,UCK,uridinekinase[EC:2.7.1.48]	0,001462534	0,00175789	0,001179363
K01424_ko00250_Alanine,aspartateandglutamatemetabolism_Metabolism_Aminoacidmetabolism_E3.5.1.1,ansA,ansB,L-asparaginase[EC:3.5.1.1];K01424_ko00460_Cyanoaminoacidmetabolism_Metabolism_Metabolismofotheraminoacids_E3.5.1.1,ansA,ansB,L-as	0,000933532	0,000794872	0,000813926
K09758_ko00250_Alanine,aspartateandglutamatemetabolism_Metabolism_Aminoacidmetabolism_asdA,aspartate4-decarboxylase[EC:4.1.1.12];K09758_ko00270_Cysteineandmethioninemetabolism_Metabolism_Aminoacidmetabolism_asdA,aspartate4-decarbox	0,000165961	3,56673E-05	0,000116275
K00854_ko00040_Pentoseandglucuronateinterconversions_Metabolism_Carbohydratemetabolism_xylB,XYLB,xylulokinase[EC:2.7.1.17]	0,00114617	0,001182117	0,001079698
K01929_ko00300_Lysinebiosynthesis_Metabolism_Aminoacidmetabolism_murF,UDP-N-acetylmuramoyl-tripeptide--D-alanyl-D-alanineligase[EC:6.3.2.10];K01929_ko01005_Lipopolysaccharidebiosynthesisproteins_Metabolism_Glycanbiosynthesisandmetabolism_	0,001058003	0,001365549	0,001162752
K00040_ko00040_Pentoseandglucuronateinterconversions_Metabolism_Carbohydratemetabolism_uxuB,fructuronatereductase[EC:1.1.1.57]	0,000238569	0,000208909	0,00023255
K01571_ko00620_Pyruvatemetabolism_Metabolism_Carbohydratemetabolism_oadA,oxaloacetatedecarboxylase,alphasubunit[EC:4.1.1.3]	0,000575678	0,000861111	0,000506628
K00248_ko00280_Valine,leucineandisoleucinedegradation_Metabolism_Aminoacidmetabolism_ACADS,bcd,butyryl-CoAdehydrogenase[EC:1.3.8.1];K00248_ko00630_Glyoxylateanddicarboxylatemetabolism_Metabolism_Carbohydratemetabolism_ACADS,bcd,buty	0,00074164	0,000682775	0,000415269
K03980_ko01005_Lipopolysaccharidebiosynthesisproteins_Metabolism_Glycanbiosynthesisandmetabolism_murJ,mviN, ,putativepeptidoglycanlipidIIflippase	0,00028006	0,000366864	0,00044849
K10039_ko02010_Ctransporters_Environmentalinformationprocessing_Membranetransport_ABC.GLN1.S,putativeglutaminetransportsystemsubstrate-bindingprotein	6,74218E-05	7,13347E-05	0,000174413
K01966_ko00280_Valine,leucineandisoleucinedegradation_Metabolism_Aminoacidmetabolism_PCCB,pccB,propionyl-CoAcarboxylasebetachain[EC:6.4.1.3];K01966_ko00630_Glyoxylateanddicarboxylatemetabolism_Metabolism_Carbohydratemetabolism_PCCB,pc	0,001628496	0,001416503	0,00132886
K02112_ko00190_Oxidativephosphorylation_Metabolism_Energymetabolism_ATPF1B,atpD,F-typeH+-transportingATPasesubunitbeta[EC:3.6.3.14];K02112_ko00195_Photosynthesis_Metabolism_Energymetabolism_ATPF1B,atpD,F-typeH+-transportingATPasesubu	0,002479047	0,001839415	0,001470051
K02790_ko02010_Ctransporters_Environmentalinformationprocessing_Membranetransport_PTS-Mal-EIIB,malX,PTSsystem,maltoseandglucose-specificIIBcomponent[EC:2.7.1.69];K02790_ko00010_Glycolysis/Gluconeogenesis_Metabolism_Carbohydratemetabolis	0,000124471	0,000163051	0,000124581
K01880_ko00970_Aminoacyl-tRNAbiosynthesis_Geneticinformationandprocessing_Transcription_GARS,glyS1,glycyl-tRNAsynthetase[EC:6.1.1.14]	0,002354576	0,001966799	0,001968373
K01011_ko04122_Sulfurrelaysystem_GeneticInformationProcessing_Folding,sortinganddegradation_TST,MPST,sseA,thiosulfate/3-mercaptopyruvatesulfurtransferase[EC:2.8.1.12.8.1.2];K01011_ko00270_Cysteineandmethioninemetabolism_Metabolism_Aminoaci	6,74218E-05	9,68113E-05	9,13591E-05
K01666_ko00360_Phenylalaninemetabolism_Metabolism_Aminoacidmetabolism_mhpE,4-hydroxy2-oxovaleratealdolase[EC:4.1.3.39];K01666_ko01220_Degradationofaromaticcompounds_Metabolism_Overview_mhpE,4-hydroxy2-oxovaleratealdolase[EC:4.1.3.39	0,000238569	0,000285339	0,000431879
K01134_ko04142_Lysosome_CellularProcesses_Transportandcatabolism_ARSA,arylsulfataseA[EC:3.1.6.8];K01134_ko00600_Sphingolipidmetabolism_Metabolism_Lipidmetabolism_ARSA,arylsulfataseA[EC:3.1.6.8]	0,000497884	0,000642012	0,000589681
K01745_ko00340_Histidinemetabolism_Metabolism_Aminoacidmetabolism_hutH,HAL,histidineammonia-lyase[EC:4.3.1.3]	0,000471953	0,000295529	0,000498322
K01251_ko00270_Cysteineandmethioninemetabolism_Metabolism_Aminoacidmetabolism_E3.3.1.1,ahcY,adenosylhomocysteinase[EC:3.3.1.1]	0,000513443	0,00030572	0,000348826
K05898_ko00984_Steroiddegradation_Metabolism_Xenobioticsbiodegradationandmetabolism_kstD,3-oxosteroid1-dehydrogenase[EC:1.3.99.4]	5,18629E-06	5,09533E-06	4,98322E-05
K02313_ko04112_Cellcycle-Caulobacter_CellularProcesses_Cellgrowthanddeath_dnaA,chromosomalreplicationinitiatorprotein;K02313_ko02020_Two-componentsystem_Environmentalinformationprocessing_Signaltrasduction_dnaA,chromosomalreplicationinitia	0,001296573	0,001518409	0,001486662
K01582_ko00310_Lysinedegradation_Metabolism_Aminoacidmetabolism_E4.1.1.18,ldcC,cadA,lysinedecarboxylase[EC:4.1.1.18];K01582_ko00960_Tropane,piperidineandpyridinealkaloidbiosynthesis_Metabolism_Biosynthesisofothersecondarymetabolites_E4.1.1.	0,000534188	0,001136259	0,001403608

K10847_ko03420_Nucleotideexcisionrepair_GeneticinformationProcessing_ReplicationandRepair_XPA,DNA-repairproteincomplementingXP-Acells	2,07452E-05	1,5286E-05	8,30537E-06
K03688_ko00130_Ubiquinoneandotherterpenoid-quinonebiosynthesis_Metabolism_Metabolismofcofactorsandvitamins_ubiB,aarF,ubiquinonebiosynthesisprotein	0,00014003	0,000366864	0,000382047
K01910_ko02020_Two-componentsystem_Environmentalinformationprocessing_Signaltrasduction_citC,[citrate(pro-3S)-lyase]ligase[EC:6.2.1.22]	6,74218E-05	0,000101907	0,000182718
K01615_ko00630_Glyoxylateanddicarboxylatemetabolism_Metabolism_Carbohydratemetabolism_E4.1.1.70,glutaconyl-CoAdecarboxylase[EC:4.1.1.70];K01615_ko00362_Benzoatedegradation_Metabolism_Xenobioticsbiodegradationandmetabolism_E4.1.1.70,glu	0,00014003	0,000163051	0,000149497
K00681_ko00460_Cyanoaminoacidmetabolism_Metabolism_Metabolismofotheraminoacids_ggt,gamma-glutamyltranspeptidase/glutathionehydrolase[EC:2.3.2.23.4.19.13];K00681_ko00480_Glutathionemetabolism_Metabolism_Metabolismofotheraminoacids_g	0,000119285	0,000147765	0,000182718
K06027_ko04721_Synapticvesiclecycle_Environmentalinformationprocessing_Signaltransduction_NSF,vesicle-fusingATPase[EC:3.6.4.6];K06027_ko04962_Vasopressin-regulatedwaterreabsorption_OrganismalSystems_Excretorysystem_NSF,vesicle-fusingATPase[EC	0,000726081	0,000300625	0,000838843
K13889_ko02010_Ctransporters_Environmentalinformationprocessing_Membranetransport_gsiB,glutathionetransportsystemsubstrate-bindingprotein	3,11177E-05	2,54767E-05	0
K00278_ko00250_Alanine,aspartateandglutamatemetabolism_Metabolism_Aminoacidmetabolism_nadB,L-aspartateoxidase[EC:1.4.3.16];K00278_ko00760_Nicotinateandnicotinamidemetabolism_Metabolism_Metabolismofcofactorsandvitamins_nadB,L-aspartate	0,002204174	0,001895464	0,001860403
K01893_ko00970_Aminoacyl-tRNAbiosynthesis_Geneticinformationandprocessing_Transcription_NARS,asnS,asparaginyl-tRNAsynthetase[EC:6.1.1.22]	0,002001909	0,001869987	0,001096309
K03150_ko00730_Thiaminemetabolism_Metabolism_Metabolismofcofactorsandvitamins_thiH,2-iminoacetatesynthase[EC:4.1.99.19]	0,001960418	0,001441979	0,001594631
K10542_ko02010_Ctransporters_Environmentalinformationprocessing_Membranetransport_mglA,methyl-galactosidetransportsystemATP-bindingprotein[EC:3.6.3.17]	0,000342295	0,000326101	0,000274077
K11444_ko02020_Two-componentsystem_Environmentalinformationprocessing_Signaltrasduction_wspR,two-componentsystem,chemotaxisfamily,responseregulatorWspR[EC:2.7.7.65]	3,11177E-05	2,03813E-05	9,13591E-05
K02471_ko02010_Ctransporters_Environmentalinformationprocessing_Membranetransport_yddA,putativeATP-bindingcassettetransporter	8,29807E-05	4,5858E-05	2,49161E-05
K00356_ko00190_Oxidativephosphorylation_Metabolism_Energymetabolism_E1.6.99.3,NADHdehydrogenase[EC:1.6.99.3]	0,000145216	0,000137574	0,00010797
K00873_ko05230_Centralcarbonmetabolismincancer_HumanDiseases_Cancers_PK,pyk,pyruvatekinase[EC:2.7.1.40];K00873_ko04930_TypeIIdiabetesmellitus_Humandiseases_Endocrineandmetabolicdiseases_PK,pyk,pyruvatekinase[EC:2.7.1.40];K00873_ko05203_	0,001327691	0,001177022	0,001254111
K01091_ko00630_Glyoxylateanddicarboxylatemetabolism_Metabolism_Carbohydratemetabolism_E3.1.3.18,gph,phosphoglycolatephosphatase[EC:3.1.3.18]	0,000990582	0,001080211	0,001494967
K01867_ko00970_Aminoacyl-tRNAbiosynthesis_Geneticinformationandprocessing_Transcription_WARS,trpS,tryptophanyl-tRNAsynthetase[EC:6.1.1.2]	0,001405485	0,001472551	0,001212584
K00680_ko00350_Tyrosinemetabolism_Metabolism_Aminoacidmetabolism_E2.3.1.-,[EC:2.3.1.-];K00680_ko00903_Limoneneandpinenedegradation_Metabolism_Metabolismofterpenoidsandpolyketides_E2.3.1.-,[EC:2.3.1.-];K00680_ko00627_Aminobenzoatedegra	0,006861464	0,006797175	0,007292117
K11072_ko02010_Ctransporters_Environmentalinformationprocessing_Membranetransport_potA,spermidine/putrescinetransportsystemATP-bindingprotein[EC:3.6.3.31]	0,001109866	0,000952827	0,000747483
K01735_ko00400_Phenylalanine,tyrosineandtryptophanbiosynthesis_Metabolism_Aminoacidmetabolism_aroB,3-dehydroquinatesynthase[EC:4.2.3.4];K01735_ko01230_Biosynthesisofaminoacids_Metabolism_Overview_aroB,3-dehydroquinatesynthase[EC:4.2.3.4	0,001021699	0,001029257	0,001295638
K01834_ko05230_Centralcarbonmetabolismincancer_HumanDiseases_Cancers_PGAM,gpmA,2,3-bisphosphoglycerate-dependentphosphoglyceratemutase[EC:5.4.2.11];K01834_ko00260_Glycine,serineandthreoninemetabolism_Metabolism_Aminoacidmetabolism	0,003184383	0,002985866	0,002998239
K02409_ko02040_Flagellarassembly_Organismalsystem_Cellmobility_fliF,flagellarM-ringproteinFliF	0,000114098	0,000122288	8,30537E-05
K12340_ko02010_Ctransporters_Environmentalinformationprocessing_Membranetransport_tolC,outermembranechannelprotein;K12340_ko00312_beta-Lactamresistance_HumanDiseases_Drugresistance_tolC,outermembranechannelprotein;K12340_ko05133_P	0,000580865	0,000973209	0,001054782
K03544_ko04112_Cellcycle-Caulobacter_CellularProcesses_Cellgrowthanddeath_clpX,CLPX,ATP-dependentClpproteaseATP-bindingsubunitClpX	0,002427184	0,002221565	0,002084648
K07309_ko00450_Selenocompoundmetabolism_Metabolism_Metabolismofotheraminoacids_ynfE,Tat-targetedselenatereductasesubunitYnfE[EC:1.97.1.9]	1,55589E-05	1,5286E-05	1,66107E-05
K00602_ko00670_Onecarbonpoolbyfolate_Metabolism_Metabolismofcofactorsandvitamins_purH,phosphoribosylaminoimidazolecarboxamideformyltransferase/IMPcyclohydrolase[EC:2.1.2.33.5.4.10];K00602_ko00230_Purinemetabolism_Metabolism_Nucleotide	0,001446975	0,001391026	0,001204279
K02536_ko00540_Lipopolysaccharidebiosynthesis_Metabolism_Glycanbiosynthesisandmetabolism_lpxD,UDP-3-O-[3-hydroxymyristoyl]glucosamineN-acyltransferase[EC:2.3.1.191]	0,000523815	0,000402531	0,000597987
K02844_ko00540_Lipopolysaccharidebiosynthesis_Metabolism_Glycanbiosynthesisandmetabolism_waaG,rfaG,UDP-glucose:(heptosyl)LPSalpha-1,3-glucosyltransferase[EC:2.4.1.-]	0,000233383	0,000275148	0,000440185
K01438_ko00330_Arginineandprolinemetabolism_Metabolism_Aminoacidmetabolism_argE,acetylornithinedeacetylase[EC:3.5.1.16];K01438_ko01210_Oxocarboxylicacidmetabolism_Metabolism_Overview_argE,acetylornithinedeacetylase[EC:3.5.1.16];K01438_ko	0,00032155	0,000300625	0,000207634
K00257_ko00281_Geranioldegradation_Metabolism_Metabolismofterpenoidsandpolyketides_E1.3.99.-,[EC:1.3.99.-]	0,0012862	0,000942637	0,000880369
K10012_ko00520_Aminosugarandnucleotidesugarmetabolism_Metabolism_Carbohydratemetabolism_arnC,pmrF,undecaprenyl-phosphate4-deoxy-4-formamido-L-arabinosetransferase[EC:2.4.2.53]	9,85395E-05	5,60487E-05	9,13591E-05
K01854_ko00052_Galactosemetabolism_Metabolism_Carbohydratemetabolism_glf,UDP-galactopyranosemutase[EC:5.4.99.9]	0,001758153	0,000998685	0,001644464
K01583_ko00330_Arginineandprolinemetabolism_Metabolism_Aminoacidmetabolism_E4.1.1.19,argininedecarboxylase[EC:4.1.1.19]	0,000134844	4,07627E-05	0,000124581
K13497_ko00400_Phenylalanine,tyrosineandtryptophanbiosynthesis_Metabolism_Aminoacidmetabolism_trpGD,anthranilatesynthase/phosphoribosyltransferase[EC:4.1.3.272.4.2.18];K13497_ko01230_Biosynthesisofaminoacids_Metabolism_Overview_trpGD,antl	9,85395E-05	4,07627E-05	0
K00214_ko00830_Retinolmetabolism_Metabolism_Metabolismofcofactorsandvitamins_BLVRA,bvdR,biliverdinreductase[EC:1.3.1.24]	4,14903E-05	8,66207E-05	1,66107E-05
K01815_ko00040_Pentoseandglucuronateinterconversions_Metabolism_Carbohydratemetabolism_kduI,4-deoxy-L-threo-5-hexosulose-uronateketol-isomerase[EC:5.3.1.17]	0,000274873	0,000224195	0,000174413
K02063_ko02010_Ctransporters_Environmentalinformationprocessing_Membranetransport_thiP,thiaminetransportsystempermeaseprotein	3,6304E-05	2,54767E-05	2,49161E-05
K10200_ko02010_Ctransporters_Environmentalinformationprocessing_Membranetransport_ABC.NGC.S,N-acetylglucosaminetransportsystemsubstrate-bindingprotein	0,000617169	0,000636917	0,001445135
K01924_ko01005_Lipopolysaccharidebiosynthesisproteins_Metabolism_Glycanbiosynthesisandmetabolism_murC,UDP-N-acetylmuramate--alanineligase[EC:6.3.2.8];K01924_ko00471_D-GlutamineandD-glutamatemetabolism_Metabolism_Metabolismofotheramir	0,001275828	0,001294215	0,001254111
K01913_ko00960_Tropane,piperidineandpyridinealkaloidbiosynthesis_Metabolism_Biosynthesisofothersecondarymetabolites_E6.2.1.-,[EC:6.2.1.-];K01913_ko00903_Limoneneandpinenedegradation_Metabolism_Metabolismofterpenoidsandpolyketides_E6.2.1.-,[	5,18629E-05	2,03813E-05	5,81376E-05
K00325_ko00760_Nicotinateandnicotinamidemetabolism_Metabolism_Metabolismofcofactorsandvitamins_pntB,NAD(P)transhydrogenasesubunitbeta[EC:1.6.1.2]	0,000129657	5,09533E-06	6,6443E-05
K13834_ko05144_Malaria_HumanDiseases_Infectiousdiseases_SPECT2,sporozoitemicronemeprotein2	1,03726E-05	0	0
K01657_ko00400_Phenylalanine,tyrosineandtryptophanbiosynthesis_Metabolism_Aminoacidmetabolism_trpE,anthranilatesynthasecomponentI[EC:4.1.3.27];K01657_ko01230_Biosynthesisofaminoacids_Metabolism_Overview_trpE,anthranilatesynthasecomponer	0,00032155	0,000463675	0,000390352
K07775_ko02020_Two-componentsystem_Environmentalinformationprocessing_Signaltrasduction_resD,two-componentsystem,OmpRfamily,responseregulatorResD	0,001472907	0,001115878	0,001362081
K00425_ko02020_Two-componentsystem_Environmentalinformationprocessing_Signaltrasduction_cydA,cytochromedubiquinoloxidasesubunitI[EC:1.10.3.-];K00425_ko00190_Oxidativephosphorylation_Metabolism_Energymetabolism_cydA,cytochromedubiquino	0,000809061	0,000662393	0,00055646
K08264_ko01200_Carbonmetabolism_Metabolism_Overview_hdrD,heterodisulfidereductasesubunitD[EC:1.8.98.1];K08264_ko00194_Photosynthesisproteins_Metabolism_Energymetabolism_hdrD,heterodisulfidereductasesubunitD[EC:1.8.98.1]	0,000165961	1,5286E-05	0,00010797
K00765_ko00340_Histidinemetabolism_Metabolism_Aminoacidmetabolism_hisG,ATPphosphoribosyltransferase[EC:2.4.2.17];K00765_ko01230_Biosynthesisofaminoacids_Metabolism_Overview_hisG,ATPphosphoribosyltransferase[EC:2.4.2.17]	0,000451207	0,000417817	0,00034052
K13533_ko02020_Two-componentsystem_Environmentalinformationprocessing_Signaltrasduction_kinE,two-componentsystem,sporulationsensorkinaseE[EC:2.7.13.3]	0	5,09533E-06	2,49161E-05
K02495_ko00830_Retinolmetabolism_Metabolism_Metabolismofcofactorsandvitamins_hemN,hemZ,oxygen-independentcoproporphyrinogenIIoxidase[EC:1.3.99.22]	0,001519583	0,001498028	0,001644464
K00789_ko00270_Cysteineandmethioninemetabolism_Metabolism_Aminoacidmetabolism_metK,S-adenosylmethioninesynthetase[EC:2.5.1.6];K00789_ko01230_Biosynthesisofaminoacids_Metabolism_Overview_metK,S-adenosylmethioninesynthetase[EC:2.5.1.6]	0,001773712	0,001701841	0,001602937
K00342_ko00190_Oxidativephosphorylation_Metabolism_Energymetabolism_nuoM,NADH-quinoneoxidoreductasesubunitM[EC:1.6.5.3]	0,001115053	0,000978304	0,000622903
K07715_ko02020_Two-componentsystem_Environmentalinformationprocessing_Signaltrasduction_glrR,qseF,two-componentsystem,NtrCfamily,responseregulatorGlrR	0,000124471	0,000142669	9,13591E-05
K01752_ko00270_Cysteineandmethioninemetabolism_Metabolism_Aminoacidmetabolism_E4.3.1.17,sdaA,L-serinedehydratase[EC:4.3.1.17];K01752_ko00260_Glycine,serineandthreoninemetabolism_Metabolism_Aminoacidmetabolism_E4.3.1.17,sdaA,L-serinede	0,000907601	0,000856016	0,000830537
K02803_ko02010_Ctransporters_Environmentalinformationprocessing_Membranetransport_PTS-Nag-EIIB,nagE,PTSsystem,N-acetylglucosamine-specificIIBcomponent[EC:2.7.1.69];K02803_ko00520_Aminosugarandnucleotidesugarmetabolism_Metabolism_Carbo	0,000165961	0,000112097	0,000116275
K01733_ko00260_Glycine,serineandthreoninemetabolism_Metabolism_Aminoacidmetabolism_thrC,threoninesynthase[EC:4.2.3.1];K01733_ko00750_VitaminB6metabolism_Metabolism_Metabolismofcofactorsandvitamins_thrC,threoninesynthase[EC:4.2.3.1];K01	0,000954278	0,000978304	0,000830537
K01226_ko00500_Starchandsucrosemetabolism_Metabolism_Carbohydratemetabolism_treC,trehalose-6-phosphatehydrolase[EC:3.2.1.93]	0,000207452	0,000168146	0,000157802
K01685_ko00040_Pentoseandglucuronateinterconversions_Metabolism_Carbohydratemetabolism_uxaA,altronatehydrolase[EC:4.2.1.7]	0,000331923	0,000387245	0,000440185
K09815_ko02010_Ctransporters_Environmentalinformationprocessing_Membranetransport_znuA,zinctransportsystemsubstrate-bindingprotein	0,000554933	0,000662393	0,000780705
K01042_ko00970_Aminoacyl-tRNAbiosynthesis_Geneticinformationandprocessing_Transcription_selA,L-seryl-tRNA(Ser)seleniumtransferase[EC:2.9.1.1];K01042_ko00450_Selenocompoundmetabolism_Metabolism_Metabolismofotheraminoacids_selA,L-seryl-tRN	9,85395E-05	0,000193623	0,000257467
K01354_ko05143_Africantrypanosomiasis_HumanDiseases_Infectiousdiseases_ptrB,oligopeptidaseB[EC:3.4.21.83];K01354_ko05142_Chagasdisease(Americantrypanosomiasis)_HumanDiseases_Infectiousdiseases_ptrB,oligopeptidaseB[EC:3.4.21.83]	3,11177E-05	5,09533E-06	4,15269E-05
K03106_ko02010_Ctransporters_Environmentalinformationprocessing_Membranetransport_SRP54,ffh,signalrecognitionparticlesubunitSRP54;K03106_ko04120_Ubiquitinmediatedproteolysis_GeneticInformationProcessing_Folding,sortinganddegradation_SRP54,I	0,002033026	0,00191075	0,001727517
K09011_ko00290_Valine,leucineandisoleucinebiosynthesis_Metabolism_Aminoacidmetabolism_cimA,D-citramalatesynthase[EC:2.3.1.182];K09011_ko01210_Oxocarboxylicacidmetabolism_Metabolism_Overview_cimA,D-citramalatesynthase[EC:2.3.1.182];K09011	0,000171148	0,000239481	0,000207634
K00694_ko00500_Starchandsucrosemetabolism_Metabolism_Carbohydratemetabolism_bcsA,cellulosesynthase(UDP-forming)[EC:2.4.1.12]	7,77944E-05	0,000137574	0,000116275
K01804_ko00040_Pentoseandglucuronateinterconversions_Metabolism_Carbohydratemetabolism_araA,L-arabinoseisomerase[EC:5.3.1.4]	0,001099494	0,000805063	0,000830537
K00372_ko00910_Nitrogenmetabolism_Metabolism_Energymetabolism_nasA,assimilatorynitratereductasecatalyticsubunit[EC:1.7.99.4]	3,6304E-05	0,000112097	0,00010797
K00366_ko00910_Nitrogenmetabolism_Metabolism_Energymetabolism_nirA,ferredoxin-nitritereductase[EC:1.7.7.1]	7,77944E-05	0,000321006	0,000207634
K07642_ko02020_Two-componentsystem_Environmentalinformationprocessing_Signaltrasduction_baeS,smeS,two-componentsystem,OmpRfamily,sensorhistidinekinaseBaeS[EC:2.7.13.3]	0,000223011	0,000132479	0,000141191
K00245_ko02020_Two-componentsystem_Environmentalinformationprocessing_Signaltrasduction_frdB,fumaratereductaseiron-sulfursubunit[EC:1.3.5.4];K00245_ko00020_Citratecycle(TCAcycle)_Metabolism_Carbohydratemetabolism_frdB,fumaratereductaseiro	7,26081E-05	0,000173241	0,000157802
K01026_ko00630_Glyoxylateanddicarboxylatemetabolism_Metabolism_Carbohydratemetabolism_pct,propionateCoA-transferase[EC:2.8.3.1];K01026_ko00620_Pyruvatemetabolism_Metabolism_Carbohydratemetabolism_pct,propionateCoA-transferase[EC:2.8.3.	0,000254128	0,000157955	0,000191024
K00104_ko00630_Glyoxylateanddicarboxylatemetabolism_Metabolism_Carbohydratemetabolism_glcD,glycolateoxidase[EC:1.1.3.15]	0,000394158	0,000270053	0,000531544

K02434_ko00970_Aminoacyl-tRNAbiosynthesis_Geneticinformationandprocessing_Transcription_gatB,PET112,aspartyl-tRNA(Asn)/glutamyl-tRNA(Gln)amidotransferasesubunitB[EC:6.3.5.66.3.5.7]	0,000912787	0,000509533	0,00055646
K00566_ko04122_Sulfurrelaysystem_GeneticInformationProcessing_Folding,sortinganddegradation_mnmA,trmU,TRMU,tRNA-specific2-thiouridylase[EC:2.8.1.-]	0,001441789	0,001401217	0,000988339
K01113_ko02020_Two-componentsystem_Environmentalinformationprocessing_Signaltrasduction_phoD,alkalinephosphataseD[EC:3.1.3.1];K01113_ko00785_Lipoicacidmetabolism_Metabolism_Metabolismofcofactorsandvitamins_phoD,alkalinephosphataseD[EC	0,000342295	0,000377055	0,000440185
K00041_ko00040_Pentoseandglucuronateinterconversions_Metabolism_Carbohydratemetabolism_uxaB,tagaturonatereductase[EC:1.1.1.58]	0,000223011	0,000519724	0,000373742
K02232_ko00830_Retinolmetabolism_Metabolism_Metabolismofcofactorsandvitamins_E6.3.5.10,cobQ,cbiP,adenosylcobyricacidsynthase[EC:6.3.5.10]	0,000435648	0,000438199	0,000431879
K01079_ko00260_Glycine,serineandthreoninemetabolism_Metabolism_Aminoacidmetabolism_serB,PSPH,phosphoserinephosphatase[EC:3.1.3.3];K01079_ko01230_Biosynthesisofaminoacids_Metabolism_Overview_serB,PSPH,phosphoserinephosphatase[EC:3.1.3	0,000726081	0,000759205	0,000431879
K00763_ko00760_Nicotinateandnicotinamidemetabolism_Metabolism_Metabolismofcofactorsandvitamins_pncB,NAPRT1,nicotinatephosphoribosyltransferase[EC:6.3.4.21]	0,00124471	0,001360454	0,000996645
K01041_ko00281_Geranioldegradation_Metabolism_Metabolismofterpenoidsandpolyketides_E2.8.3.-,[EC:2.8.3.-];K01041_ko00626_Naphthalenedegradation_Metabolism_Xenobioticsbiodegradationandmetabolism_E2.8.3.-,[EC:2.8.3.-]	0,000705336	0,000754109	0,000465101
K10548_ko02010_Ctransporters_Environmentalinformationprocessing_Membranetransport_ABC.GGU.A,gguA,putativemultiplesugartransportsystemATP-bindingprotein	0,000160775	0,000107002	8,30537E-05
K13378_ko00190_Oxidativephosphorylation_Metabolism_Energymetabolism_nuoCD,NADH-quinoneoxidoreductasesubunitC/D[EC:1.6.5.3]	0,000529002	0,000652203	0,000373742
K03092_ko02020_Two-componentsystem_Environmentalinformationprocessing_Signaltrasduction_SIG54,rpoN,RNApolymerasesigma-54factor;K03092_ko05111_Vibriocholeraepathogeniccycle_HumanDiseases_Infectiousdiseases_SIG54,rpoN,RNApolymerasesigm	0,000492698	0,000743919	0,000481712
K01255_ko00480_Glutathionemetabolism_Metabolism_Metabolismofotheraminoacids_CARP,pepA,leucylaminopeptidase[EC:3.4.11.1]	0,000108912	0,000173241	0,000157802
K00831_ko00260_Glycine,serineandthreoninemetabolism_Metabolism_Aminoacidmetabolism_serC,PSAT1,phosphoserineaminotransferase[EC:2.6.1.52];K00831_ko00750_VitaminB6metabolism_Metabolism_Metabolismofcofactorsandvitamins_serC,PSAT1,phosp	0,001115053	0,000856016	0,000888675
K01223_ko00010_Glycolysis/Gluconeogenesis_Metabolism_Carbohydratemetabolism_E3.2.1.86B,bglA,6-phospho-beta-glucosidase[EC:3.2.1.86]	0,001198033	0,000963018	0,001129531
K03420_ko03050_Proteasome_GeneticInformationProcessing_Folding,sortinganddegradation_psmR,proteasomeregulatorysubunit	4,14903E-05	6,62393E-05	5,81376E-05
K00812_ko00250_Alanine,aspartateandglutamatemetabolism_Metabolism_Aminoacidmetabolism_aspB,aspartateaminotransferase[EC:2.6.1.1];K00812_ko00330_Arginineandprolinemetabolism_Metabolism_Aminoacidmetabolism_aspB,aspartateaminotransfera	0,000954278	0,001080211	0,001013255
K10558_ko02010_Ctransporters_Environmentalinformationprocessing_Membranetransport_IsrA,ego,AI-2transportsystemATP-bindingprotein	2,59315E-05	1,01907E-05	2,49161E-05
K01120_ko00230_Purinemetabolism_Metabolism_Nucleotidemetabolism_cpdP,3',5'-cyclic-nucleotidephosphodiesterase[EC:3.1.4.17]	2,07452E-05	4,07627E-05	3,32215E-05
K01883_ko00970_Aminoacyl-tRNAbiosynthesis_Geneticinformationandprocessing_Transcription_CARS,cysS,cysteinyl-tRNAsynthetase[EC:6.1.1.16]	0,002230105	0,001819034	0,001511578
K01520_ko00240_Pyrimidinemetabolism_Metabolism_Nucleotidemetabolism_dut,DUT,dUTPpyrophosphatase[EC:3.6.1.23]	0,000777944	0,000723537	0,00078901
K00970_ko03018_RNAdegradation_GeneticInformationProcessing_Folding,sortinganddegradation_pcnB,poly(A)polymerase[EC:2.7.7.19]	0,000622355	0,000672584	0,000631208
K00965_ko00520_Aminosugarandnucleotidesugarmetabolism_Metabolism_Carbohydratemetabolism_galT,GALT,UDPglucose--hexose-1-phosphateuridylyltransferase[EC:2.7.7.12];K00965_ko00052_Galactosemetabolism_Metabolism_Carbohydratemetabolism_ga	0,000658659	0,000805063	0,000606292
K00130_ko00260_Glycine,serineandthreoninemetabolism_Metabolism_Aminoacidmetabolism_betB,gbsA,betaine-aldehydedehydrogenase[EC:1.2.1.8]	1,03726E-05	1,5286E-05	6,6443E-05
K10005_ko02010_Ctransporters_Environmentalinformationprocessing_Membranetransport_gluB,glutamatetransportsystemsubstrate-bindingprotein	2,07452E-05	0	0
K14534_ko00630_Glyoxylateanddicarboxylatemetabolism_Metabolism_Carbohydratemetabolism_abfD,4-hydroxybutyryl-CoAdehydratase/vinylacetyl-CoA-Delta-isomerase[EC:4.2.1.1205.3.3.3];K14534_ko01200_Carbonmetabolism_Metabolism_Overview_abfD,4	0,000119285	0,000117193	8,30537E-05
K07793_ko02020_Two-componentsystem_Environmentalinformationprocessing_Signaltrasduction_tctA,putativetricarboxylictransportmembraneprotein	0,00042009	0,000336292	0,000265772
K14978_ko02020_Two-componentsystem_Environmentalinformationprocessing_Signaltrasduction_ssrA,two-componentsystem,LuxRfamily,secretionsystemsensorhistidinekinaseSsrA	1,55589E-05	0	8,30537E-06
K08770_ko04920_Adipocytokinesignalingpathway_Organismalsystem_Endocrinsystem_UBC,ubiquitinC	1,55589E-05	0	5,81376E-05
K01699_ko00630_Glyoxylateanddicarboxylatemetabolism_Metabolism_Carbohydratemetabolism_pduC,propanedioldehydrataselargesubunit[EC:4.2.1.28]	1,03726E-05	1,01907E-05	1,66107E-05
K02389_ko02040_Flagellarassembly_Organismalsystem_Cellmobility_flgD,flagellarbasal-bodyrodmodificationproteinFlgD	0,000103726	6,1144E-05	7,47483E-05
K00033_ko00030_Pentosephosphatepathway_Metabolism_Carbohydratemetabolism_PGD,gnd,6-phosphogluconatedehydrogenase[EC:1.1.1.44];K00033_ko00480_Glutathionemetabolism_Metabolism_Metabolismofotheraminoacids_PGD,gnd,6-phosphogluconat	0,000347482	0,000234385	0,000265772
K03465_ko00670_Onecarbonpoolbyfolate_Metabolism_Metabolismofcofactorsandvitamins_E2.1.1.148,thyX,thy1,thymidylatesynthase(FAD)[EC:2.1.1.148];K03465_ko00240_Pyrimidinemetabolism_Metabolism_Nucleotidemetabolism_E2.1.1.148,thyX,thy1,thymic	0,000311177	0,000377055	0,00066443
K01647_ko00020_Citratecycle(TCAcycle)_Metabolism_Carbohydratemetabolism_CS,gltA,citratesynthase[EC:2.3.3.1];K01647_ko00630_Glyoxylateanddicarboxylatemetabolism_Metabolism_Carbohydratemetabolism_CS,gltA,citratesynthase[EC:2.3.3.1];K01647_ko(	0,000378599	0,000565582	0,000614598
K01270_ko00480_Glutathionemetabolism_Metabolism_Metabolismofotheraminoacids_pepD,dipeptidaseD[EC:3.4.13.-]	0,001322504	0,00145217	0,001312249
K01756_ko00250_Alanine,aspartateandglutamatemetabolism_Metabolism_Aminoacidmetabolism_purB,ADSL,adenylosuccinatelyase[EC:4.3.2.2];K01756_ko00230_Purinemetabolism_Metabolism_Nucleotidemetabolism_purB,ADSL,adenylosuccinatelyase[EC:4.3.2	0,001685545	0,001355359	0,001735823
K07259_ko01005_Lipopolysaccharidebiosynthesisproteins_Metabolism_Glycanbiosynthesisandmetabolism_dacB,D-alanyl-D-alaninecarboxypeptidase/D-alanyl-D-alanine-endopeptidase(penicillin-bindingprotein4)[EC:3.4.16.43.4.21.-]	0,000305991	0,000280243	0,000298993
K00648_ko00061_Fattyacidbiosynthesis_Metabolism_Lipidmetabolism_fabH,3-oxoacyl-[acyl-carrier-protein]synthaseIII[EC:2.3.1.180];K00648_ko01212_Fattyacidmetabolism_Metabolism_Overview_fabH,3-oxoacyl-[acyl-carrier-protein]synthaseIII[EC:2.3.1.180]	0,001255083	0,001273833	0,001088004
K01812_ko00040_Pentoseandglucuronateinterconversions_Metabolism_Carbohydratemetabolism_uxaC,glucuronateisomerase[EC:5.3.1.12]	0,000814248	0,001049639	0,000622903
K03404_ko00830_Retinolmetabolism_Metabolism_Metabolismofcofactorsandvitamins_chlD,bchD,magnesiumchelatasesubunitD[EC:6.6.1.1]	4,14903E-05	3,0572E-05	5,81376E-05
K01220_ko00052_Galactosemetabolism_Metabolism_Carbohydratemetabolism_E3.2.1.85,lacG,6-phospho-beta-galactosidase[EC:3.2.1.85]	8,8167E-05	7,643E-05	4,15269E-05
K01465_ko00240_Pyrimidinemetabolism_Metabolism_Nucleotidemetabolism_URA4,pyrC,dihydroorotase[EC:3.5.2.3]	0,000985395	0,000774491	0,000863759
K00329_ko00190_Oxidativephosphorylation_Metabolism_Energymetabolism_E1.6.5.3,NADHdehydrogenase[EC:1.6.5.3]	0,000150402	5,60487E-05	9,13591E-05
K07716_ko04112_Cellcycle-Caulobacter_CellularProcesses_Cellgrowthanddeath_pleC,two-componentsystem,cellcyclesensorhistidinekinasePleC[EC:2.7.13.3];K07716_ko02020_Two-componentsystem_Environmentalinformationprocessing_Signaltrasduction_pleC,	2,07452E-05	5,09533E-05	2,49161E-05
K00560_ko00670_Onecarbonpoolbyfolate_Metabolism_Metabolismofcofactorsandvitamins_thyA,TYMS,thymidylatesynthase[EC:2.1.1.45];K00560_ko00240_Pyrimidinemetabolism_Metabolism_Nucleotidemetabolism_thyA,TYMS,thymidylatesynthase[EC:2.1.1.45]	0,001441789	0,001110783	0,001295638
K03388_ko01200_Carbonmetabolism_Metabolism_Overview_hdrA,heterodisulfidereductasesubunitA[EC:1.8.98.1];K03388_ko00194_Photosynthesisproteins_Metabolism_Energymetabolism_hdrA,heterodisulfidereductasesubunitA[EC:1.8.98.1]	0,000259315	0,000214004	0,000182718
K00980_ko00564_Glycerophospholipidmetabolism_Metabolism_Lipidmetabolism_tagD,glycerol-3-phosphatecytidylyltransferase[EC:2.7.7.39]	0,000155589	0,000203813	0,000224245
K02397_ko02040_Flagellarassembly_Organismalsystem_Cellmobility_flgL,flagellarhook-associatedprotein3FlgL	5,18629E-05	7,643E-05	6,6443E-05
K07091_ko02010_Ctransporters_Environmentalinformationprocessing_Membranetransport_lptF,lipopolysaccharideexportsystempermeaseprotein	0,00028006	0,000137574	0,000207634
K09835_ko00906_Carotenoidbiosynthesis_Metabolism_Metabolismofterpenoidsandpolyketides_crtISO,crtH,prolycopeneisomerase[EC:5.2.1.13]	0,000103726	5,09533E-05	4,98322E-05
K00012_ko00520_Aminosugarandnucleotidesugarmetabolism_Metabolism_Carbohydratemetabolism_UGDH,ugd,UDPglucose6-dehydrogenase[EC:1.1.1.22];K00012_ko00052_Galactosemetabolism_Metabolism_Carbohydratemetabolism_UGDH,ugd,UDPglucose6	0,002121193	0,001564267	0,001893625
K00941_ko00730_Thiaminemetabolism_Metabolism_Metabolismofcofactorsandvitamins_thiD,hydroxymethylpyrimidine/phosphomethylpyrimidinekinase[EC:2.7.1.492.7.4.7]	0,00032155	0,000336292	0,00032391
K03573_ko03430_Mismatchrepair_GeneticinformationProcessing_ReplicationandRepair_mutH,DNAmismatchrepairproteinMutH	0,000243756	0,000295529	0,00023255
K00983_ko00520_Aminosugarandnucleotidesugarmetabolism_Metabolism_Carbohydratemetabolism_E2.7.7.43,neuA,CMAS,N-acylneuraminatecytidylyltransferase[EC:2.7.7.43]	0,001789271	0,005849443	0,006627687
K00768_ko00830_Retinolmetabolism_Metabolism_Metabolismofcofactorsandvitamins_E2.4.2.21,cobU,cobT,nicotinate-nucleotide--dimethylbenzimidazolephosphoribosyltransferase[EC:2.4.2.21]	0,000409717	0,000529915	0,000614598
K04345_ko04540_Gapjunction_Cellgrowthanddeath_Cellularcommunity_PKA,proteinkinaseA[EC:2.7.11.11];K04345_ko04210_Apoptosis_Cellularprocesses_Cellgrowthanddeath_PKA,proteinkinaseA[EC:2.7.11.11];K04345_ko04113_Meiosis-yeast_CellularProcesses_	2,59315E-05	5,09533E-06	1,66107E-05
K01755_ko00250_Alanine,aspartateandglutamatemetabolism_Metabolism_Aminoacidmetabolism_argH,ASL,argininosuccinatelyase[EC:4.3.2.1];K01755_ko00330_Arginineandprolinemetabolism_Metabolism_Aminoacidmetabolism_argH,ASL,argininosuccinatelyas	0,001312132	0,000723537	0,000980034
K00568_ko00130_Ubiquinoneandotherterpenoid-quinonebiosynthesis_Metabolism_Metabolismofcofactorsandvitamins_ubiG,2-polyprenyl-6-hydroxyphenylmethylase/3-demethylubiquinone-93-methyltransferase[EC:2.1.1.2222.1.1.64]	0,000108912	0,000163051	0,000298993
K00262_ko00250_Alanine,aspartateandglutamatemetabolism_Metabolism_Aminoacidmetabolism_E1.4.1.4,gdhA,glutamatedehydrogenase(NADP+)[EC:1.4.1.4];K00262_ko00330_Arginineandprolinemetabolism_Metabolism_Aminoacidmetabolism_E1.4.1.4,gdhA,	0,002432371	0,00198718	0,001893625
K03100_ko04120_Ubiquitinmediatedproteolysis_GeneticInformationProcessing_Folding,sortinganddegradation_lepB,signalpeptidaseI[EC:3.4.21.89]	0,001389926	0,001416503	0,001461745
K02433_ko00970_Aminoacyl-tRNAbiosynthesis_Geneticinformationandprocessing_Transcription_gatA,QRSL1,aspartyl-tRNA(Asn)/glutamyl-tRNA(Gln)amidotransferasesubunitA[EC:6.3.5.66.3.5.7]	0,000497884	0,000448389	0,000498322
K00604_ko00970_Aminoacyl-tRNAbiosynthesis_Geneticinformationandprocessing_Transcription_MTFMT,fmt,methionyl-tRNAformyltransferase[EC:2.1.2.9];K00604_ko00670_Onecarbonpoolbyfolate_Metabolism_Metabolismofcofactorsandvitamins_MTFMT,fmt,r	0,001052817	0,000912065	0,000855453
K07651_ko02020_Two-componentsystem_Environmentalinformationprocessing_Signaltrasduction_resE,two-componentsystem,OmpRfamily,sensorhistidinekinaseResE[EC:2.7.13.3]	0,000134844	0,000157955	0,000124581
K03272_ko00540_Lipopolysaccharidebiosynthesis_Metabolism_Glycanbiosynthesisandmetabolism_gmhC,hldE,waaE,rfaE,D-beta-D-heptose7-phosphatekinase/D-beta-D-heptose1-phosphateadenosyltransferase[EC:2.7.1.1672.7.7.70]	0,000129657	0,000127383	0,000182718
K01112_ko00051_Fructoseandmannosemetabolism_Metabolism_Carbohydratemetabolism_E3.1.3.-,[EC:3.1.3.-]	0,000285246	0,000254767	0,000332215
K01580_ko04940_TypeIdiabetesmellitus_Humandiseases_Endocrineandmetabolicdiseases_E4.1.1.15,gadB,gadA,GAD,glutamatedecarboxylase[EC:4.1.1.15];K01580_ko00250_Alanine,aspartateandglutamatemetabolism_Metabolism_Aminoacidmetabolism_E4.1.1.1	0,000274873	0,000168146	0,000348826
K00283_ko00260_Glycine,serineandthreoninemetabolism_Metabolism_Aminoacidmetabolism_gcvPB,glycinedehydrogenasesubunit2[EC:1.4.4.2];K00283_ko01200_Carbonmetabolism_Metabolism_Overview_gcvPB,glycinedehydrogenasesubunit2[EC:1.4.4.2]	0,000653473	0,000275148	0,00034052
K01925_ko01005_Lipopolysaccharidebiosynthesisproteins_Metabolism_Glycanbiosynthesisandmetabolism_murD,UDP-N-acetylmuramoylalanine--D-glutamateligase[EC:6.3.2.9];K01925_ko00471_D-GlutamineandD-glutamatemetabolism_Metabolism_Metabolism	0,001462534	0,001513314	0,00156141
K00010_ko00521_Streptomycinbiosynthesis_Metabolism_Biosynthesisofthersecondarymetabolites_iolG,myo-inositol2-dehydrogenase/D-chiro-inositol1-dehydrogenase[EC:1.1.1.181.1.1.369];K00010_ko00630_Glyoxylateanddicarboxylatemetabolism_Metabolism	0,000606796	0,000422913	0,0007724
K02799_ko02010_Ctransporters_Environmentalinformationprocessing_Membranetransport_PTS-Mtl-EIIB,mtlA,PTSsystem,mannitol-specificIIBcomponent[EC:2.7.1.69];K02799_ko00051_Fructoseandmannosemetabolism_Metabolism_Carbohydratemetabolism_PT	8,8167E-05	4,07627E-05	3,32215E-05
K00058_ko00260_Glycine,serineandthreoninemetabolism_Metabolism_Aminoacidmetabolism_serA,PHGDH,D-3-phosphoglyceratedehydrogenase[EC:1.1.1.95];K00058_ko01230_Biosynthesisofaminoacids_Metabolism_Overview_serA,PHGDH,D-3-phosphoglycerat	0,001867065	0,001712032	0,001619548

K00077_ko00770_PantothenateandCoABiosynthesis_Metabolism_Metabolismofcofactorsandvitamins_panE,apbA,2-dehydropantoate2-reductase[EC:1.1.1.169]	0,00050307	0,000371959	0,000431879
K00302_ko00260_Glycine,serineandthreonineMetabolism_Metabolism_Aminoacidmetabolism_soxA,sarcosineoxidase,subunitalpha[EC:1.5.3.1]	0,000482325	0,000499343	0,000257467
K10541_ko02010_Ctransporters_Environmentalinformationprocessing_Membranetransport_mglC,methyl-galactosidetransportsystempermeaseprotein	0,000248942	0,000214004	0,000174413
K07248_ko00630_Glyoxylateanddicarboxylatemetabolism_Metabolism_Carbohydratemetabolism_aldA,lactaldehydedehydrogenase/glycolaldehydedehydrogenase[EC:1.2.1.221.2.1.21];K07248_ko00620_Pyruvatemetabolism_Metabolism_Carbohydratemetabolisr	1,55589E-05	2,03813E-05	0
K02817_ko02010_Ctransporters_Environmentalinformationprocessing_Membranetransport_PTS-Tre-EIIA,treP,PTSsystem,trehalose-specificIIAcomponent[EC:2.7.1.69];K02817_ko00500_Starchandsucrosemetabolism_Metabolism_Carbohydratemetabolism_PTS-Tr	7,77944E-05	1,01907E-05	4,15269E-05
K00343_ko00190_Oxidativephosphorylation_Metabolism_Energymetabolism_nuoN,NADH-quinoneoxidoreductasesubunitN[EC:1.6.5.3]	0,000570492	0,00053501	0,000373742
K10011_ko00520_Aminosugarandnucleotidesugarmetabolism_Metabolism_Carbohydratemetabolism_arnA,pmrI,UDP-4-amino-4-deoxy-L-arabinoseformyltransferase/UDP-glucuronicaciddehydrogenase(UDP-4-keto-hexauronicaciddecarboxylating)[EC:2.1.2.131.1.	3,11177E-05	1,5286E-05	8,30537E-06
K07654_ko02020_Two-componentsystem_Environmentalinformationprocessing_Signaltrasduction_mtrB,two-componentsystem,OmpRfamily,sensorhistidinekinaseMtrB[EC:2.7.13.3]	1,03726E-05	2,03813E-05	0
K01085_ko00010_Glycolysis/Gluconeogenesis_Metabolism_Carbohydratemetabolism_agp,glucose-1-phosphatase[EC:3.1.3.10]	0,000150402	6,62393E-05	3,32215E-05
K12392_ko04142_Lysosome_CellularProcesses_Transportandcatabolism_AP1B1,AP-1complexsubunitbeta-1	1,03726E-05	0	1,66107E-05
K00135_ko00250_Alanine,aspartateandglutamatemetabolism_Metabolism_Aminoacidmetabolism_gabD,succinate-semialdehydedehydrogenase/glutarate-semialdehydedehydrogenase[EC:1.2.1.161.2.1.791.2.1.20];K00135_ko00310_Lysinedegradation_Metabolis	7,26081E-05	4,07627E-05	6,6443E-05
K03400_ko02020_Two-componentsystem_Environmentalinformationprocessing_Signaltrasduction_luxC,long-chain-fatty-acyl-CoAreductase[EC:1.2.1.50]	2,07452E-05	2,03813E-05	0
K10108_ko02010_Ctransporters_Environmentalinformationprocessing_Membranetransport_malE,maltose/maltodextrintransportsystemsubstrate-bindingprotein;K10108_ko02030_Bacterialchemotaxis_Organismalsystem_Cellmobility_malE,maltose/maltodextrin	0,000342295	0,000142669	0,000207634
K02234_ko00830_RetinolMetabolism_Metabolism_Metabolismofcofactorsandvitamins_cobW,cobalaminbiosynthesisproteinCobW	0,000544561	0,000463675	0,000548155
K00322_ko00760_Nicotinateandnicotinamidemetabolism_Metabolism_Metabolismofcofactorsandvitamins_sthA,udhA,NAD(P)transhydrogenase[EC:1.6.1.1]	5,18629E-06	5,09533E-06	0
K05934_ko00830_RetinolMetabolism_Metabolism_Metabolismofcofactorsandvitamins_E2.1.1.131,cobJ,cbiH,precorrin-3BC17-methyltransferase[EC:2.1.1.131]	0,000223011	0,000315911	0,000166107
K00014_ko00400_Phenylalanine,tyrosineandtryptophanbiosynthesis_Metabolism_Aminoacidmetabolism_aroE,shikimatedehydrogenase[EC:1.1.1.25];K00014_ko01230_Biosynthesisofaminoacids_Metabolism_Overview_aroE,shikimatedehydrogenase[EC:1.1.1.25]	0,000560119	0,000448389	0,000656124
K01586_ko00300_Lysinebiosynthesis_Metabolism_Aminoacidmetabolism_lysA,diaminopimelatedecarboxylase[EC:4.1.1.20];K01586_ko01230_Biosynthesisofaminoacids_Metabolism_Overview_lysA,diaminopimelatedecarboxylase[EC:4.1.1.20]	0,000907601	0,000820349	0,000813926
K01067_ko00620_Pyruvatemetabolism_Metabolism_Carbohydratemetabolism_E3.1.2.1,ACH1,acetyl-CoAhydrolase[EC:3.1.2.1]	0,000337109	0,000193623	0,000274077
K01577_ko00630_Glyoxylateanddicarboxylatemetabolism_Metabolism_Carbohydratemetabolism_oxc,oxalyl-CoAdecarboxylase[EC:4.1.1.8]	0,000197079	5,60487E-05	0,000224245
K01137_ko04142_Lysosome_CellularProcesses_Transportandcatabolism_GNS,N-acetylglucosamine-6-sulfatase[EC:3.1.6.14];K01137_ko00531_Glycosaminoglycandegradation_Metabolism_Glycanbiosynthesisandmetabolism_GNS,N-acetylglucosamine-6-sulfatase[I	0,000124471	9,68113E-05	0,000157802
K01939_ko00250_Alanine,aspartateandglutamatemetabolism_Metabolism_Aminoacidmetabolism_purA,ADSS,adenylosuccinatesynthase[EC:6.3.4.4];K01939_ko00230_Purinemetabolism_Metabolism_Nucleotidemetabolism_purA,ADSS,adenylosuccinatesynthase[	0,001208406	0,001085306	0,000714262
K02527_ko00540_Lipopolysaccharidebiosynthesis_Metabolism_Glycanbiosynthesisandmetabolism_kdtA,waaA,3-deoxy-D-manno-octulosonic-acidtransferase[EC:2.4.99.122.4.99.132.4.99.142.4.99.15]	0,000409717	0,00038215	0,000307299
K01028_ko00280_Valine,leucineandisoleucinedegradation_Metabolism_Aminoacidmetabolism_E2.8.3.5A,scoA,3-oxoacidCoA-transferasesubunitA[EC:2.8.3.5];K01028_ko00630_Glyoxylateanddicarboxylatemetabolism_Metabolism_Carbohydratemetabolism_E2.8.	0,000300805	0,000264957	0,000440185
K00790_ko00520_Aminosugarandnucleotidesugarmetabolism_Metabolism_Carbohydratemetabolism_murA,UDP-N-acetylglucosamine1-carboxyvinyltransferase[EC:2.5.1.7];K00790_ko01005_Lipopolysaccharidebiosynthesisproteins_Metabolism_Glycanbiosynthes	0,001462534	0,001492933	0,001353776
K01136_ko04142_Lysosome_CellularProcesses_Transportandcatabolism_IDS,iduronate2-sulfatase[EC:3.1.6.13];K01136_ko00531_Glycosaminoglycandegradation_Metabolism_Glycanbiosynthesisandmetabolism_IDS,iduronate2-sulfatase[EC:3.1.6.13]	0,000197079	0,000101907	0,000149497
K01961_ko00630_Glyoxylateanddicarboxylatemetabolism_Metabolism_Carbohydratemetabolism_accC,acetyl-CoAcarboxylase,biotincarboxylasesubunit[EC:6.4.1.26.3.4.14];K01961_ko00620_Pyruvatemetabolism_Metabolism_Carbohydratemetabolism_accC,acety	0,000736453	0,000708251	0,000872064
K00067_ko00521_Streptomycinbiosynthesis_Metabolism_Biosynthesisofothersecondarymetabolites_rfbD,rmlD,dTDP-4-dehydrorhamnosereductase[EC:1.1.1.133];K00067_ko00523_Polyketidesugarunitbiosynthesis_Metabolism_Metabolismofterpenoidsandpolyke	0,000793503	0,000963018	0,000980034
K02412_ko02040_Flagellarassembly_Organismalsystem_Cellmobility_fliI,flagellum-specificATPsynthase[EC:3.6.3.14]	0,000243756	0,000219099	0,000132886
K13038_ko00770_PantothenateandCoABiosynthesis_Metabolism_Metabolismofcofactorsandvitamins_coaBC,dfp,phosphopantothenoylcysteinedecarboxylase/phosphopantothenate--cysteineligase[EC:4.1.1.366.3.2.5]	0,000767571	0,000856016	0,00055646
K03283_ko04144_Endocytosis_CellularProcesses_Transportandcatabolism_HSPA1_8,heatshock70kDaprotein1/8;K03283_ko02020_Two-componentsystem_Environmentalinformationprocessing_Signaltrasduction_HSPA1_8,heatshock70kDaprotein1/8;K03283_ko0	3,6304E-05	1,5286E-05	8,30537E-06
K11749_ko04112_Cellcycle-Caulobacter_CellularProcesses_Cellgrowthanddeath_rseP,regulatorofsigmaEprotease[EC:3.4.24.-]	0,001109866	0,000927351	0,001137836
K00975_ko00520_Aminosugarandnucleotidesugarmetabolism_Metabolism_Carbohydratemetabolism_glgC,glucose-1-phosphateadenylyltransferase[EC:2.7.7.27];K00975_ko00500_Starchandsucrosemetabolism_Metabolism_Carbohydratemetabolism_glgC,glucose	0,002105634	0,00221647	0,001835487
K02749_ko02010_Ctransporters_Environmentalinformationprocessing_Membranetransport_PTS-Arb-EIIB,glvB,PTSsystem,arbutin-likeIIBcomponent[EC:2.7.1.69];K02749_ko00010_Glycolysis/Gluconeogenesis_Metabolism_Carbohydratemetabolism_PTS-Arb-EIIB,g	4,66766E-05	0	4,15269E-05
K00928_ko00270_Cysteineandmethionninemetabolism_Metabolism_Aminoacidmetabolism_lysC,aspartatekinase[EC:2.7.2.4];K00928_ko00260_Glycine,serineandthreonineMetabolism_Metabolism_Aminoacidmetabolism_lysC,aspartatekinase[EC:2.7.2.4];K00928_k	0,001317318	0,001177022	0,00122089
K01679_ko05200_PathwaysincancerHumanDiseases_Cancers_E4.2.1.2B,fumC,fumaratehydratase,classII[EC:4.2.1.2];K01679_ko05211_RenalcellcarcinomaHumanDiseases_Cancers_E4.2.1.2B,fumC,fumaratehydratase,classII[EC:4.2.1.2];K01679_ko00020_Citratec	0,000160775	0,000168146	0,000157802
K03735_ko00564_Glycerophospholipidmetabolism_Metabolism_Lipidmetabolism_eutB,ethanolamineammonia-lyaselargesubunit[EC:4.3.1.7]	6,74218E-05	2,03813E-05	1,66107E-05
K08641_ko02020_Two-componentsystem_Environmentalinformationprocessing_Signaltrasduction_vanX,D-alanyl-D-alaninedipeptidase[EC:3.4.13.22]	0,000124471	9,1716E-05	0,000149497
K01232_ko00500_Starchandsucrosemetabolism_Metabolism_Carbohydratemetabolism_E3.2.1.122,glvA,maltose-6'-phosphateglucosidase[EC:3.2.1.122]	0,000248942	0,000107002	8,30537E-05
K01466_ko00230_Purinemetabolism_Metabolism_Nucleotidemetabolism_allB,allantoinase[EC:3.5.2.5]	6,22355E-05	4,07627E-05	2,49161E-05
K05845_ko02010_Ctransporters_Environmentalinformationprocessing_Membranetransport_opuC,osmoprotectanttransportsystemsubstrate-bindingprotein	0,000197079	0,000112097	0,00023255
K03601_ko03430_Mismatchrepair_GeneticinformationProcessing_ReplicationandRepair_xseA,exodeoxyribonucleaseVIIlargesubunit[EC:3.1.11.6]	0,00092316	0,001008876	0,000988339
K03431_ko00520_Aminosugarandnucleotidesugarmetabolism_Metabolism_Carbohydratemetabolism_glmM,phosphoglucosaminemutase[EC:5.4.2.10]	0,000912787	0,000861111	0,000656124
K13922_ko00630_Glyoxylateanddicarboxylatemetabolism_Metabolism_Carbohydratemetabolism_pduP,propionaldehydedehydrogenase[EC:1.2.1.87]	0,000160775	6,1144E-05	2,49161E-05
K00131_ko00010_Glycolysis/Gluconeogenesis_Metabolism_Carbohydratemetabolism_gapN,glyceraldehyde-3-phosphatedehydrogenase(NADP+)[EC:1.2.1.9];K00131_ko00030_Pentosephosphatepathway_Metabolism_Carbohydratemetabolism_gapN,glyceraldehy	5,18629E-06	3,56673E-05	0
K00382_ko00260_Glycine,serineandthreonineMetabolism_Metabolism_Aminoacidmetabolism_DLD,lpd,pdhD,dihydrolipoamidedehydrogenase[EC:1.8.1.4];K00382_ko00280_Valine,leucineandisoleucinedegradation_Metabolism_Aminoacidmetabolism_DLD,lpd,pd	0,000497884	0,000580868	0,000440185
K00052_ko00290_Valine,leucineandisoleucinebiosynthesis_Metabolism_Aminoacidmetabolism_leuB,3-isopropylmalatedehydrogenase[EC:1.1.1.85];K00052_ko00630_Glyoxylateanddicarboxylatemetabolism_Metabolism_Carbohydratemetabolism_leuB,3-isopropy	0,000679404	0,000733728	0,000506628
K01451_ko00360_Phenylalaninemetabolism_Metabolism_Aminoacidmetabolism_hipO,hippuratehydrolase[EC:3.5.1.32]	0,000186706	0,000259862	0,000240856
K11754_ko00785_Lipoicacidmetabolism_Metabolism_Metabolismofcofactorsandvitamins_folC,dihydrofolatesynthase/folylpolyglutamatesynthase[EC:6.3.2.126.3.2.17]	0,001000954	0,001156641	0,001104614
K00128_ko00330_Arginineandprolinemetabolism_Metabolism_Aminoacidmetabolism_E1.2.1.3,aldehydedehydrogenase(NAD+)[EC:1.2.1.3];K00128_ko00340_Histidinemetabolism_Metabolism_Aminoacidmetabolism_E1.2.1.3,aldehydedehydrogenase(NAD+)[EC:1	0,000404531	0,000356673	0,000348826
K01581_ko00330_Arginineandprolinemetabolism_Metabolism_Aminoacidmetabolism_E4.1.1.17,ODC1,speC,speF,ornithinedecarboxylase[EC:4.1.1.17];K01581_ko00480_Glutathionemetabolism_Metabolism_Metabolismofotheraminoacids_E4.1.1.17,ODC1,speC,sp	0,000129657	0,000112097	0,000257467
K01945_ko00230_Purinemetabolism_Metabolism_Nucleotidemetabolism_purD,phosphoribosylamine--glycineligase[EC:6.3.4.13]	0,001140984	0,00114645	0,000996645
K02118_ko00190_Oxidativephosphorylation_Metabolism_Energymetabolism_ATPVB,ntpB,atpB,V/A-typeH+-transportingATPasesubunitB	0,000425276	0,000443294	0,000390352
K10793_ko00330_Arginineandprolinemetabolism_Metabolism_Aminoacidmetabolism_prdA,D-prolinereductase(dithiol)PrdA[EC:1.21.4.1]	6,22355E-05	8,15253E-05	3,32215E-05
K00140_ko00280_Valine,leucineandisoleucinedegradation_Metabolism_Aminoacidmetabolism_mmsA,iolA,ALDH6A1,malonate-semialdehydedehydrogenase(acetylating)/methylmalonate-semialdehydedehydrogenase[EC:1.2.1.181.2.1.27];K00140_ko00630_Glyox	3,6304E-05	4,07627E-05	0,00010797
K12452_ko00520_Aminosugarandnucleotidesugarmetabolism_Metabolism_Carbohydratemetabolism_rfbH,CDP-6-deoxy-D-xylo-4-hexulose-3-dehydrase	0,000337109	0,000208909	0,00021594
K00958_ko00920_Sulfurmetabolism_Metabolism_Energymetabolism_sat,met3,sulfateadenylyltransferase[EC:2.7.7.4];K00958_ko00450_Selenocompoundmetabolism_Metabolism_Metabolismofotheraminoacids_sat,met3,sulfateadenylyltransferase[EC:2.7.7.4];K0	1,03726E-05	0	1,66107E-05
K10545_ko02010_Ctransporters_Environmentalinformationprocessing_Membranetransport_xylG,D-xylosetransportsystemATP-bindingprotein[EC:3.6.3.17]	7,77944E-05	3,56673E-05	3,32215E-05
K05350_ko00940_Phenylpropanoidbiosynthesis_Metabolism_Biosynthesisofothersecondarymetabolites_bglB,beta-glucosidase[EC:3.2.1.21];K05350_ko00500_Starchandsucrosemetabolism_Metabolism_Carbohydratemetabolism_bglB,beta-glucosidase[EC:3.2.1.21	0,000342295	0,000392341	0,000290688
K06001_ko00260_Glycine,serineandthreonineMetabolism_Metabolism_Aminoacidmetabolism_trpB,tryptophansynthasebetachain[EC:4.2.1.20];K06001_ko00400_Phenylalanine,tyrosineandtryptophanbiosynthesis_Metabolism_Aminoacidmetabolism_trpB,tryptop	0,000627541	0,000601249	0,000581376
K01686_ko00040_Pentoseandglucuronateinterconversions_Metabolism_Carbohydratemetabolism_uxuA,mannonatedehydratase[EC:4.2.1.8]	0,000575678	0,000718442	0,000390352
K02775_ko02010_Ctransporters_Environmentalinformationprocessing_Membranetransport_PTS-Gat-EIIC,gatC,PTSsystem,galactitol-specificIICcomponent;K02775_ko00052_Galactosemetabolism_Metabolism_Carbohydratemetabolism_PTS-Gat-EIIC,gatC,PTSsyste	0,000326736	0,000315911	0,000298993
K02172_ko00312_beta-Lactamresistance_HumanDiseases_Drugresistance_blaR1,blaregulatorproteinblaR1	0,00014003	6,1144E-05	0,000124581
K10540_ko02010_Ctransporters_Environmentalinformationprocessing_Membranetransport_mglB,methyl-galactosidetransportsystemsubstrate-bindingprotein;K10540_ko02030_Bacterialchemotaxis_Organismalsystem_Cellmobility_mglB,methyl-galactosidetrans	0,000456394	0,00030572	0,000124581
K13381_ko00520_Aminosugarandnucleotidesugarmetabolism_Metabolism_Carbohydratemetabolism_chiA,bifunctionalchitinase/lysozyme[EC:3.2.1.143.2.1.17]	0	5,09533E-06	0
K04113_ko01220_Degradationofaromaticcompounds_Metabolism_Overview_bcrB,badE,benzoyl-CoAreductasesubunitB[EC:1.3.7.8];K04113_ko00362_Benzoatedegradation_Metabolism_Xenobioticsbiodegradationandmetabolism_bcrB,badE,benzoyl-CoAreductas	0,000150402	9,68113E-05	0,000157802
K00925_ko00630_Glyoxylateanddicarboxylatemetabolism_Metabolism_Carbohydratemetabolism_ackA,acetatekinase[EC:2.7.2.1];K00925_ko00620_Pyruvatemetabolism_Metabolism_Carbohydratemetabolism_ackA,acetatekinase[EC:2.7.2.1];K00925_ko00430_Ta	0,001628496	0,001273833	0,001320554
K02372_ko00061_Fattyacidbiosynthesis_Metabolism_Lipidmetabolism_fabZ,3-hydroxyacyl-[acyl-carrier-protein]dehydratase[EC:4.2.1.59];K02372_ko01212_Fattyacidmetabolism_Metabolism_Overview_fabZ,3-hydroxyacyl-[acyl-carrier-protein]dehydratase[EC:4.2	0,000508257	0,000779586	0,000697651
K05825_ko00300_Lysinebiosynthesis_Metabolism_Aminoacidmetabolism_LYSN,2-aminoadipatetransaminase[EC:2.6.1.-];K05825_ko01210_Oxocarboxylicacidmetabolism_Metabolism_Overview_LYSN,2-aminoadipatetransaminase[EC:2.6.1.-];K05825_ko01230_Bio	0,000197079	7,13347E-05	0,000157802
K00627_ko00020_Citratecycle(TCAcycle)_Metabolism_Carbohydratemetabolism_DLAT,aceF,pdhC,pyruvatedehydrogenaseE2component(dihydrolipoamideacetyltransferase)[EC:2.3.1.12];K00627_ko00010_Glycolysis/Gluconeogenesis_Metabolism_Carbohydratem	0,000129657	6,1144E-05	0,000166107

K00394_ko00920_Sulfurmetabolism_Metabolism_Energymetabolism_aprA,adenylylsulfatereductase,subunitA[EC:1.8.99.2]	0,000160775	1,01907E-05	0,00010797
K01572_ko00620_Pyruvatemetabolism_Metabolism_Carbohydratemetabolism_oadB,oxaloacetatedecarboxylase,betasubunit[EC:4.1.1.3]	0,001353622	0,001391026	0,001104614
K10192_ko02010_Ctransporters_Environmentalinformationprocessing_Membranetransport_togB,oligogalacturonidetransportsystemsubstrate-bindingprotein	4,66766E-05	3,0572E-05	4,98322E-05
K01689_ko04066_HIF-1signalingpathway_Environmentalinformationprocessing_Signaltrasduction_ENO,eno,enolase[EC:4.2.1.11];K01689_ko03018_RNAdegradation_GeneticInformationProcessing_Folding,sortinganddegradation_ENO,eno,enolase[EC:4.2.1.11];K0	0,00234939	0,002119659	0,001769044
K07405_ko00500_Starchandsucrosemetabolism_Metabolism_Carbohydratemetabolism_E3.2.1.1A,alpha-amylase[EC:3.2.1.1]	0,000596424	0,000784681	0,000490017
K07406_ko00052_Galactosemetabolism_Metabolism_Carbohydratemetabolism_melA,alpha-galactosidase[EC:3.2.1.22];K07406_ko00603_Glycosphingolipidbiosynthesis-globoseries_Metabolism_Glycanbiosynthesisandmetabolism_melA,alpha-galactosidase[EC:3.2	9,33532E-05	9,1716E-05	0,000174413
K00756_ko00240_Pyrimidinemetabolism_Metabolism_Nucleotidemetabolism_E2.4.2.2,pdp,pyrimidine-nucleosidephosphorylase[EC:2.4.2.2]	0,000269687	0,000448389	0,000514933
K03040_ko03020_RNApolymerase_GeneticInformationProcessing_Transcription_rpoA,DNA-directedRNApolymerasesubunitalpha[EC:2.7.7.6];K03040_ko00230_Purinemetabolism_Metabolism_Nucleotidemetabolism_rpoA,DNA-directedRNApolymerasesubunitalp	0,001908555	0,001599935	0,001478356
K11996_ko04122_Sulfurrelaysystem_GeneticInformationProcessing_Folding,sortinganddegradation_MOCS3,UBA4,moeB,adenylyltransferaseandsulfurtransferase	0,000829807	0,00068787	0,000755789
K01740_ko00270_Cysteineandmethioninemetabolism_Metabolism_Aminoacidmetabolism_E2.5.1.49,metY,O-acetylhomoserine(thiol)-lyase[EC:2.5.1.49]	0,001115053	0,001105687	0,001204279
K00968_ko00564_Glycerophospholipidmetabolism_Metabolism_Lipidmetabolism_PCYT1,choline-phosphatecytidylyltransferase[EC:2.7.7.15];K00968_ko00440_Phosphonateandphosphinatemetabolism_Metabolism_Metabolismofotheraminoacids_PCYT1,choline-p	0,000176334	0,000188527	0,000249161
K00003_ko00270_Cysteineandmethioninemetabolism_Metabolism_Aminoacidmetabolism_E1.1.1.3,homoserinedehydrogenase[EC:1.1.1.3];K00003_ko00260_Glycine,serineandthreoninemetabolism_Metabolism_Aminoacidmetabolism_E1.1.1.3,homoserinedehyd	0,000746826	0,000529915	0,000614598
K05663_ko02010_Ctransporters_Environmentalinformationprocessing_Membranetransport_ABC.ATM,mitochondrialABCtransporterATM	0	0	8,30537E-06
K00605_ko00260_Glycine,serineandthreoninemetabolism_Metabolism_Aminoacidmetabolism_gcvT,AMT,aminomethyltransferase[EC:2.1.2.10];K00605_ko00670_Onecarbonpoolbyfolate_Metabolism_Metabolismofcofactorsandvitamins_gcvT,AMT,aminomethyltr	0,000477139	0,000275148	0,000315604
K01222_ko00010_Glycolysis/Gluconeogenesis_Metabolism_Carbohydratemetabolism_E3.2.1.86A,celF,6-phospho-beta-glucosidase[EC:3.2.1.86]	0,000108912	0,000147765	0,000240856
K14153_ko00730_Thiaminemetabolism_Metabolism_Metabolismofcofactorsandvitamins_thiDE,hydroxymethylpyrimidinekinase/phosphomethylpyrimidinekinase/thiamine-phosphatediphosphorylase[EC:2.7.1.492.7.4.72.5.1.3]	5,18629E-06	0	8,30537E-06
K01443_ko00520_Aminosugarandnucleotidesugarmetabolism_Metabolism_Carbohydratemetabolism_nagA,AMDHD2,N-acetylglucosamine-6-phosphatedeacetylase[EC:3.5.1.25]	0,000554933	0,000565582	0,000631208
K01476_ko05146_Amoebiasis_HumanDiseases_Infectiousdiseases_E3.5.3.1,rocF,arg,arginase[EC:3.5.3.1];K01476_ko00330_Arginineandprolinemetabolism_Metabolism_Aminoacidmetabolism_E3.5.3.1,rocF,arg,arginase[EC:3.5.3.1];K01476_ko01230_Biosynthesiso	0,000160775	0,000122288	0,000182718
K05847_ko02010_Ctransporters_Environmentalinformationprocessing_Membranetransport_opuA,osmoprotectanttransportsystemATP-bindingprotein	0,000191893	0,000193623	0,000224245
K13444_ko04142_Lysosome_CellularProcesses_Transportandcatabolism_SUMF1,FGE,sulfatasemodifyingfactor1	0,000290432	0,000412722	0,000274077
K01720_ko00630_Glyoxylateanddicarboxylatemetabolism_Metabolism_Carbohydratemetabolism_prpD,2-methylcitratedehydratase[EC:4.2.1.79]	0,000165961	0,000132479	0,000166107
K09759_ko00970_Aminoacyl-tRNAbiosynthesis_Geneticinformationandprocessing_Transcription_aspC,nondiscriminatingaspartyl-tRNAsynthetase[EC:6.1.1.23]	0,000150402	7,643E-05	5,81376E-05
K12603_ko03018_RNAdegradation_GeneticInformationProcessing_Folding,sortinganddegradation_CNOT6,CCR4,CCR4-NOTtranscriptioncomplexsubunit6[EC:3.1.13.4]	5,18629E-06	1,01907E-05	0
K00381_ko00920_Sulfurmetabolism_Metabolism_Energymetabolism_cysI,sulfitereductase(NADPH)hemoproteinbeta-component[EC:1.8.1.2]	0	2,03813E-05	2,49161E-05
K00766_ko00400_Phenylalanine,tyrosineandtryptophanbiosynthesis_Metabolism_Aminoacidmetabolism_trpD,anthranilatephosphoribosyltransferase[EC:2.4.2.18];K00766_ko01230_Biosynthesisofaminoacids_Metabolism_Overview_trpD,anthranilatephosphoribc	0,000171148	0,000290434	0,000332215
K02808_ko02010_Ctransporters_Environmentalinformationprocessing_Membranetransport_PTS-Scr-EIIA,scrA,PTSsystem,sucrose-specificIIAcomponent[EC:2.7.1.69];K02808_ko00500_Starchandsucrosemetabolism_Metabolism_Carbohydratemetabolism_PTS-Scr-	0,000191893	0,000112097	0,000124581
K01875_ko00970_Aminoacyl-tRNAbiosynthesis_Geneticinformationandprocessing_Transcription_SARS,serS,seryl-tRNAsynthetase[EC:6.1.1.11]	0,00206933	0,001951513	0,001619548
K00948_ko00030_Pentosephosphatepathway_Metabolism_Carbohydratemetabolism_PRPS,prsA,ribose-phosphatepyrophosphokinase[EC:2.7.6.1];K00948_ko00230_Purinemetabolism_Metabolism_Nucleotidemetabolism_PRPS,prsA,ribose-phosphatepyrophosphc	0,001472907	0,001192308	0,001054782
K01703_ko00290_Valine,leucineandisoleucinebiosynthesis_Metabolism_Aminoacidmetabolism_leuC,3-isopropylmalate/(R)-2-methylmalatedehydrataselargesubunit[EC:4.2.1.334.2.1.35];K01703_ko00630_Glyoxylateanddicarboxylatemetabolism_Metabolism_Carl	0,000829807	0,000616535	0,000813926
K01524_ko00230_Purinemetabolism_Metabolism_Nucleotidemetabolism_ppx-gppA,exopolyphosphatase/guanosine-5'-triphosphate,3'-diphosphatepyrophosphatase[EC:3.6.1.113.6.1.40]	0,000653473	0,000672584	0,00068104
K13601_ko00830_Retinolmetabolism_Metabolism_Metabolismofcofactorsandvitamins_bchQ,bacteriochlorophyllC8methyltransferase[EC:2.1.1.-]	5,18629E-06	5,09533E-06	8,30537E-06
K01668_ko00350_Tyrosinemetabolism_Metabolism_Aminoacidmetabolism_E4.1.99.2,tyrosinephenol-lyase[EC:4.1.99.2]	1,03726E-05	1,01907E-05	8,30537E-06
K00917_ko00052_Galactosemetabolism_Metabolism_Carbohydratemetabolism_lacC,tagatose6-phosphatekinase[EC:2.7.1.144]	0,000103726	9,1716E-05	0,000199329
K07783_ko02020_Two-componentsystem_Environmentalinformationprocessing_Signaltrasduction_uhpC,MFStransporter,OPAfamily,sugarphosphatesensorproteinUhpC	8,29807E-05	1,01907E-05	0,000157802
K00901_ko04066_HIF-1signalingpathway_Environmentalinformationprocessing_Signaltrasduction_E2.7.1.107,DGK,dgkA,diacylglycerolkinase(ATPdependent)[EC:2.7.1.107];K00901_ko00561_Glycerolipidmetabolism_Metabolism_Lipidmetabolism_E2.7.1.107,DGK,(	0,000108912	0,000275148	0,000191024
K01358_ko04112_Cellcycle-Caulobacter_CellularProcesses_Cellgrowthanddeath_clpP,CLPP,ATP-dependentClpprotease,proteasesubunit[EC:3.4.21.92]	0,002256037	0,002833006	0,002707551
K02474_ko00520_Aminosugarandnucleotidesugarmetabolism_Metabolism_Carbohydratemetabolism_wbpO,UDP-N-acetyl-D-galactosaminedehydrogenase[EC:1.1.1.-]	0,000586051	0,000361769	0,000539849
K01491_ko00670_Onecarbonpoolbyfolate_Metabolism_Metabolismofcofactorsandvitamins_folD,methylenetetrahydrofolatedehydrogenase(NADP+)/methenyltetrahydrofolatecyclohydrolase[EC:1.5.1.53.5.4.9];K01491_ko01200_Carbonmetabolism_Metabolism_(	0,00088167	0,000708251	0,000905286
K01866_ko00970_Aminoacyl-tRNAbiosynthesis_Geneticinformationandprocessing_Transcription_YARS,tyrS,tyrosyl-tRNAsynthetase[EC:6.1.1.1]	0,002074517	0,001783367	0,001802266
K10896_ko03460_Fanconianemiapathway_GeneticinformationProcessing_ReplicationandRepair_FANCM,fanconianemiagroupMprotein	3,6304E-05	3,0572E-05	8,30537E-05
K07106_ko00520_Aminosugarandnucleotidesugarmetabolism_Metabolism_Carbohydratemetabolism_murQ,N-acetylmuramicacid6-phosphateetherase[EC:4.2.1.126]	0,000259315	0,000412722	0,000348826
K00197_ko01200_Carbonmetabolism_Metabolism_Overview_cdhE,acsC,acetyl-CoAdecarbonylase/synthasecomplexsubunitgamma[EC:2.1.1.245];K00197_ko00194_Photosynthesisproteins_Metabolism_Energymetabolism_cdhE,acsC,acetyl-CoAdecarbonylase/synt	5,70492E-05	0,000198718	0,000124581
K00066_ko02020_Two-componentsystem_Environmentalinformationprocessing_Signaltrasduction_algD,GDP-mannose6-dehydrogenase[EC:1.1.1.132];K00066_ko00520_Aminosugarandnucleotidesugarmetabolism_Metabolism_Carbohydratemetabolism_algD,GD	0	0	8,30537E-06
K03342_ko00785_Lipoicacidmetabolism_Metabolism_Metabolismofcofactorsandvitamins_pabBC,para-aminobenzoatesynthetase/4-amino-4-deoxychorismatelyase[EC:2.6.1.854.1.3.38]	2,59315E-05	3,0572E-05	4,15269E-05
K07792_ko02020_Two-componentsystem_Environmentalinformationprocessing_Signaltrasduction_dcuB,anaerobicC4-dicarboxylatetransporterDcuB	0,000134844	3,0572E-05	3,32215E-05
K05308_ko00052_Galactosemetabolism_Metabolism_Carbohydratemetabolism_gnaD,gluconate/galactonatedehydratase[EC:4.2.1.140];K05308_ko00030_Pentosephosphatepathway_Metabolism_Carbohydratemetabolism_gnaD,gluconate/galactonatedehydratas	4,14903E-05	2,03813E-05	2,49161E-05
K00241_ko00020_Citratecycle(TCAcycle)_Metabolism_Carbohydratemetabolism_sdhC,succinatedehydrogenasecytochromeb556subunit;K00241_ko00630_Glyoxylateanddicarboxylatemetabolism_Metabolism_Carbohydratemetabolism_sdhC,succinatedehydrogen	0,000736453	0,000270053	0,000274077
K13043_ko00330_Arginineandprolinemetabolism_Metabolism_Aminoacidmetabolism_argF,N-succinyl-L-ornithinetranscarbamylase[EC:2.1.3.11]	0,000430462	0,000198718	0,000149497
K03531_ko04112_Cellcycle-Caulobacter_CellularProcesses_Cellgrowthanddeath_ftsZ,celldivisionproteinFtsZ	0,001317318	0,001278929	0,001079698
K00224_ko00351_1,1,1-Trichloro-2,2-bis(4-chlorophenyl)ethane(DDT)degradation_Metabolism_Xenobioticsbiodegradationandmetabolism_E1.3.1.-,[EC:1.3.1.-];K00224_ko00361_Chlorocyclohexaneandchlorobenzenedegradation_Metabolism_Xenobioticsbiodegra	0,000653473	0,000259862	0,000265772
K01487_ko00230_Purinemetabolism_Metabolism_Nucleotidemetabolism_E3.5.4.3,guaD,guaninedeaminase[EC:3.5.4.3]	0,000233383	0,00015286	0,00032391
K13598_ko02020_Two-componentsystem_Environmentalinformationprocessing_Signaltrasduction_ntrY,two-componentsystem,NtrCfamily,nitrogenregulationsensorhistidinekinaseNtrY[EC:2.7.13.3]	0,000259315	0,000601249	0,000614598
K11755_ko00340_Histidinemetabolism_Metabolism_Aminoacidmetabolism_hisIE,phosphoribosyl-ATPpyrophosphohydrolase/phosphoribosyl-AMPcyclohydrolase[EC:3.6.1.313.5.4.19];K11755_ko01230_Biosynthesisofaminoacids_Metabolism_Overview_hisIE,phos	0,000337109	0,000198718	0,000315604
K00811_ko00250_Alanine,aspartateandglutamatemetabolism_Metabolism_Aminoacidmetabolism_ASP5,aspartateaminotransferase,chloroplastic[EC:2.6.1.1];K00811_ko00330_Arginineandprolinemetabolism_Metabolism_Aminoacidmetabolism_ASP5,aspartatear	0,000435648	0,000672584	0,000423574
K00013_ko00340_Histidinemetabolism_Metabolism_Aminoacidmetabolism_hisD,histidinoldehydrogenase[EC:1.1.1.23];K00013_ko01230_Biosynthesisofaminoacids_Metabolism_Overview_hisD,histidinoldehydrogenase[EC:1.1.1.23]	0,000373413	0,000463675	0,000531544
K01787_ko00520_Aminosugarandnucleotidesugarmetabolism_Metabolism_Carbohydratemetabolism_RENBP,N-acylglucosamine2-epimerase[EC:5.1.3.8]	0,00042009	0,000906969	0,000490017
K01408_ko05010_Alzheimer'sdisease_HumanDiseases_Degenerativediseases_IDE,ide,insulysin[EC:3.4.24.56]	0,000285246	0,000285339	0,000423574
K03279_ko00540_Lipopolysaccharidebiosynthesis_Metabolism_Glycanbiosynthesisandmetabolism_waaJ,rfaJ,UDP-glucose:(galactosyl)LPSalpha-1,2-glucosyltransferase[EC:2.4.1.58]	0,000202265	0,000249671	0,000257467
K11711_ko02020_Two-componentsystem_Environmentalinformationprocessing_Signaltrasduction_dctS,two-componentsystem,LuxRfamily,sensorhistidinekinaseDctS[EC:2.7.13.3]	9,33532E-05	3,56673E-05	5,81376E-05
K02012_ko02010_Ctransporters_Environmentalinformationprocessing_Membranetransport_afuA,fbpA,iron(III)transportsystemsubstrate-bindingprotein	0,000451207	0,000264957	0,000456795
K03585_ko00312_beta-Lactamresistance_HumanDiseases_Drugresistance_acrA,mexA,adeI,smeD,membranefusionprotein	0,001109866	0,00129931	0,001071393
K13010_ko00520_Aminosugarandnucleotidesugarmetabolism_Metabolism_Carbohydratemetabolism_per,rfbE,perosaminesynthetase[EC:2.6.1.102]	0,00068459	0,000861111	0,000622903
K11614_ko02020_Two-componentsystem_Environmentalinformationprocessing_Signaltrasduction_yufL,malK,two-componentsystem,CitBfamily,sensorhistidinekinaseMalK[EC:2.7.13.3]	1,55589E-05	1,5286E-05	1,66107E-05
K01805_ko00051_Fructoseandmannosemetabolism_Metabolism_Carbohydratemetabolism_xylA,xyloseisomerase[EC:5.3.1.5];K01805_ko00040_Pentoseandglucuronateinterconversions_Metabolism_Carbohydratemetabolism_xylA,xyloseisomerase[EC:5.3.1.5]	0,000658659	0,000896779	0,000548155
K03072_ko02010_Ctransporters_Environmentalinformationprocessing_Membranetransport_secD,preproteintranslocasesubunitSecD;K03072_ko04120_Ubiquitinmediatedproteolysis_GeneticInformationProcessing_Folding,sortinganddegradation_secD,preprotein	0,000171148	0,000157955	0,000199329
K01845_ko00830_Retinolmetabolism_Metabolism_Metabolismofcofactorsandvitamins_hemL,glutamate-1-semialdehyde2,1-aminomutase[EC:5.4.3.8]	0,000290432	0,000392341	0,000415269
K03742_ko00760_Nicotinateandnicotinamidemetabolism_Metabolism_Metabolismofcofactorsandvitamins_pncC,nicotinamide-nucleotideamidase[EC:3.5.1.42]	0,00050307	0,000366864	0,000631208
K00045_ko00051_Fructoseandmannosemetabolism_Metabolism_Carbohydratemetabolism_E1.1.1.67,mtlK,mannitol2-dehydrogenase[EC:1.1.1.67]	4,66766E-05	2,03813E-05	1,66107E-05
K04705_ko04144_Endocytosis_CellularProcesses_Transportandcatabolism_STAM,signaltransducingadaptormolecule;K04705_ko04630_Jak-STATsignalingpathway_Environmentalinformationprocessing_Signaltrasduction_STAM,signaltransducingadaptormolecule	0	0	1,66107E-05
K01478_ko00330_Arginineandprolinemetabolism_Metabolism_Aminoacidmetabolism_E3.5.3.6,arcA,arginenedeiminase[EC:3.5.3.6]	0,000165961	0,00015286	0,00010797

K13954_ko00350_Tyrosinemetabolism_Metabolism_Aminoacidmetabolism_yiaY,alcoholdehydrogenase[EC:1.1.1.1];K13954_ko00010_Glycolysis/Gluconeogenesis_Metabolism_Carbohydratemetabolism_yiaY,alcoholdehydrogenase[EC:1.1.1.1];K13954_ko00071_F	0,000186706	0,000239481	0,000174413
K01452_ko00520_Aminosugarandnucleotidesugarmetabolism_Metabolism_Carbohydratemetabolism_E3.5.1.41,chitindeacetylase[EC:3.5.1.41]	8,8167E-05	0,000219099	0,000182718
K01758_ko00270_Cysteineandmethioninemetabolism_Metabolism_Aminoacidmetabolism_CTH,cystathioninegamma-lyase[EC:4.4.1.1];K01758_ko00260_Glycine,serineandthreoninemetabolism_Metabolism_Aminoacidmetabolism_CTH,cystathioninegamma-lyase	0,00042009	0,000580868	0,000689346
K04835_ko00630_Glyoxylateanddicarboxylatemetabolism_Metabolism_Carbohydratemetabolism_E4.3.1.2,methylaspartateammonia-lyase[EC:4.3.1.2]	1,55589E-05	2,03813E-05	1,66107E-05
K03621_ko00561_Glycerolipidmetabolism_Metabolism_Lipidmetabolism_plsX,glycerol-3-phosphateacyltransferasePlsX[EC:2.3.1.15];K03621_ko00564_Glycerophospholipidmetabolism_Metabolism_Lipidmetabolism_plsX,glycerol-3-phosphateacyltransferasePlsX[E	0,000523815	0,00053501	0,000631208
K06675_ko04111_Cellcycle-yeast_CellularProcesses_Cellgrowthanddeath_SMC4,structuralmaintenanceofchromosome4	0	1,01907E-05	0
K00147_ko00330_Arginineandprolinemetabolism_Metabolism_Aminoacidmetabolism_proA,glutamate-5-semialdehydedehydrogenase[EC:1.2.1.41];K00147_ko00332_Carbapenembiosynthesis_Metabolism_Biosynthesisofothersecondarymetabolites_proA,glutam	0,000570492	0,000667489	0,000581376
K00788_ko00730_Thiaminemetabolism_Metabolism_Metabolismofcofactorsandvitamins_thiE,thiamine-phosphatepyrophosphorylase[EC:2.5.1.3]	0,000834993	0,000850921	0,001320554
K02224_ko00830_Retinolmetabolism_Metabolism_Metabolismofcofactorsandvitamins_cobB-cbiA,cobyrinicacida,c-diamidesynthase[EC:6.3.5.96.3.5.11]	0,00032155	0,000402531	0,000373742
K00282_ko00260_Glycine,serineandthreoninemetabolism_Metabolism_Aminoacidmetabolism_gcvPA,glycinedehydrogenasesubunit1[EC:1.4.4.2];K00282_ko01200_Carbonmetabolism_Metabolism_Overview_gcvPA,glycinedehydrogenasesubunit1[EC:1.4.4.2]	0,000373413	0,000346483	0,000348826
K11616_ko02020_Two-componentsystem_Environmentalinformationprocessing_Signaltrasduction_maeN,malate:Na+symporter	4,66766E-05	6,62393E-05	4,15269E-05
K06042_ko00830_Retinolmetabolism_Metabolismofcofactorsandvitamins_cobH-cbiC,precorrin-8X/cobalt-precorrin-8methylmutase[EC:5.4.99.615.4.99.60]	0,000119285	6,1144E-05	7,47483E-05
K02083_ko00230_Purinemetabolism_Metabolism_Nucleotidemetabolism_allC,allantoatedeiminase[EC:3.5.3.9]	3,6304E-05	1,5286E-05	4,98322E-05
K04487_ko04122_Sulfurrelaysystem_GeneticInformationProcessing_Folding,sortinganddegradation_iscS,NFS1,cysteinedesulfurase[EC:2.8.1.7];K04487_ko00730_Thiaminemetabolism_Metabolism_Metabolismofcofactorsandvitamins_iscS,NFS1,cysteinedesulfurase	0,001587005	0,001895464	0,001594631
K11717_ko00450_Selenocompoundmetabolism_Metabolism_Metabolismofotheraminoacids_sufS,cysteinedesulfurase/selenocysteinelyase[EC:2.8.1.74.4.1.16]	0,001078749	0,001518409	0,001395302
K00880_ko00052_Galactosemetabolism_Metabolism_Carbohydratemetabolism_lyxK,L-xylulokinase[EC:2.7.1.53];K00880_ko00040_Pentoseandglucuronateinterconversions_Metabolism_Carbohydratemetabolism_lyxK,L-xylulokinase[EC:2.7.1.53]	2,07452E-05	4,07627E-05	9,13591E-05
K02040_ko02010_Ctransporters_Environmentalinformationprocessing_Membranetransport_pstS,phosphatetransportsystemsubstrate-bindingprotein;K02040_ko02020_Two-componentsystem_Environmentalinformationprocessing_Signaltrasduction_pstS,phosph	0,000803875	0,000815253	0,000863759
K00639_ko00260_Glycine,serineandthreoninemetabolism_Metabolism_Aminoacidmetabolism_kbl,GCAT,glycineC-acetyltransferase[EC:2.3.1.29]	0,000637914	0,000636917	0,000398658
K00001_ko00350_Tyrosinemetabolism_Metabolism_Aminoacidmetabolism_E1.1.1.1,adh,alcoholdehydrogenase[EC:1.1.1.1];K00001_ko00010_Glycolysis/Gluconeogenesis_Metabolism_Carbohydratemetabolism_E1.1.1.1,adh,alcoholdehydrogenase[EC:1.1.1.1];K0(	0,000523815	0,000443294	0,000548155
K06282_ko00633_Nitrotoluenedegradation_Metabolism_Xenobioticsbiodegradationandmetabolism_hyaA,hybO,hydrogenasesmallsubunit[EC:1.12.99.6]	6,22355E-05	3,56673E-05	3,32215E-05
K10209_ko00906_Carotenoidbiosynthesis_Metabolism_Metabolismofterpenoidsandpolyketides_crtN,4,4'-diapophytoenedesaturase[EC:1.3.8.2]	0	1,01907E-05	3,32215E-05
K13927_ko02020_Two-componentsystem_Environmentalinformationprocessing_Signaltrasduction_citXG,holo-ACPsynthase/triphosphoribosyl-dephospho-CoAsynthase[EC:2.7.7.612.4.2.52]	0,000108912	6,1144E-05	3,32215E-05
K00620_ko00330_Arginineandprolinemetabolism_Metabolism_Aminoacidmetabolism_argJ,glutamateN-acetyltransferase/amino-acidN-acetyltransferase[EC:2.3.1.352.3.1.1];K00620_ko01210_Oxocarboxylicacidmetabolism_Metabolism_Overview_argJ,glutamateI	0,000404531	0,000529915	0,000539849
K03629_ko03440_Homologousrecombination_GeneticinformationProcessing_ReplicationandRepair_recF,DNAreplicationandrepairproteinRecF	0,00110468	0,001166831	0,001287333
K09516_ko00830_Retinolmetabolism_Metabolismofcofactorsandvitamins_RETSAT,all-trans-retinol13,14-reductase[EC:1.3.99.23]	4,14903E-05	6,1144E-05	4,15269E-05
K11912_ko02010_Ctransporters_Environmentalinformationprocessing_Membranetransport_ppkA,serine/threonine-proteinkinasePpkA[EC:2.7.11.1]	0,000378599	0,000336292	0,000539849
K08372_ko02020_Two-componentsystem_Environmentalinformationprocessing_Signaltrasduction_pepD,putativeserineproteasePepD[EC:3.4.21.-]	0,000108912	7,643E-05	3,32215E-05
K03074_ko02010_Ctransporters_Environmentalinformationprocessing_Membranetransport_secF,preproteintranslocasesubunitSecF;K03074_ko04120_Ubiquitinmediatedproteolysis_GeneticInformationProcessing_Folding,sortinganddegradation_secF,preproteint	0,00014003	0,000147765	0,000332215
K00652_ko00780_Biotinmetabolism_Metabolism_Metabolismofcofactorsandvitamins_bioF,8-amino-7-oxononanoatesynthase[EC:2.3.1.47]	0,00074164	0,000667489	0,000523238
K02502_ko00340_Histidinemetabolism_Metabolism_Aminoacidmetabolism_hisZ,ATPphosphoribosyltransferaseregulatorysubunit;K02502_ko01230_Biosynthesisofaminoacids_Metabolism_Overview_hisZ,ATPphosphoribosyltransferaseregulatorysubunit	0,000295619	0,000219099	0,000249161
K09490_ko04141_Proteinprocessinginendoplasmicreticulum_GeneticInformationProcessing_Folding,sortinganddegradation_HSPA5,BIP,heatshock70kDaprotein5;K09490_ko04120_Ubiquitinmediatedproteolysis_GeneticInformationProcessing_Folding,sortinganddd	3,11177E-05	2,54767E-05	8,30537E-06
K03412_ko02020_Two-componentsystem_Environmentalinformationprocessing_Signaltrasduction_cheB,two-componentsystem,chemotaxisfamily,responseregulatorCheB[EC:3.1.1.61];K03412_ko02030_Bacterialchemotaxis_Organismalsystem_Cellmobility_cheB,(	0,000119285	9,1716E-05	8,30537E-05
K01940_ko00250_Alanine,aspartateandglutamatemetabolism_Metabolism_Aminoacidmetabolism_argG,ASS1,argininosuccinatesynthase[EC:6.3.4.5];K01940_ko00330_Arginineandprolinemetabolism_Metabolism_Aminoacidmetabolism_argG,ASS1,argininosuccina	0,001571446	0,001171927	0,000855453
K01813_ko00051_Fructoseandmannosemetabolism_Metabolism_Carbohydratemetabolism_rhaA,L-rhamnoseisomerase[EC:5.3.1.14]	0,000285246	0,000280243	0,000207634
K03473_ko00750_VitaminB6metabolism_Metabolism_Metabolismofcofactorsandvitamins_pdxB,erythronate-4-phosphatedehydrogenase[EC:1.1.1.290]	0,000197079	0,000280243	0,000207634
K03151_ko04122_Sulfurrelaysystem_GeneticInformationProcessing_Folding,sortinganddegradation_thiI,thiaminebiosynthesisproteinThiI;K03151_ko00730_Thiaminemetabolism_Metabolism_Metabolismofcofactorsandvitamins_thiI,thiaminebiosynthesisproteinTI	0,000529002	0,000575773	0,000631208
K00850_ko04151_PI3K-Aktsignalingpathway_Environmentalinformationprocessing_Signaltrasduction_pfkA,PFK,6-phosphofructokinase1[EC:2.7.1.11];K00850_ko03018_RNAdegradation_GeneticInformationProcessing_Folding,sortinganddegradation_pfkA,PFK,6-ph	0,002084889	0,001976989	0,001727517
K13126_ko03018_RNAdegradation_GeneticInformationProcessing_Folding,sortinganddegradation_PABPC,polyadenylate-bindingprotein;K13126_ko03015_mRNAsurveillancepathway_GeneticinformationProcessing_Transcription_PABPC,polyadenylate-bindingpro	1,03726E-05	1,5286E-05	2,49161E-05
K01923_ko00230_Purinemetabolism_Metabolism_Nucleotidemetabolism_purC,phosphoribosylaminoimidazole-succinocarboxamidesynthase[EC:6.3.2.6]	0,000954278	0,000968113	0,000739178
K11358_ko00250_Alanine,aspartateandglutamatemetabolism_Metabolism_Aminoacidmetabolism_yhdR,aspartateaminotransferase[EC:2.6.1.1];K11358_ko00330_Arginineandprolinemetabolism_Metabolism_Aminoacidmetabolism_yhdR,aspartateaminotransfera	0,000295619	0,000249671	0,00021594
K02410_ko02030_Bacterialchemotaxis_Organismalsystem_Cellmobility_fliG,flagellarmotorswitchproteinFliG;K02410_ko02040_Flagellarassembly_Organismalsystem_Cellmobility_fliG,flagellarmotorswitchproteinFliG	0,000233383	0,000168146	0,000141191
K03553_ko03440_Homologousrecombination_GeneticinformationProcessing_ReplicationandRepair_recA,recombinationproteinRecA	0,001571446	0,001416503	0,001353776
K01782_ko00310_Lysinedegradation_Metabolism_Aminoacidmetabolism_fadJ,3-hydroxyacyl-CoAdehydrogenase/enoyl-CoAhydratase/3-hydroxybutyryl-CoAepimerase[EC:1.1.1.354.2.1.175.1.2.3];K01782_ko00380_Tryptophanmetabolism_Metabolism_Aminoacid	5,18629E-06	1,01907E-05	0
K00894_ko00564_Glycerophospholipidmetabolism_Metabolism_Lipidmetabolism_ETNK,EKI,ethanolaminekinase[EC:2.7.1.82]	5,18629E-06	3,56673E-05	3,32215E-05
K11720_ko02010_Ctransporters_Environmentalinformationprocessing_Membranetransport_lptG,lipopolysaccharideexportsystempermeaseprotein	0,000269687	0,000428008	0,000199329
K00972_ko00520_Aminosugarandnucleotidesugarmetabolism_Metabolism_Carbohydratemetabolism_UAP1,UDP-N-acetylglucosamine/UDP-N-acetylgalactosaminediphosphorylase[EC:2.7.7.232.7.7.83]	0,000114098	0,000178337	0,000199329
K10206_ko00300_Lysinebiosynthesis_Metabolism_Aminoacidmetabolism_E2.6.1.83,LL-diaminopimelateaminotransferase[EC:2.6.1.83];K10206_ko01230_Biosynthesisofaminoacids_Metabolism_Overview_E2.6.1.83,LL-diaminopimelateaminotransferase[EC:2.6.1.8	0,000767571	0,000504438	0,000797316
K00031_ko04146_Peroxisome_CellularProcesses_Transportandcatabolism_IDH1,IDH2,icd,isocitratedehydrogenase[EC:1.1.1.42];K00031_ko00020_Citratecycle(TCAcycle)_Metabolism_Carbohydratemetabolism_IDH1,IDH2,icd,isocitratedehydrogenase[EC:1.1.1.42];I	0,000497884	0,000529915	0,000614598
K01000_ko01005_Lipopolysaccharidebiosynthesisproteins_Metabolism_Glycanbiosynthesisandmetabolism_mraY,phospho-N-acetylmuramoyl-pentapeptide-transferase[EC:2.7.8.13]	0,00156626	0,001615221	0,001702601
K05343_ko00500_Starchandsucrosemetabolism_Metabolism_Carbohydratemetabolism_treS,maltosealpha-D-glucosyltransferase/alpha-amylase[EC:5.4.99.163.2.1.1]	0,000103726	9,1716E-05	9,96645E-05
K01196_ko00500_Starchandsucrosemetabolism_Metabolism_Carbohydratemetabolism_AGL,glycogendebranchingenzyme[EC:2.4.1.253.2.1.33]	0	1,01907E-05	0
K00097_ko00750_VitaminB6metabolism_Metabolism_Metabolismofcofactorsandvitamins_pdxA,4-hydroxythreonine-4-phosphatedehydrogenase[EC:1.1.1.262]	0,000466766	0,000591059	0,000298993
K15023_ko01200_Carbonmetabolism_Metabolism_Overview_acsE,5-methyltetrahydrofolatecorrinoid/ironsulfurproteinmethyltransferase[EC:2.1.1.258];K15023_ko00194_Photosynthesisproteins_Metabolism_Energymetabolism_acsE,5-methyltetrahydrofolatecor	5,18629E-06	0,000168146	6,6443E-05
K13599_ko02020_Two-componentsystem_Environmentalinformationprocessing_Signaltrasduction_ntrX,two-componentsystem,NtrCfamily,nitrogenregulationresponseregulatorNtrX	9,33532E-05	3,56673E-05	0,00010797
K00821_ko00330_Arginineandprolinemetabolism_Metabolism_Aminoacidmetabolism_argD,acetylornithine/N-succinyldiaminopimelateaminotransferase[EC:2.6.1.112.6.1.17];K00821_ko00300_Lysinebiosynthesis_Metabolism_Aminoacidmetabolism_argD,acetylo	0,000430462	0,000351578	0,00023255
K07281_ko00630_Glyoxylateanddicarboxylatemetabolism_Metabolism_Carbohydratemetabolism_ipct,1L-myo-inositol1-phosphatecytidylyltransferase[EC:2.7.7.74]	0,000165961	0,000208909	0,000191024
K02338_ko03030_DNAreplication_GeneticinformationProcessing_ReplicationandRepair_DPO3B,dnaN,DNApolymeraseIIIsubunitbeta[EC:2.7.7.7];K02338_ko03440_Homologousrecombination_GeneticinformationProcessing_ReplicationandRepair_DPO3B,dnaN,DN	0,000949091	0,001080211	0,001378692
K09808_ko02010_Ctransporters_Environmentalinformationprocessing_Membranetransport_ABC.LPT.P,lolC,lolE,lipoprotein-releasingsystempermeaseprotein	0,000259315	0,000438199	0,000373742
K14170_ko00400_Phenylalanine,tyrosineandtryptophanbiosynthesis_Metabolism_Aminoacidmetabolism_pheA,chorismatemutase/prephenatedehydratase[EC:5.4.99.54.2.1.51];K14170_ko01230_Biosynthesisofaminoacids_Metabolism_Overview_pheA,chorismat	0,000388972	0,00038215	0,000332215
K01839_ko00030_Pentosephosphatepathway_Metabolism_Carbohydratemetabolism_deoB,phosphopentomutase[EC:5.4.2.7];K01839_ko00230_Purinemetabolism_Metabolism_Nucleotidemetabolism_deoB,phosphopentomutase[EC:5.4.2.7]	0,000487511	0,000504438	0,000581376
K07717_ko02020_Two-componentsystem_Environmentalinformationprocessing_Signaltrasduction_ycbA,glnK,two-componentsystem,sensorhistidinekinaseYcbA[EC:2.7.13.3]	1,55589E-05	3,0572E-05	2,49161E-05
K14652_ko00740_Riboflavinmetabolism_Metabolism_Metabolismofcofactorsandvitamins_ribBA,3,4-dihydroxy2-butanone4-phosphatesynthase/GTPcyclohydrolaseII[EC:4.1.99.123.5.4.25]	0,000917974	0,000703156	0,00055646
K08720_ko00312_beta-Lactamresistance_HumanDiseases_Drugresistance_ompU,outermembraneproteinOmpU;K08720_ko05111_Vibriocholeraepathogeniccycle_HumanDiseases_Infectiousdiseases_ompU,outermembraneproteinOmpU	2,59315E-05	1,01907E-05	0
K00832_ko00270_Cysteineandmethioninemetabolism_Metabolism_Aminoacidmetabolism_tyrB,aromatic-amino-acidtransaminase[EC:2.6.1.57];K00832_ko00360_Phenylalaninemetabolism_Metabolism_Aminoacidmetabolism_tyrB,aromatic-amino-acidtransamin	2,59315E-05	0,000214004	0,000166107
K00030_ko00020_Citratecycle(TCAcycle)_Metabolism_Carbohydratemetabolism_IDH3,isocitratedehydrogenase(NAD+)[EC:1.1.1.41];K00030_ko01210_Oxocarboxylicacidmetabolism_Metabolism_Overview_IDH3,isocitratedehydrogenase(NAD+)[EC:1.1.1.41];K0003	0,000103726	5,60487E-05	0,000141191
K00743_ko00601_Glycosphingolipidbiosynthesis-lactoandneolactoseries_Metabolism_Glycanbiosynthesisandmetabolism_GGTA1,N-acetyllactosaminide3-alpha-galactosyltransferase[EC:2.4.1.87]	0,000145216	0,000168146	0,000166107
K00845_ko00524_Butirosinandneomycinbiosynthesis_Metabolism_Biosynthesisofothersecondarymetabolites_glk,glucokinase[EC:2.7.1.2];K00845_ko00521_Streptomycinbiosynthesis_Metabolism_Biosynthesisofothersecondarymetabolites_glk,glucokinase[EC:2.7.	0,00184632	0,001645793	0,001852098
K00290_ko00300_Lysinebiosynthesis_Metabolism_Aminoacidmetabolism_LYS1,saccharopinedehydrogenase(NADP+,L-lysineforming)[EC:1.5.1.7];K00290_ko00310_Lysinedegradation_Metabolism_Aminoacidmetabolism_LYS1,saccharopinedehydrogenase(NADP+,L-l	0,00156626	0,000947732	0,00066443
K03273_ko00540_Lipopolysaccharidebiosynthesis_Metabolism_Glycanbiosynthesisandmetabolism_gmhB,D-glycero-D-manno-heptose1,7-bisphosphatephosphatase[EC:3.1.3.823.1.3.83]	0,000202265	0,000208909	0,00023255
K04115_ko01220_Degradationofaromaticcompounds_Metabolism_Overview_bcrD,badG,benzoyl-CoAreductasesubunitD[EC:1.3.7.8];K04115_ko00362_Benzoatedegradation_Metabolism_Xenobioticsbiodegradationandmetabolism_bcrD,badG,benzoyl-CoAreducta	1,03726E-05	2,03813E-05	1,66107E-05

K02472_ko00520_Aminosugarandnucleotidesugarmetabolism_Metabolism_Carbohydratemetabolism_wecC,UDP-N-acetyl-D-mannosaminuronicaciddehydrogenase[EC:1.1.1.336]	0,000160775	0,000310815	0,000224245
K00626_ko02020_Two-componentsystem_Environmentalinformationprocessing_Signaltrasduction_E2.3.1.9,atoB,acetyl-CoAC-acetyltransferase[EC:2.3.1.9];K00626_ko00310_Lysinedegradation_Metabolism_Aminoacidmetabolism_E2.3.1.9,atoB,acetyl-CoAC-acety	0,000492698	0,000407627	0,00034052
K01791_ko00520_Aminosugarandnucleotidesugarmetabolism_Metabolism_Carbohydratemetabolism_wecB,UDP-N-acetylglucosamine2-epimerase(non-hydrolysing)[EC:5.1.3.14]	0,001701104	0,00175789	0,001785655
K11693_ko01005_Lipopolysaccharidebiosynthesisproteins_Metabolism_Glycanbiosynthesisandmetabolism_femX,fmhB,peptidoglycanpentaglycineglycinetransferase(thefirstglycine)[EC:2.3.2.16]	0,000233383	0,000484057	0,000697651
K11752_ko00740_Riboflavinmetabolism_Metabolism_Metabolismofcofactorsandvitamins_ribD,diaminohydroxyphosphoribosylaminopyrimidinedeaminase/5-amino-6-(5-phosphoribosylamino)uracilreductase[EC:3.5.4.261.1.1.193]	0,000352668	0,000336292	0,000257467
K11103_ko02020_Two-componentsystem_Environmentalinformationprocessing_Signaltrasduction_dctA,aerobicC4-dicarboxylatetransportprotein	3,11177E-05	3,56673E-05	6,6443E-05
K01468_ko00340_Histidinemetabolism_Metabolism_Aminoacidmetabolism_hutI,AMDHD1,imidazolonepropionase[EC:3.5.2.7]	0,000388972	0,000585963	0,000465101
K01914_ko00250_Alanine,aspartateandglutamatemetabolism_Metabolism_Aminoacidmetabolism_asnA,aspartate--ammonialigase[EC:6.3.1.1];K01914_ko00460_Cyanoaminoacidmetabolism_Metabolism_Metabolismofotheraminoacids_asnA,aspartate--ammonia	0,000648286	0,000733728	0,000739178
K01628_ko00051_Fructoseandmannosemetabolism_Metabolism_Carbohydratemetabolism_fucA,L-fuculose-phosphatealdolase[EC:4.1.2.17]	0,000352668	0,000244576	0,000298993
K01696_ko00260_Glycine,serineandthreoninemetabolism_Metabolism_Aminoacidmetabolism_trpB,tryptophansynthasebetachain[EC:4.2.1.20];K01696_ko00400_Phenylalanine,tyrosineandtryptophanbiosynthesis_Metabolism_Aminoacidmetabolism_trpB,tryptop	0,000399344	0,000377055	0,000332215
K11753_ko00740_Riboflavinmetabolism_Metabolism_Metabolismofcofactorsandvitamins_ribF,riboflavinkinase/FMNadenylyltransferase[EC:2.7.1.262.7.7.2]	0,000430462	0,000642012	0,000589681
K10559_ko02010_Ctransporters_Environmentalinformationprocessing_Membranetransport_rhaS,rhamnosetransportsystemsubstrate-bindingprotein	3,6304E-05	5,09533E-06	6,6443E-05
K04788_ko01053_Biosynthesisofsiderophoregroupnonribosomalpeptides_Metabolism_Metabolismofterpenoidsandpolyketides_mbtB,mycobactinphenyloxazolinesynthetase	0	0	8,30537E-06
K08965_ko00270_Cysteineandmethioninemetabolism_Metabolism_Aminoacidmetabolism_mtnW,2,3-diketo-5-methylthiopentyl-1-phosphateenolase[EC:5.3.2.5]	5,18629E-06	5,09533E-06	1,66107E-05
K05286_ko00563_Glycosylphosphatidylinositol(GPI)-anchorbiosynthesis_Metabolism_Glycanbiosynthesisandmetabolism_PIGB,phosphatidylinositolglycan,classB[EC:2.4.1.-]	5,18629E-06	1,01907E-05	0
K00865_ko00260_Glycine,serineandthreoninemetabolism_Metabolism_Aminoacidmetabolism_glxK,glyceratekinase[EC:2.7.1.31];K00865_ko00630_Glyoxylateanddicarboxylatemetabolism_Metabolism_Carbohydratemetabolism_glxK,glyceratekinase[EC:2.7.1.31];	0,000326736	0,000453485	0,000373742
K01060_ko00311_Penicillinandcephalosporinbiosynthesis_Metabolism_Biosynthesisofothersecondarymetabolites_E3.1.1.41,cephalosporin-Cdeacetylase[EC:3.1.1.41]	0,000119285	0,00038215	0,000174413
K14575_ko03008_Ribosomebiogenesisineukaryotes_GeneticinformationProcessing_Transcription_AFG2,DRG1,SPATA5,AAAfamilyATPase	5,18629E-06	5,09533E-06	8,30537E-06
K08289_ko00670_Onecarbonpoolbyfolate_Metabolism_Metabolismofcofactorsandvitamins_purT,phosphoribosylglycinamideformyltransferase2[EC:2.1.2.2];K08289_ko00230_Purinemetabolism_Metabolism_Nucleotidemetabolism_purT,phosphoribosylglycinamid	0,000373413	0,000198718	0,000174413
K01665_ko00785_Lipoicacidmetabolism_Metabolism_Metabolismofcofactorsandvitamins_pabB,para-aminobenzoatesynthetasecomponentI[EC:2.6.1.85]	0,000150402	0,000341387	0,000282383
K01760_ko00270_Cysteineandmethioninemetabolism_Metabolism_Aminoacidmetabolism_metC,cystathionineбeta-lyase[EC:4.4.1.8];K01760_ko00450_Selenocompoundmetabolism_Metabolism_Metabolismofotheraminoacids_metC,cystathionineбeta-lyase[EC:4	8,8167E-05	4,5858E-05	6,6443E-05
K00044_ko00140_Steroidhormonebiosynthesis_Metabolism_Lipidmetabolism_HSD17B1,17beta-estradiol17-dehydrogenase[EC:1.1.1.62];K00044_ko04912_GnRHsignalingpathway_Organismalsystem_Endocrinsystem_HSD17B1,17beta-estradiol17-dehydrogenase[	2,59315E-05	4,5858E-05	4,15269E-05
K01500_ko00791_Atrazinedegradation_Humandiseases_Xenobioticsbiodegradationandmetabolism_E3.5.4.-,[EC:3.5.4.-]	0,00028006	0,000366864	0,000282383
K00884_ko00520_Aminosugarandnucleotidesugarmetabolism_Metabolism_Carbohydratemetabolism_NAGK,nagK,N-acetylglucosaminekinase[EC:2.7.1.59]	6,22355E-05	5,09533E-05	4,98322E-05
K02190_ko00830_Retinolmetabolism_Metabolismofcofactorsandvitamins_cbiK,sirohydrochlorincobaltochelatase[EC:4.99.1.3]	0,000290432	0,000402531	0,000257467
K01682_ko00020_Citratecycle(TCAcycle)_Metabolism_Carbohydratemetabolism_acnB,aconitatehydratase2/2-methylisocitratedehydratase[EC:4.2.1.34.2.1.99];K01682_ko00630_Glyoxylateanddicarboxylatemetabolism_Metabolism_Carbohydratemetabolism_acnI	0	2,54767E-05	0
K00008_ko00051_Fructoseandmannosemetabolism_Metabolism_Carbohydratemetabolism_SORD,gutB,L-iditol2-dehydrogenase[EC:1.1.1.14];K00008_ko00040_Pentoseandglucuronateinterconversions_Metabolism_Carbohydratemetabolism_SORD,gutB,L-iditol2-r	0,000497884	0,000417817	0,00068104
K10547_ko02010_Ctransporters_Environmentalinformationprocessing_Membranetransport_ABC.GGU.P,gguB,putativemultiplesugartransportsystempermeaseprotein	0,000108912	3,56673E-05	4,15269E-05
K01998_ko02010_Ctransporters_Environmentalinformationprocessing_Membranetransport_livM,branched-chainaminoacidtransportsystempermeaseprotein	0,000985395	0,001961703	0,002109564
K00132_ko00630_Glyoxylateanddicarboxylatemetabolism_Metabolism_Carbohydratemetabolism_E1.2.1.10,acetaldehydedehydrogenase(acetylating)(EC:1.2.1.10];K00132_ko00620_Pyruvatemetabolism_Metabolism_Carbohydratemetabolism_E1.2.1.10,acetaldel	8,8167E-05	4,5858E-05	7,47483E-05
K01505_ko00630_Glyoxylateanddicarboxylatemetabolism_Metabolism_Carbohydratemetabolism_E3.5.99.7,1-aminocyclopropane-1-carboxylatedeaminase[EC:3.5.99.7]	5,18629E-06	2,54767E-05	8,30537E-06
K02454_ko02010_Ctransporters_Environmentalinformationprocessing_Membranetransport_gspE,generalsecretionpathwayproteinE	8,29807E-05	3,0572E-05	5,81376E-05
K13015_ko00520_Aminosugarandnucleotidesugarmetabolism_Metabolism_Carbohydratemetabolism_wbpA,UDP-N-acetyl-D-glucosaminedehydrogenase[EC:1.1.1.136]	6,22355E-05	0,000107002	7,47483E-05
K01889_ko00970_Aminoacyl-tRNAbiosynthesis_Geneticinformationandprocessing_Transcription_FARSA,pheS,phenylalanyl-tRNAsynthetasealphachain[EC:6.1.1.20]	0,001410671	0,001365549	0,001719212
K07799_ko02020_Two-componentsystem_Environmentalinformationprocessing_Signaltrasduction_mdtA,putativemultidrugeffluxtransporterMdtA	0,000217824	0,000377055	0,000357131
K13925_ko05100_Bacterialinvasionofepithelialcells_Humandiseases_Infectiousdiseases_pfbA,plasminandfibronectin-bindingproteinA	2,07452E-05	2,03813E-05	2,49161E-05
K10546_ko02010_Ctransporters_Environmentalinformationprocessing_Membranetransport_ABC.GGU.S,chvE,putativemultiplesugartransportsystemsubstrate-bindingprotein	0,000155589	6,1144E-05	6,6443E-05
K01933_ko00230_Purinemetabolism_Metabolism_Nucleotidemetabolism_purM,phosphoribosylformylglycinamidinecyclo-ligase[EC:6.3.3.1]	0,001006141	0,000769395	0,0007724
K02013_ko02010_Ctransporters_Environmentalinformationprocessing_Membranetransport_ABC.FEV.A,ironcomplextransportersystemATP-bindingprotein[EC:3.6.3.34]	0,000892042	0,00091716	0,001154447
K00027_ko02020_Two-componentsystem_Environmentalinformationprocessing_Signaltrasduction_E1.1.1.38,sfcA,maeA,malatedehydrogenase(oxaloacetate-decarboxylating)[EC:1.1.1.38];K00027_ko00620_Pyruvatemetabolism_Metabolism_Carbohydratemetabo	0,000591237	0,000473866	0,000490017
K00929_ko00630_Glyoxylateanddicarboxylatemetabolism_Metabolism_Carbohydratemetabolism_E2.7.2.7,buk,butyratekinase[EC:2.7.2.7]	0,000394158	0,000555391	0,000274077
K01999_ko02010_Ctransporters_Environmentalinformationprocessing_Membranetransport_livK,branched-chainaminoacidtransportsystemsubstrate-bindingprotein	0,00068459	0,000397436	0,000614598
K01726_ko00630_Glyoxylateanddicarboxylatemetabolism_Metabolism_Carbohydratemetabolism_E4.2.1.-,[EC:4.2.1.-];K01726_ko00903_Limoneneandpinenedegradation_Metabolism_Metabolismofterpenoidsandpolyketides_E4.2.1.-,[EC:4.2.1.-];K01726_ko0036	0,001317318	0,001131164	0,001353776
K13040_ko02020_Two-componentsystem_Environmentalinformationprocessing_Signaltrasduction_ttrS,two-componentsystem,LuxRfamily,sensorhistidinekinaseTtrS[EC:2.7.13.3]	1,03726E-05	3,0572E-05	2,49161E-05
K11640_ko02020_Two-componentsystem_Environmentalinformationprocessing_Signaltrasduction_natK,two-componentsystem,LytTfamily,sensorhistidinekinaseNatK[EC:2.7.13.3]	3,6304E-05	1,01907E-05	3,32215E-05
K00384_ko00450_Selenocompoundmetabolism_Metabolism_Metabolismofotheraminoacids_trxB,thioredoxinreductase(NADPH)[EC:1.8.1.9];K00384_ko00240_Pyrimidinemetabolism_Metabolism_Nucleotidemetabolism_trxB,thioredoxinreductase(NADPH)[EC:1.8	0,000928346	0,001100592	0,001619548
K13815_ko02020_Two-componentsystem_Environmentalinformationprocessing_Signaltrasduction_rpfG,two-componentsystem,responseregulatorRpfG	3,6304E-05	4,5858E-05	0,00010797
K01956_ko00250_Alanine,aspartateandglutamatemetabolism_Metabolism_Aminoacidmetabolism_carA,CPA1,carbamoyl-phosphatesynthasesmallsubunit[EC:6.3.5.5];K01956_ko00240_Pyrimidinemetabolism_Metabolism_Nucleotidemetabolism_carA,CPA1,carbar	0,001052817	0,001263643	0,000980034
K00082_ko00740_Riboflavinmetabolism_Metabolism_Metabolismofcofactorsandvitamins_ribD2,5-amino-6-(5-phosphoribosylamino)uracilreductase[EC:1.1.1.193]	3,6304E-05	3,0572E-05	4,98322E-05
K00048_ko00630_Glyoxylateanddicarboxylatemetabolism_Metabolism_Carbohydratemetabolism_fucO,lactaldehydereductase[EC:1.1.1.77];K00048_ko00630_Glyoxylateanddicarboxylatemetabolism_Metabolism_Carbohydratemetabolism_fucO,lactaldehydereduc	0,000466766	0,000315911	0,000274077
K14571_ko03008_Ribosomebiogenesisineukaryotes_GeneticinformationProcessing_Transcription_RIX7,NVL,ribosomebiogenesisATPase	7,77944E-05	6,62393E-05	5,81376E-05
K00057_ko00564_Glycerophospholipidmetabolism_Metabolism_Lipidmetabolism_gpsA,glycerol-3-phosphatedehydrogenase(NAD(P)+)[EC:1.1.1.94]	0,000840179	0,001029257	0,000764094
K08068_ko00520_Aminosugarandnucleotidesugarmetabolism_Metabolism_Carbohydratemetabolism_siaA,neuC1,UDP-N-acetylglucosamine2-epimerase(hydrolysing)[EC:3.2.1.183]	0	1,5286E-05	1,66107E-05
K02010_ko02010_Ctransporters_Environmentalinformationprocessing_Membranetransport_afuC,fbpC,iron(III)transportersystemATP-bindingprotein[EC:3.6.3.30]	0,000285246	0,000336292	0,000240856
K00036_ko05230_Centralcarbonmetabolismincancer_HumanDiseases_Cancers_G6PD,zwf,glucose-6-phosphate1-dehydrogenase[EC:1.1.1.49];K00036_ko00030_Pentosephosphatepathway_Metabolism_Carbohydratemetabolism_G6PD,zwf,glucose-6-phosphate1-d	0,000119285	0,000275148	0,000116275
K00303_ko00260_Glycine,serineandthreoninemetabolism_Metabolism_Aminoacidmetabolism_soxB,sarcosineoxidase,subunitbeta[EC:1.5.3.1]	7,77944E-05	5,09533E-06	2,49161E-05
K01796_ko04146_Peroxisome_CellularProcesses_Transportandcatabolism_E5.1.99.4,AMACR,mcr,alpha-methylacyl-CoAracemase[EC:5.1.99.4];K01796_ko00120_Primarybileacidbiosynthesis_Metabolism_Lipidmetabolism_E5.1.99.4,AMACR,mcr,alpha-methylacyl-C	1,03726E-05	3,56673E-05	4,15269E-05
K00364_ko00230_Purinemetabolism_Metabolism_Nucleotidemetabolism_E1.7.1.7,guaC,GMPreductase[EC:1.7.1.7]	0,000119285	5,60487E-05	8,30537E-06
K10536_ko00330_Arginineandprolinemetabolism_Metabolism_Aminoacidmetabolism_E3.5.3.12,agmatinedeiminase[EC:3.5.3.12]	0,000482325	0,000692965	0,000473406
K00043_ko00630_Glyoxylateanddicarboxylatemetabolism_Metabolism_Carbohydratemetabolism_gbd,4-hydroxybutyratedehydrogenase[EC:1.1.1.61];K00043_ko01200_Carbonmetabolism_Metabolism_Overview_gbd,4-hydroxybutyratedehydrogenase[EC:1.1.1.6	5,70492E-05	0,000107002	1,66107E-05
K01921_ko01005_Lipopolysaccharidebiosynthesisproteins_Metabolism_Glycanbiosynthesisandmetabolism_ddl,D-alanine-D-alanineligase[EC:6.3.2.4];K01921_ko00473_D-Alaninemetabolism_Metabolism_Metabolismofotheraminoacids_ddl,D-alanine-D-alanineliga	0,001182474	0,001436884	0,001752433
K00134_ko04066_HIF-1signalingpathway_Environmentalinformationprocessing_Signaltrasduction_GAPDH,gapA,glyceraldehyde3-phosphatedehydrogenase[EC:1.2.1.12];K00134_ko05010_Alzheimer'sdisease_HumanDiseases_Degenerativediseases_GAPDH,gapA,gl	0,002691685	0,001997371	0,001827182
K03195_ko02010_Ctransporters_Environmentalinformationprocessing_Membranetransport_virB10,lvhB10,typeIVsecretionsystemproteinVirB10	4,66766E-05	8,15253E-05	9,96645E-05
K01624_ko00051_Fructoseandmannosemetabolism_Metabolism_Carbohydratemetabolism_FBA,fbaA,fructose-bisphosphatealdolase,classII[EC:4.1.2.13];K01624_ko00010_Glycolysis/Gluconeogenesis_Metabolism_Carbohydratemetabolism_FBA,fbaA,fructose-bisp	0,002432371	0,001747699	0,001187668
K01785_ko00052_Galactosemetabolism_Metabolism_Carbohydratemetabolism_galM,GALM,aldose1-epimerase[EC:5.1.3.3];K01785_ko00010_Glycolysis/Gluconeogenesis_Metabolism_Carbohydratemetabolism_galM,GALM,aldose1-epimerase[EC:5.1.3.3]	0,001436603	0,00137574	0,001303943
K00380_ko00920_Sulfurmetabolism_Metabolism_Energymetabolism_cysJ,sulfitereductase(NADPH)flavoproteinalpha-component[EC:1.8.1.2]	9,33532E-05	0,000127383	6,6443E-05
K14260_ko00250_Alanine,aspartateandglutamatemetabolism_Metabolism_Aminoacidmetabolism_alaA,alanine-synthesizingtransaminase[EC:2.6.1.662.6.1.2];K14260_ko00290_Valine,leucineandisoleucinebiosynthesis_Metabolism_Aminoacidmetabolism_alaA,ala	0,000746826	0,000234385	0,000514933
K00116_ko00020_Citratecycle(TCAcycle)_Metabolism_Carbohydratemetabolism_mqo,malatedehydrogenase(quinone)[EC:1.1.5.4];K00116_ko00620_Pyruvatemetabolism_Metabolism_Carbohydratemetabolism_mqo,malatedehydrogenase(quinone)[EC:1.1.5.4];K0	1,55589E-05	1,5286E-05	4,98322E-05
K00860_ko00920_Sulfurmetabolism_Metabolism_Energymetabolism_cysC,adenylylsulfatekinase[EC:2.7.1.25];K00860_ko00230_Purinemetabolism_Metabolism_Nucleotidemetabolism_cysC,adenylylsulfatekinase[EC:2.7.1.25]	7,77944E-05	0,000112097	4,98322E-05
K13607_ko00960_Tropane,piperidineandpyridinealkaloidbiosynthesis_Metabolism_Biosynthesisofothersecondarymetabolites_fldA,cinnamoyl-CoA:phenyllactateCoA-transferase[EC:2.8.3.17]	0,000134844	2,54767E-05	6,6443E-05

K00099_ko00900_Terpenoidbackbonebiosynthesis_Metabolism_Metabolismofterpenoidsandpolyketides_dxr,1-deoxy-D-xylulose-5-phosphatereductoisomerase[EC:1.1.1.267]	0,000897228	0,000932446	0,000647819
K12506_ko00900_Terpenoidbackbonebiosynthesis_Metabolism_Metabolismofterpenoidsandpolyketides_ispDF,2-C-methyl-D-erythritol4-phosphatecytidylyltransferase/2-C-methyl-D-erythritol2,4-cyclodiphosphatesynthase[EC:2.7.7.604.6.1.12]	6,74218E-05	7,13347E-05	0,000116275
K13498_ko00400_Phenylalanine,tyrosineandtryptophanbiosynthesis_Metabolism_Aminoacidmetabolism_trpCF,indole-3-glycerolphosphatesynthase/phosphoribosylanthranilateisomerase[EC:4.1.1.485.3.1.24];K13498_ko01230_BiosynthesisofaminoacidsMetabol	2,59315E-05	1,01907E-05	0
K02563_ko04112_Cellcycle-Caulobacter_CellularProcesses_Cellgrowthanddeath_murG,UDP-N-acetylglucosamine--N-acetylmuramyl-(pentapeptide)pyrophosphoryl-undecaprenolN-acetylglucosaminetransferase[EC:2.4.1.227];K02563_ko01005_Lipopolysaccharide	0,000938719	0,00122288	0,001079698
K00112_ko00564_Glycerophospholipidmetabolism_Metabolism_Lipidmetabolism_glpB,glycerol-3-phosphatedehydrogenasesubunitB[EC:1.1.5.3]	4,66766E-05	1,5286E-05	1,66107E-05
K07404_ko00030_Pentosephosphatepathway_Metabolism_Carbohydratemetabolism_pgl,6-phosphogluconolactonase[EC:3.1.1.31];K07404_ko01200_Carbonmetabolism_Metabolism_Overview_pgl,6-phosphogluconolactonase[EC:3.1.1.31]	0,000233383	0,000239481	0,000199329
K02491_ko02020_Two-componentsystem_Environmentalinformationprocessing_Signaltrasduction_kinA,two-componentsystem,sporulationsensorkinaseA[EC:2.7.13.3]	5,18629E-06	0	2,49161E-05
K10715_ko02020_Two-componentsystem_Environmentalinformationprocessing_Signaltrasduction_rpfC,two-componentsystem,sensorhistidinekinaseRpfC[EC:2.7.13.3]	2,07452E-05	1,01907E-05	0
K00002_ko00010_Glycolysis/Gluconeogenesis_Metabolism_Carbohydratemetabolism_AKR1A1,adh,alcoholdehydrogenase(NADP+)[EC:1.1.1.2];K00002_ko00040_PentoseandglucuronateinterconversionsMetabolism_Carbohydratemetabolism_AKR1A1,adh,alcoho	8,29807E-05	5,60487E-05	4,15269E-05
K13529_ko03410_Baseexcisionrepair_GeneticinformationProcessing_ReplicationandRepair_ada-alkA,AraCfamilytranscriptionalregulator,regulatoryproteinofadaptativeresponse/DNA-3-methyladenineglycosylaseII[EC:3.2.2.21]	2,59315E-05	2,54767E-05	0
K01613_ko00564_Glycerophospholipidmetabolism_Metabolism_Lipidmetabolism_psd,PISD,phosphatidylserinedecarboxylase[EC:4.1.1.65]	0,000383786	0,00045858	0,00044849
K01684_ko00052_Galactosemetabolism_Metabolism_Carbohydratemetabolism_dgoD,galactonatedehydratase[EC:4.2.1.6]	0,000145216	8,15253E-05	0,000207634
K00164_ko00310_Lysinedegradation_Metabolism_Aminoacidmetabolism_OGDH,sucA,2-oxoglutaratedehydrogenaseE1component[EC:1.2.4.2];K00164_ko00380_Tryptophanmetabolism_Metabolism_Aminoacidmetabolism_OGDH,sucA,2-oxoglutaratedehydrogena	2,59315E-05	1,5286E-05	1,66107E-05
K00826_ko00290_Valine,leucineandisoleucinebiosynthesis_Metabolism_Aminoacidmetabolism_E2.6.1.42,ilvE,branched-chainaminoacidaminotransferase[EC:2.6.1.42];K00826_ko00280_Valine,leucineandisoleucinedegradation_Metabolism_Aminoacidmetabolism	0,001234337	0,000799967	0,00089698
K00145_ko00330_Arginineandprolinemetabolism_Metabolism_Aminoacidmetabolism_argC,N-acetyl-gamma-glutamyl-phosphatereductase[EC:1.2.1.38];K00145_ko01210_Oxocarboxylicacidmetabolism_Metabolism_Overview_argC,N-acetyl-gamma-glutamyl-pho	0,000560119	0,000514629	0,000373742
K07250_ko00250_Alanine,aspartateandglutamatemetabolism_Metabolism_Aminoacidmetabolism_gabT,4-aminobutyrateaminotransferase/(S)-3-amino-2-methylpropionatetransaminase[EC:2.6.1.192.6.1.22];K07250_ko00280_Valine,leucineandisoleucinedegrada	4,66766E-05	2,54767E-05	1,66107E-05
K03430_ko00440_Phosphonateandphosphinatemetabolism_Metabolism_Metabolismofotheraminoacids_phnW,2-aminoethylphosphonate-pyruvatetransaminase[EC:2.6.1.37]	7,26081E-05	0,000101907	0,000132886
K01711_ko00520_Aminosugarandnucleotidesugarmetabolism_Metabolism_Carbohydratemetabolism_gmd,GMDS,GDPmannose4,6-dehydratase[EC:4.2.1.47];K01711_ko00051_Fructoseandmannosemetabolism_Metabolism_Carbohydratemetabolism_gmd,GMDS,	0,001052817	0,001166831	0,000838843
K00259_ko00250_Alanine,aspartateandglutamatemetabolism_Metabolism_Aminoacidmetabolism_ald,alaninedehydrogenase[EC:1.4.1.1];K00259_ko00430_Taurineandhypotaurinemetabolism_Metabolism_Metabolismofotheraminoacids_ald,alaninedehydrogena	0,000497884	0,000346483	0,000406963
K00133_ko00270_Cysteineandmethionninemetabolism_Metabolism_Aminoacidmetabolism_asd,aspartate-semialdehydedehydrogenase[EC:1.2.1.11];K00133_ko00260_Glycine,serineandthreoninemetabolism_Metabolism_Aminoacidmetabolism_asd,aspartate-ser	0,000954278	0,001054734	0,000921896
K13747_ko00330_Arginineandprolinemetabolism_Metabolism_Aminoacidmetabolism_nspC,carboxynorspermidinedecarboxylase[EC:4.1.1.96]	0,000430462	0,000351578	0,00023255
K08478_ko02020_Two-componentsystem_Environmentalinformationprocessing_Signaltrasduction_pgtC,phosphoglyceratetransportregulatoryproteinPgtC	8,29807E-05	8,15253E-05	0,000132886
K08325_ko00630_Glyoxylateanddicarboxylatemetabolism_Metabolism_Carbohydratemetabolism_yqhD,NADP-dependentalcoholdehydrogenase[EC:1.1.-.-]	3,11177E-05	7,643E-05	0,000174413
K04103_ko00380_Tryptophanmetabolism_Metabolism_Aminoacidmetabolism_E4.1.1.74,ipdC,indolepyruvatedecarboxylase[EC:4.1.1.74]	5,18629E-06	0	3,32215E-05
K01259_ko00330_Arginineandprolinemetabolism_Metabolism_Aminoacidmetabolism_pip,prolineiminopeptidase[EC:3.4.11.5]	5,18629E-05	0,000132479	0,000191024
K00818_ko00330_Arginineandprolinemetabolism_Metabolism_Aminoacidmetabolism_E2.6.1.11,argD,acetylornithineaminotransferase[EC:2.6.1.11];K00818_ko01210_Oxocarboxylicacidmetabolism_Metabolism_Overview_E2.6.1.11,argD,acetylornithineaminotrar	0,000414903	0,000478961	0,000465101
K03271_ko00540_Lipopolysaccharidebiosynthesis_Metabolism_Glycanbiosynthesisandmetabolism_gmhA,lpcA,D-sedoheptulose7-phosphateisomerase[EC:5.3.1.28]	0,000186706	0,00015286	0,000373742
K00847_ko00520_Aminosugarandnucleotidesugarmetabolism_Metabolism_Carbohydratemetabolism_E2.7.1.4,scrK,fructokinase[EC:2.7.1.4];K00847_ko00051_Fructoseandmannosemetabolism_Metabolism_Carbohydratemetabolism_E2.7.1.4,scrK,fructokinase[EC	0,000731267	0,001182117	0,000838843
K07796_ko02020_Two-componentsystem_Environmentalinformationprocessing_Signaltrasduction_cusC,silC,Cu(I)/Ag(I)effluxsystemoutermembraneproteinCusC/SilC	0,00014003	0,000203813	0,000274077
K11688_ko02020_Two-componentsystem_Environmentalinformationprocessing_Signaltrasduction_dctP,C4-dicarboxylate-bindingproteinDctP	0,001021699	0,000692965	0,000863759
K00640_ko00270_Cysteineandmethioninemetabolism_Metabolism_Aminoacidmetabolism_cysE,serineO-acetyltransferase[EC:2.3.1.30];K00640_ko00920_Sulfurmetabolism_Metabolism_Energymetabolism_cysE,serineO-acetyltransferase[EC:2.3.1.30];K00640_koC	0,000933532	0,00145217	0,001295638
K13787_ko00900_Terpenoidbackbonebiosynthesis_Metabolism_Metabolismofterpenoidsandpolyketides_idsA,geranylgeranyldiphosphatesynthase,typeI[EC:2.5.1.12.5.1.102.5.1.29]	2,07452E-05	6,1144E-05	2,49161E-05
K04785_ko01053_Biosynthesisofsiderophoregroupnonribosomalpeptides_Metabolism_Metabolismofterpenoidsandpolyketides_irp3,ybtU,yersiniabactinsynthetase,thiazolinylreductasecomponent	0	1,01907E-05	1,66107E-05
K01736_ko00400_Phenylalanine,tyrosineandtryptophanbiosynthesis_Metabolism_Aminoacidmetabolism_aroC,chorismatesynthase[EC:4.2.3.5];K01736_ko01230_BiosynthesisofaminoacidsMetabolism_Overview_aroC,chorismatesynthase[EC:4.2.3.5]	0,000539374	0,000647107	0,000531544
K02036_ko02010_Ctransporters_Environmentalinformationprocessing_Membranetransport_pstB,phosphatetransportsystemATP-bindingprotein[EC:3.6.3.27]	0,000492698	0,000509533	0,000564765
K13985_ko04723_Retrogradeendocannabinoidsignaling_Environmentalinformationprocessing_Signaltransduction_NAPEPLD,N-acyl-phosphatidylethanolamine-hydrolysingphospholipaseD[EC:3.1.4.54]	4,14903E-05	9,68113E-05	0,000157802
K03382_ko00791_Atrazinedegradation_Humandiseases_Xenobioticsbiodegradationandmetabolism_atzB,hydroxyatrazineethylaminohydrolase[EC:3.5.99.3]	4,66766E-05	4,07627E-05	4,98322E-05
K00575_ko02020_Two-componentsystem_Environmentalinformationprocessing_Signaltrasduction_cheR,chemotaxisproteinmethyltransferaseCheR[EC:2.1.1.80];K00575_ko02030_Bacterialchemotaxis_Organismalsystem_Cellmobility_cheR,chemotaxisproteinmetl	0,000145216	5,60487E-05	9,13591E-05
K03524_ko00780_Biotinmetabolism_Metabolism_Metabolismofcofactorsandvitamins_birA,BirAfamilytranscriptionalregulator,biotinoperonrepressor/biotin-[acetyl-CoA-carboxylase]ligase[EC:6.3.4.15]	0,000466766	0,00045858	0,000531544
K13280_ko04120_Ubiquitinmediatedproteolysis_GeneticInformationProcessing_Folding,sortinganddegradation_SEC11,sipW,signalpeptidase,endoplasmicreticulum-type[EC:3.4.-.-]	0,000689777	0,000738823	0,000971729
K02401_ko02040_Flagellarassembly_Organismalsystem_Cellmobility_flhB,flagellarbiosyntheticproteinFlhB	0,000186706	0,000122288	4,98322E-05
K04517_ko00400_Phenylalanine,tyrosineandtryptophanbiosynthesis_Metabolism_Aminoacidmetabolism_tyrA2,prephenatedehydrogenase[EC:1.3.1.12];K04517_ko00401_Novobiocinbiosynthesis_Metabolism_Biosynthesisofothersecondarymetabolites_tyrA2,prep	0,000285246	0,000203813	0,000274077
K00249_ko00280_Valine,leucineandisoleucinedegradation_Metabolism_Aminoacidmetabolism_ACADM,acd,acyl-CoAdehydrogenase[EC:1.3.8.7];K00249_ko00630_Glyoxylateanddicarboxylatemetabolism_Metabolism_Carbohydratemetabolism_ACADM,acd,acyl-C	7,26081E-05	2,54767E-05	9,13591E-05
K13017_ko00520_Aminosugarandnucleotidesugarmetabolism_Metabolism_Carbohydratemetabolism_wbpE,wlbC,UDP-2-acetamido-2-deoxy-ribo-hexuluronateaminotransferase[EC:2.6.1.98]	0,000103726	0,000101907	0,000166107
K00748_ko00540_Lipopolysaccharidebiosynthesis_Metabolism_Glycanbiosynthesisandmetabolism_lpxB,lipid-A-disaccharidesynthase[EC:2.4.1.182]	0,000331923	0,000443294	0,000332215
K02108_ko00190_Oxidativephosphorylation_Metabolism_Energymetabolism_ATPF0A,atpB,F-typeH+-transportingATPasesubunita;K02108_ko00195_Photosynthesis_Metabolism_Energymetabolism_ATPF0A,atpB,F-typeH+-transportingATPasesubunita	0,00068459	0,00068787	0,000838843
K00946_ko00730_Thiaminemetabolism_Metabolism_Metabolismofcofactorsandvitamins_thiL,thiamine-monophosphatekinase[EC:2.7.4.16]	0,000352668	0,000361769	0,000406963
K07645_ko02020_Two-componentsystem_Environmentalinformationprocessing_Signaltrasduction_qseC,two-componentsystem,OmpRfamily,sensorhistidinekinaseQseC[EC:2.7.13.3]	2,59315E-05	2,03813E-05	0
K02849_ko00540_Lipopolysaccharidebiosynthesis_Metabolism_Glycanbiosynthesisandmetabolism_waaQ,rfaQ,heptosyltransferaseIII[EC:2.4.-.-]	4,14903E-05	2,03813E-05	3,32215E-05
K01564_ko00791_Atrazinedegradation_Humandiseases_Xenobioticsbiodegradationandmetabolism_E3.8.1.-,[EC:3.8.1.-];K01564_ko00625_Chloroalkaneandchloroalkenedegradation_Metabolism_Xenobioticsbiodegradationandmetabolism_E3.8.1.-,[EC:3.8.1.-]	0,000103726	0,000132479	4,98322E-05
K02492_ko00830_Retinolmetabolism_Metabolism_Metabolismofcofactorsandvitamins_hemA,glutamyl-tRNAreductase[EC:1.2.1.70]	0,000165961	0,00038215	0,000373742
K03462_ko00760_Nicotinateandnicotinamidemetabolism_Metabolism_Metabolismofcofactorsandvitamins_NAMPT,nicotinamidephosphoribosyltransferase[EC:2.4.2.12]	4,14903E-05	4,07627E-05	2,49161E-05
K00009_ko00051_Fructoseandmannosemetabolism_Metabolism_Carbohydratemetabolism_mtlD,mannitol-1-phosphate5-dehydrogenase[EC:1.1.1.17]	7,26081E-05	8,15253E-05	0,000116275
K00459_ko00910_Nitrogenmetabolism_Metabolism_Energymetabolism_ncd2,npd,nitronatemonooxygenase[EC:1.13.12.16]	0,000285246	0,000270053	0,000498322
K03856_ko00400_Phenylalanine,tyrosineandtryptophanbiosynthesis_Metabolism_Aminoacidmetabolism_AROA2,aroA,3-deoxy-7-phosphoheptulonatesynthase[EC:2.5.1.54];K03856_ko01230_Biosynthesisofaminoacids_Metabolism_Overview_AROA2,aroA,3-deoxy	0,000337109	0,000428008	0,000207634
K05816_ko02010_Ctransporters_Environmentalinformationprocessing_Membranetransport_ugpC,sn-glycerol3-phosphatetransportsystemATP-bindingprotein[EC:3.6.3.20]	5,18629E-05	1,01907E-05	5,81376E-05
K04566_ko00970_Aminoacyl-tRNAbiosynthesis_Geneticinformationandprocessing_Transcription_lysK,lysyl-tRNAsynthetase,classI[EC:6.1.1.6]	3,6304E-05	4,07627E-05	4,15269E-05
K03831_ko04122_Sulfurrelaysystem_GeneticInformationProcessing_Folding,sortinganddegradation_mogA,molybdopterinadenylyltransferase[EC:2.7.7.75]	3,11177E-05	5,60487E-05	7,47483E-05
K03280_ko00540_Lipopolysaccharidebiosynthesis_Metabolism_Glycanbiosynthesisandmetabolism_waaK,rfaK,UDP-N-acetylglucosamine:(glucosyl)LPSalpha-1,2-N-acetylglucosaminyltransferase[EC:2.4.1.56]	3,11177E-05	1,5286E-05	8,30537E-05
K01039_ko00630_Glyoxylateanddicarboxylatemetabolism_Metabolism_Carbohydratemetabolism_gctA,glutaconateCoA-transferase,subunitA[EC:2.8.3.12];K01039_ko00643_Styrenedegradation_Metabolism_Xenobioticsbiodegradationandmetabolism_gctA,glutac	7,77944E-05	5,60487E-05	2,49161E-05
K03390_ko01200_Carbonmetabolism_Metabolism_Overview_hdrC,heterodisulfidereductasesubunitC[EC:1.8.98.1];K03390_ko00194_Photosynthesisproteins_Metabolism_Energymetabolism_hdrC,heterodisulfidereductasesubunitC[EC:1.8.98.1]	7,26081E-05	5,60487E-05	4,15269E-05
K02341_ko03030_DNAreplication_GeneticinformationProcessing_ReplicationandRepair_DPO3D2,holB,DNApolymeraseIIIsubunitdelta'[EC:2.7.7.7];K02341_ko03440_Homologousrecombination_GeneticinformationProcessing_ReplicationandRepair_DPO3D2,holB,D	0,000803875	0,001064925	0,000930202
K00721_ko00513_Variousty pesofN-glycanbiosynthesis_Metabolism_Glycanbiosynthesisandmetabolism_DPM1,dolichol-phosphatemannosyltransferase[EC:2.4.1.83]	0,001727035	0,001472551	0,001544799
K00086_ko00630_Glyoxylateanddicarboxylatemetabolism_Metabolism_Carbohydratemetabolism_dhaT,1,3-propanedioldehydrogenase[EC:1.1.1.202];K00086_ko00561_Glycerolipidmetabolism_Metabolism_Lipidmetabolism_dhaT,1,3-propanedioldehydrogenase[	0,000114098	8,15253E-05	0,000149497
K02188_ko00830_Retinolmetabolism_Metabolism_Metabolismofcofactorsandvitamins_cbiD,cobalt-precorrin-5B(C1)-methyltransferase[EC:2.1.1.195]	0,000191893	0,000331197	0,000274077
K00931_ko00330_Arginineandprolinemetabolism_Metabolism_Aminoacidmetabolism_proB,glutamate5-kinase[EC:2.7.2.11];K00931_ko00332_Carbapenembiosynthesis_Metabolism_Biosynthesisofothersecondarymetabolites_proB,glutamate5-kinase[EC:2.7.2.11]	0,000435648	0,000489152	0,000332215
K01626_ko00400_Phenylalanine,tyrosineandtryptophanbiosynthesis_Metabolism_Aminoacidmetabolism_E2.5.1.54,aroF,aroG,aroH,3-deoxy-7-phosphoheptulonatesynthase[EC:2.5.1.54];K01626_ko01230_BiosynthesisofaminoacidsMetabolism_Overview_E2.5.1.5	0,000466766	0,000264957	0,000307299
K00215_ko00300_Lysinebiosynthesis_Metabolism_Aminoacidmetabolism_dapB,4-hydroxy-tetrahydrodipicolinatereductase[EC:1.17.1.8];K00215_ko01230_Biosynthesisofaminoacids_Metabolism_Overview_dapB,4-hydroxy-tetrahydrodipicolinatereductase[EC:1.17	0,000715708	0,000820349	0,000805621
K01046_ko00561_Glycerolipidmetabolism_Metabolism_Lipidmetabolism_E3.1.1.3,triacylglycerollipase[EC:3.1.1.3]	0,000171148	0,000142669	0,000166107
K00261_ko00250_Alanine,aspartateandglutamatemetabolism_Metabolism_Aminoacidmetabolism_GLUD1_2,gdhA,glutamatedehydrogenase(NAD(P)+)[EC:1.4.1.3];K00261_ko00330_Arginineandprolinemetabolism_Metabolism_Aminoacidmetabolism_GLUD1_2,g	0,000715708	0,00015286	0,000290688

K02770_ko02010_Ctransporters_Environmentalinformationprocessing_Membranetransport_PTS-Fru-EIIC,fruA,PTSsystem,fructose-specificIICcomponent;K02770_ko00051_Fructoseandmannosemetabolism_Metabolism_Carbohydratemetabolism_PTS-Fru-EIIC,fruA	6,74218E-05	3,0572E-05	4,98322E-05
K02361_ko00130_Ubiquinoneandotherterpenoid-quinonebiosynthesis_Metabolism_Metabolismofcofactorsandvitamins_entC,isochorismatesynthase[EC:5.4.4.2];K02361_ko01053_Biosynthesisofsiderophoregroupnonribosomalpeptides_Metabolism_Metabolismo	0,000108912	0,000101907	0,000199329
K07798_ko02020_Two-componentsystem_Environmentalinformationprocessing_Signaltrasduction_cusB,silB,Cu(I)/Ag(I)effluxsystemmembraneproteinCusB/SilB	0,00018152	0,000132479	0,000456795
K05823_ko00300_Lysinebiosynthesis_Metabolism_Aminoacidmetabolism_E3.5.1.47,N-acetyldiaminopimelatedeacetylase[EC:3.5.1.47];K05823_ko01230_Biosynthesisofaminoacids_Metabolism_Overview_E3.5.1.47,N-acetyldiaminopimelatedeacetylase[EC:3.5.1.4	3,6304E-05	1,01907E-05	8,30537E-06
K01903_ko00020_Citratecycle(TCAcycle)_Metabolism_Carbohydratemetabolism_sucC,succinyl-CoAsynthetasebetasubunit[EC:6.2.1.5];K01903_ko00630_Glyoxylateanddicarboxylatemetabolism_Metabolism_Carbohydratemetabolism_sucC,succinyl-CoAsynthetasel	4,14903E-05	0,000107002	0,000182718
K01846_ko00630_Glyoxylateanddicarboxylatemetabolism_Metabolism_Carbohydratemetabolism_E5.4.99.1,methylaspartatemutase[EC:5.4.99.1]	5,70492E-05	5,60487E-05	5,81376E-05
K02377_ko00520_Aminosugarandnucleotidesugarmetabolism_Metabolism_Carbohydratemetabolism_TSTA3,fcl,GDP-L-fucosesynthase[EC:1.1.1.271];K02377_ko00051_Fructoseandmannosemetabolism_Metabolism_Carbohydratemetabolism_TSTA3,fcl,GDP-L-fuc	0,000793503	0,000682775	0,00068104
K00005_ko00630_Glyoxylateanddicarboxylatemetabolism_Metabolism_Carbohydratemetabolism_gldA,glyceroldehydrogenase[EC:1.1.1.6];K00005_ko00561_Glycerolipidmetabolism_Metabolism_Lipidmetabolism_gldA,glyceroldehydrogenase[EC:1.1.1.6]	0,000176334	0,000122288	0,000149497
K11646_ko00400_Phenylalanine,tyrosineandtryptophanbiosynthesis_Metabolism_Aminoacidmetabolism_K11646,3-dehydroquinatesynthaseII[EC:1.4.1.24]	3,11177E-05	0	1,66107E-05
K01473_ko00330_Arginineandprolinemetabolism_Metabolism_Aminoacidmetabolism_hyuA,N-methylhydantoinaseA[EC:3.5.2.14]	0,000119285	7,13347E-05	9,13591E-05
K02613_ko00360_Phenylalaninemetabolism_Metabolism_Aminoacidmetabolism_paaE,ring-1,2-phenylacetyl-CoAepoxidasesubunitPaaE	2,07452E-05	5,09533E-06	0
K07714_ko02020_Two-componentsystem_Environmentalinformationprocessing_Signaltrasduction_atoC,two-componentsystem,NtrCfamily,responseregulatorAtoC	0,000368227	0,00038215	0,000490017
K01917_ko00480_Glutathionemetabolism_Metabolism_Metabolismofotheraminoacids_E6.3.1.8,glutathionylspermidinesynthase[EC:6.3.1.8]	8,8167E-05	2,54767E-05	7,47483E-05
K01008_ko00450_Selenocompoundmetabolism_Metabolismofotheraminoacids_selD,SEPHS,selenide,waterdikinase[EC:2.7.9.3]	0,000160775	0,000259862	0,000182718
K01772_ko00830_Retinolmetabolism_Metabolism_Metabolismofcofactorsandvitamins_hemH,FECH,ferrochelatase[EC:4.99.1.1]	4,14903E-05	5,09533E-06	3,32215E-05
K09065_ko00330_Arginineandprolinemetabolism_Metabolism_Aminoacidmetabolism_argF,N-acetylornithinecarbamoyltransferase[EC:2.1.3.9]	7,26081E-05	5,60487E-05	4,15269E-05
K01012_ko00780_Biotinmetabolism_Metabolism_Metabolismofcofactorsandvitamins_bioB,biotinsynthase[EC:2.8.1.6]	0,000342295	0,000667489	0,000423574
K02018_ko02010_Ctransporters_Environmentalinformationprocessing_Membranetransport_modB,molybdatetransportsystempermeaseprotein	0,000331923	0,000188527	0,000224245
K03275_ko00540_Lipopolysaccharidebiosynthesis_Metabolism_Glycanbiosynthesisandmetabolism_waaO,rfaI,UDP-glucose:(glucosyl)LPSalpha-1,3-glucosyltransferase[EC:2.4.1.-]	5,70492E-05	7,643E-05	5,81376E-05
K01620_ko00260_Glycine,serineandthreoninemetabolism_Metabolism_Aminoacidmetabolism_ltaE,threoninealdolase[EC:4.1.2.5];K01620_ko01230_Biosynthesisofaminoacids_Metabolism_Overview_ltaE,threoninealdolase[EC:4.1.2.5]	0,000357854	0,000387245	0,000315604
K04516_ko00400_Phenylalanine,tyrosineandtryptophanbiosynthesis_Metabolism_Aminoacidmetabolism_AROA1,aroA,chorismatemutase[EC:5.4.99.5];K04516_ko01230_Biosynthesisofaminoacids_Metabolism_Overview_AROA1,aroA,chorismatemutase[EC:5.4.99.	0,000331923	0,000351578	0,00021594
K03475_ko02010_Ctransporters_Environmentalinformationprocessing_Membranetransport_PTS-Ula-EIIC,ulaA,sgaT,PTSsystem,ascorbate-specificIICcomponent;K03475_ko00052_Galactosemetabolism_Metabolism_Carbohydratemetabolism_PTS-Ula-EIIC,ulaA,sgaT	0,000129657	0,000157955	0,000249161
K03340_ko00300_Lysinebiosynthesis_Metabolism_Aminoacidmetabolism_dapdh,diaminopimelatedehydrogenase[EC:1.4.1.16];K03340_ko01230_Biosynthesisofaminoacids_Metabolism_Overview_dapdh,diaminopimelatedehydrogenase[EC:1.4.1.16]	0,000456394	0,000346483	0,000398658
K05877_ko02020_Two-componentsystem_Environmentalinformationprocessing_Signaltrasduction_tap,methyl-acceptingchemotaxisproteinIV,peptidesensorreceptor;K05877_ko02030_Bacterialchemotaxis_Organismalsystem_Cellmobility_tap,methyl-acceptingch	1,55589E-05	0	1,66107E-05
K00609_ko00250_Alanine,aspartateandglutamatemetabolism_Metabolism_Aminoacidmetabolism_pyrB,PYR2,aspartatecarbamoyltransferasecatalyticsubunit[EC:2.1.3.2];K00609_ko00240_Pyrimidinemetabolism_Metabolism_Nucleotidemetabolism_pyrB,PYR2,as	0,000834993	0,000906969	0,000714262
K01470_ko00330_Arginineandprolinemetabolism_Metabolism_Aminoacidmetabolism_E3.5.2.10,creatinineamidohydrolase[EC:3.5.2.10]	0,000217824	0,000214004	0,000207634
K13020_ko00520_Aminosugarandnucleotidesugarmetabolism_Metabolism_Carbohydratemetabolism_wlbA,bplA,UDP-N-acetyl-2-amino-2-deoxyglucuronatedehydrogenase[EC:1.1.1.335]	0,000606796	0,000947732	0,000888675
K09696_ko02010_Ctransporters_Environmentalinformationprocessing_Membranetransport_natB,sodiumtransportsystempermeaseprotein;K09696_ko02020_Two-componentsystem_Environmentalinformationprocessing_Signaltrasduction_natB,sodiumtransport	6,74218E-05	7,13347E-05	6,6443E-05
K10532_ko04142_Lysosome_CellularProcesses_Transportandcatabolism_HGSNAT,heparan-alpha-glucosaminideN-acetyltransferase[EC:2.3.1.78];K10532_ko00531_Glycosaminoglycandegradation_Metabolism_Glycanbiosynthesisandmetabolism_HGSNAT,heparan-	7,77944E-05	0,000163051	0,00032391
K00494_ko02020_Two-componentsystem_Environmentalinformationprocessing_Signaltrasduction_luxA,alkanalmonooxygenasealphachain[EC:1.14.14.3]	0	2,03813E-05	0
K00912_ko00540_Lipopolysaccharidebiosynthesis_Metabolism_Glycanbiosynthesisandmetabolism_lpxK,tetraacyldisaccharide4'-kinase[EC:2.7.1.130]	0,000186706	0,000295529	0,000298993
K02044_ko02010_Ctransporters_Environmentalinformationprocessing_Membranetransport_phnD,phosphonatetransportsystemsubstrate-bindingprotein	0,000108912	9,68113E-05	7,47483E-05
K02015_ko02010_Ctransporters_Environmentalinformationprocessing_Membranetransport_ABC.FEV.P,ironcomplextransportsystempermeaseprotein	0,001140984	0,001569363	0,001245806
K00696_ko00500_Starchandsucrosemetabolism_Metabolism_Carbohydratemetabolism_E2.4.1.14,sucrose-phosphatesynthase[EC:2.4.1.14]	5,18629E-06	0	0
K03426_ko04146_Peroxisome_CellularProcesses_Transportandcatabolism_E3.6.1.22,NUDT12,nudC,NAD+diphosphatase[EC:3.6.1.22];K03426_ko00760_Nicotinateandnicotinamidemetabolism_Metabolism_Metabolismofcofactorsandvitamins_E3.6.1.22,NUDT12,nu	0,000539374	0,000351578	0,000390352
K01739_ko00270_Cysteineandmethioninemetabolism_Metabolism_Aminoacidmetabolism_metB,cystathioninegamma-synthase[EC:2.5.1.48];K01739_ko00920_Sulfurmetabolism_Metabolism_Energymetabolism_metB,cystathioninegamma-synthase[EC:2.5.1.48];I	5,70492E-05	3,56673E-05	1,66107E-05
K00874_ko00030_Pentosephosphatepathway_Metabolism_Carbohydratemetabolism_kdgK,2-dehydro-3-deoxygluconokinase[EC:2.7.1.45];K00874_ko01200_Carbonmetabolism_Metabolism_Overview_kdgK,2-dehydro-3-deoxygluconokinase[EC:2.7.1.45]	0,000866111	0,001019067	0,00078901
K02967_ko03010_Ribosome_GeneticinformationProcessing_Transcription_RP-S2,MRPS2,rpsB,smallsubunitribosomalproteinS2	0,001732221	0,001472551	0,001436829
K01243_ko00270_Cysteineandmethioninemetabolism_Metabolism_Aminoacidmetabolism_mtnN,mtn,pfs,adenosylhomocysteinenucleosidase[EC:3.2.2.9];K01243_ko01230_Biosynthesisofaminoacids_Metabolism_Overview_mtnN,mtn,pfs,adenosylhomocysteinen	0,000383786	0,000636917	0,000631208
K03894_ko00310_Lysinedegradation_Metabolism_Aminoacidmetabolism_iucA,N2-citryl-N6-acetyl-N6-hydroxylysinesynthase[EC:6.3.2.38]	0	1,01907E-05	0
K01576_ko00627_Aminobenzoatedegradation_Metabolism_Xenobioticsbiodegradationandmetabolism_mdlC,benzoylformatedecarboxylase[EC:4.1.1.7]	0	1,01907E-05	8,30537E-06
K01484_ko00330_Arginineandprolinemetabolism_Metabolism_Aminoacidmetabolism_astB,succinylargininedihydrolase[EC:3.5.3.23]	1,03726E-05	0	0
K08963_ko00270_Cysteineandmethioninemetabolism_Metabolism_Aminoacidmetabolism_mtnA,methylthioribose-1-phosphateisomerase[EC:5.3.1.23]	0,00018152	0,000224195	0,000207634
K00625_ko00630_Glyoxylateanddicarboxylatemetabolism_Metabolism_Carbohydratemetabolism_E2.3.1.8,pta,phosphateacetyltransferase[EC:2.3.1.8];K00625_ko00620_Pyruvatemetabolism_Metabolism_Carbohydratemetabolism_E2.3.1.8,pta,phosphateacetyltr	0,000933532	0,000866207	0,000539849
K02071_ko02010_Ctransporters_Environmentalinformationprocessing_Membranetransport_metN,D-methioninetransportsystemATP-bindingprotein	0,000430462	0,000341387	0,000465101
K01246_ko03410_Baseexcisionrepair_GeneticinformationProcessing_ReplicationandRepair_tag,DNA-3-methyladenineglycosylase[EC:3.2.2.20]	0,000347482	0,000254767	0,000348826
K01607_ko01220_Degradationofaromaticcompounds_Metabolism_Overview_pcaC,4-carboxymuconolactonedecarboxylase[EC:4.1.1.44];K01607_ko00362_Benzoatedegradation_Metabolism_Xenobioticsbiodegradationandmetabolism_pcaC,4-carboxymuconolacto	0,001151357	0,001187213	0,000747483
K00784_ko03013_RNAtransport_GeneticinformationProcessing_Transcription_rnz,ribonucleaseZ[EC:3.1.26.11]	0,001166916	0,001365549	0,00122089
K01918_ko00770_PantothenateandCoAbiosynthesis_Metabolism_Metabolismofcofactorsandvitamins_panC,pantoate--beta-alanineligase[EC:6.3.2.1];K01918_ko00410_beta-Alaninemetabolism_Metabolism_Metabolismofotheraminoacids_panC,pantoate--beta-al	0,000477139	0,000356673	0,000307299
K01856_ko01220_Degradationofaromaticcompounds_Metabolism_Overview_catB,muconatecycloisomerase[EC:5.5.1.1];K01856_ko00362_Benzoatedegradation_Metabolism_Xenobioticsbiodegradationandmetabolism_catB,muconatecycloisomerase[EC:5.5.1.1];K	0,000114098	0,000259862	0,000141191
K00757_ko00240_Pyrimidinemetabolism_Metabolism_Nucleotidemetabolism_udp,UPP,uridinephosphorylase[EC:2.4.2.3];K00757_ko00983_Drugmetabolism-otherenzymes_Metabolism_Xenobioticsbiodegradationandmetabolism_udp,UPP,uridinephosphorylase[I	0,000580865	0,000489152	0,000456795
K02227_ko00830_Retinolmetabolism_Metabolism_Metabolismofcofactorsandvitamins_cbiB,cobD,adenosylcobinamide-phosphatesynthase[EC:6.3.1.10]	0,000373413	0,000285339	0,000382047
K03740_ko05150_Staphylococcusaureusinfection_HumanDiseases_Infectiousdiseases_dltD,D-alaninetransferprotein	4,66766E-05	6,1144E-05	6,6443E-05
K03551_ko03440_Homologousrecombination_GeneticinformationProcessing_ReplicationandRepair_ruvB,hollidayjunctionDNAhelicaseRuvB[EC:3.6.4.12]	0,001125425	0,000973209	0,000847148
K00841_ko00300_Lysinebiosynthesis_Metabolism_Aminoacidmetabolism_patA,aminotransferase[EC:2.6.1.-];K00841_ko01230_Biosynthesisofaminoacids_Metabolism_Overview_patA,aminotransferase[EC:2.6.1.-]	7,26081E-05	6,1144E-05	4,98322E-05
K11261_ko01200_Carbonmetabolism_Metabolism_Overview_fwdE,fmdE,formylmethanofurandehydrogenasesubunitE[EC:1.2.99.5];K11261_ko00194_Photosynthesisproteins_Metabolism_Energymetabolism_fwdE,fmdE,formylmethanofurandehydrogenasesubun	0,000243756	0,000315911	0,000307299
K00273_ko04146_Peroxisome_CellularProcesses_Transportandcatabolism_DAO,aao,D-amino-acidoxidase[EC:1.4.3.3];K00273_ko00330_Arginineandprolinemetabolism_Metabolism_Aminoacidmetabolism_DAO,aao,D-amino-acidoxidase[EC:1.4.3.3];K00273_ko002	7,77944E-05	5,09533E-05	4,98322E-05
K10686_ko04120_Ubiquitinmediatedproteolysis_GeneticInformationProcessing_Folding,sortinganddegradation_UBE1C,UBA3,ubiquitin-activatingenzymeE1C[EC:6.3.2.19]	1,55589E-05	1,01907E-05	8,30537E-06
K00926_ko00330_Arginineandprolinemetabolism_Metabolism_Aminoacidmetabolism_arcC,carbamatekinase[EC:2.7.2.2];K00926_ko00910_Nitrogenmetabolism_Metabolism_Energymetabolism_arcC,carbamatekinase[EC:2.7.2.2];K00926_ko00230_Purinemetabol	0,000295619	0,000224195	0,000265772
K01714_ko00300_Lysinebiosynthesis_Metabolism_Aminoacidmetabolism_dapA,4-hydroxy-tetrahydrodipicolinatesynthase[EC:4.3.3.7];K01714_ko01230_Biosynthesisofaminoacids_Metabolism_Overview_dapA,4-hydroxy-tetrahydrodipicolinatesynthase[EC:4.3.3.7	0,000803875	0,000779586	0,00078901
K01239_ko00760_Nicotinateandnicotinamidemetabolism_Metabolism_Metabolismofcofactorsandvitamins_iunH,purinenucleosidase[EC:3.2.2.1];K01239_ko00230_Purinemetabolism_Metabolism_Nucleotidemetabolism_iunH,purinenucleosidase[EC:3.2.2.1]	0,000171148	0,000254767	0,000182718
K11520_ko02020_Two-componentsystem_Environmentalinformationprocessing_Signaltrasduction_manS,two-componentsystem,OmpRfamily,manganesesensingsensorhistidinekinase[EC:2.7.13.3]	2,07452E-05	0,000137574	9,13591E-05
K00018_ko00260_Glycine,serineandthreoninemetabolism_Metabolism_Aminoacidmetabolism_hprA,glyceratedehydrogenase[EC:1.1.1.29];K00018_ko00630_Glyoxylateanddicarboxylatemetabolism_Metabolism_Carbohydratemetabolism_hprA,glyceratedehydrog	0,00046158	0,000341387	0,000415269
K07345_ko05133_Pertussis_HumanDiseases_Infectiousdiseases_fimA,majortype1subunitfimbrin(pilin)	6,22355E-05	2,54767E-05	4,98322E-05
K09584_ko04141_Proteinprocessinginendoplasmicreticulum_GeneticInformationProcessing_Folding,sortinganddegradation_PDIA6,TXNDC7,proteindisulfide-isomeraseA6[EC:5.3.4.1]	1,03726E-05	0	1,66107E-05
K14375_ko00522_Biosynthesisof12-,14-and16-memberedmacrolides_Metabolism_Metabolismofterpenoidsandpolyketides_aveBl,dTDP-L-oleandrosyltransferase[EC:2.4.1.-];K14375_ko01052_TypeIpolyketidestructures_Metabolism_Metabolismofterpenoidsandpo	3,11177E-05	0	2,49161E-05
K00956_ko00920_Sulfurmetabolism_Metabolism_Energymetabolism_cysN,sulfateadenylyltransferasesubunit1[EC:2.7.7.4];K00956_ko00450_Selenocompoundmetabolism_Metabolism_Metabolismofotheraminoacids_cysN,sulfateadenylyltransferasesubunit1[EC:2	0,000160775	0,000137574	0,000116275
K00053_ko00290_Valine,leucineandisoleucinebiosynthesis_Metabolism_Aminoacidmetabolism_ilvC,ketol-acidreductoisomerase[EC:1.1.1.86];K00053_ko01210_Oxocarboxylicacidmetabolism_Metabolism_Overview_ilvC,ketol-acidreductoisomerase[EC:1.1.1.86];K	0,000803875	0,000494247	0,000506628
K00611_ko00330_Arginineandprolinemetabolism_Metabolism_Aminoacidmetabolism_OTC,argF,argI,ornithinecarbamoyltransferase[EC:2.1.3.3];K00611_ko01230_Biosynthesisofaminoacids_Metabolism_Overview_OTC,argF,argI,ornithinecarbamoyltransferase[EC:	0,000736453	0,000499343	0,000431879
K03778_ko00620_Pyruvatemetabolism_Metabolism_Carbohydratemetabolism_ldhA,D-lactatedehydrogenase[EC:1.1.1.28]	0,000212638	0,000275148	0,000282383

K02048_ko02010_Ctransporters_Environmentalinformationprocessing_Membranetransport_cysP,sbp,sulfatetransportsystemsubstrate-bindingprotein;K02048_ko00920_Sulfurmetabolism_Metabolism_Energymetabolism_cysP,sbp,sulfatetransportsystemsubstrate	4,66766E-05	3,56673E-05	8,30537E-05
K10561_ko02010_Ctransporters_Environmentalinformationprocessing_Membranetransport_rhaQ,rhamnosetransportsystempermeaseprotein	0	5,09533E-06	8,30537E-06
K10942_ko02020_Two-componentsystem_Environmentalinformationprocessing_Signaltrasduction_flrB,fleS,two-componentsystem,sensorhistidinekinaseFlrB[EC:2.7.13.3];K10942_ko05111_Vibriocholeraepathogeniccycle_HumanDiseases_Infectiousdiseases_flrB,f	2,59315E-05	5,09533E-06	4,15269E-05
K01639_ko00520_Aminosugarandnucleotidesugarmetabolism_Metabolism_Carbohydratemetabolism_E4.1.3.3,nanA,NPL,N-acetylneuraminatelyase[EC:4.1.3.3]	0,000539374	0,000438199	0,000548155
K01599_ko00830_Retinolmetabolism_Metabolism_Metabolismofcofactorsandvitamins_hemE,UROD,uroporphyrinogendecarboxylase[EC:4.1.1.37]	0,000549747	0,000713347	0,001386997
K02340_ko03030_DNAreplication_GeneticinformationProcessing_ReplicationandRepair_DPO3D1,holA,DNApolymeraseIIIsubunitdelta[EC:2.7.7.7];K02340_ko03440_Homologousrecombination_GeneticinformationProcessing_ReplicationandRepair_DPO3D1,holA,D	0,000710522	0,000845825	0,00100495
K00024_ko00270_Cysteineandmethioninemetabolism_Metabolism_Aminoacidmetabolism_mdh,malatedehydrogenase[EC:1.1.1.37];K00024_ko00020_Citratecycle(TCAcycle)_Metabolism_Carbohydratemetabolism_mdh,malatedehydrogenase[EC:1.1.1.37];K00024	0,00120322	0,00107002	0,00066443
K13771_ko05132_Salmonellainfection_HumanDiseases_Infectiousdiseases_nsrR,Rrf2familytranscriptionalregulator,nitricoxide-sensitivetranscriptionalrepressor	4,14903E-05	3,0572E-05	2,49161E-05
K05275_ko00750_VitaminB6metabolism_Metabolism_Metabolismofcofactorsandvitamins_E1.1.1.65,pyridoxine4-dehydrogenase[EC:1.1.1.65]	6,22355E-05	5,60487E-05	7,47483E-05
K02007_ko02010_Ctransporters_Environmentalinformationprocessing_Membranetransport_cbiM,cobalt/nickeltransportsystempermeaseprotein	0,000124471	0,000122288	0,00010797
K09459_ko00440_Phosphonateandphosphinatemetabolism_Metabolism_Metabolismofotheraminoacids_E4.1.1.82,phosphonopyruvatedecarboxylase[EC:4.1.1.82]	0,000129657	8,15253E-05	0,000207634
K09487_ko04151_PI3K-Aktsignalingpathway_Environmentalinformationprocessing_Signaltrasduction_HSP90B,TRA1,heatshockprotein90kDabeta;K09487_ko04141_Proteinprocessinginendoplasmicreticulum_GeneticInformationProcessing_Folding,sortinganddegra	0	1,5286E-05	0
K03185_ko00130_Ubiquinoneandotherterpenoid-quinonebiosynthesis_Metabolism_Metabolismofcofactorsandvitamins_ubiH,2-octaprenyl-6-methoxyphenolhydroxylase[EC:1.14.13.-]	1,03726E-05	0	0
K00952_ko00760_Nicotinateandnicotinamidemetabolism_Metabolism_Metabolismofcofactorsandvitamins_nadM,nicotinamide-nucleotideadenylyltransferase[EC:2.7.7.1]	1,55589E-05	3,56673E-05	8,30537E-06
K11473_ko00630_Glyoxylateanddicarboxylatemetabolism_Metabolism_Carbohydratemetabolism_glcF,glycolateoxidaseiron-sulfursubunit	0,000171148	0,000117193	0,000124581
K01997_ko02010_Ctransporters_Environmentalinformationprocessing_Membranetransport_livH,branched-chainaminoacidtransportsystempermeaseprotein	0,000611982	0,000351578	0,000440185
K13490_ko02020_Two-componentsystem_Environmentalinformationprocessing_Signaltrasduction_wspE,two-componentsystem,chemotaxisfamily,sensorhistidinekinaseandresponseregulatorWspE	0	1,01907E-05	0
K03841_ko04151_PI3K-Aktsignalingpathway_Environmentalinformationprocessing_Signaltrasduction_FBP,fbp,fructose-1,6-bisphosphataseI[EC:3.1.3.11];K03841_ko00051_Fructoseandmannosemetabolism_Metabolism_Carbohydratemetabolism_FBP,fbp,fructose	1,03726E-05	0	7,47483E-05
K02548_ko00130_Ubiquinoneandotherterpenoid-quinonebiosynthesis_Metabolism_Metabolismofcofactorsandvitamins_menA,1,4-dihydroxy-2-naphthoateoctaprenyltransferase[EC:2.5.1.742.5.1.-]	0,000347482	0,000356673	0,000357131
K01738_ko00270_Cysteineandmethioninemetabolism_Metabolism_Aminoacidmetabolism_cysK,cysteinesynthaseA[EC:2.5.1.47];K01738_ko00920_Sulfurmetabolism_Metabolism_Energymetabolism_cysK,cysteinesynthaseA[EC:2.5.1.47];K01738_ko01230_Biosynth	0,001037258	0,001243261	0,001287333
K00297_ko00670_Onecarbonpoolbyfolate_Metabolism_Metabolismofcofactorsandvitamins_metF,MTHFR,methylenetetrahydrofolatereductase(NADPH)[EC:1.5.1.20];K00297_ko01200_Carbonmetabolism_Metabolism_Overview_metF,MTHFR,methylenetetrahydr	0,000373413	0,00053501	0,000382047
K03230_ko02010_Ctransporters_Environmentalinformationprocessing_Membranetransport_yscV,sctV,hrcV,typeIIIsecretionproteinV	5,70492E-05	1,01907E-05	8,30537E-06
K10440_ko02010_Ctransporters_Environmentalinformationprocessing_Membranetransport_rbsC,ribosetransportsystempermeaseprotein	0,000777944	0,000718442	0,001038171
K01709_ko00520_Aminosugarandnucleotidesugarmetabolism_Metabolism_Carbohydratemetabolism_rfbG,CDP-glucose4,6-dehydratase[EC:4.2.1.45]	0,000254128	0,000219099	0,000141191
K07806_ko02020_Two-componentsystem_Environmentalinformationprocessing_Signaltrasduction_arnB,pmrH,UDP-4-amino-4-deoxy-L-arabinose-oxoglutarateaminotransferase[EC:2.6.1.87];K07806_ko00520_Aminosugarandnucleotidesugarmetabolism_Metaboli	5,70492E-05	5,60487E-05	2,49161E-05
K02319_ko00230_Purinemetabolism_Metabolism_Nucleotidemetabolism_DPA,polB1,DNApolymeraseI[EC:2.7.7.7];K02319_ko00240_Pyrimidinemetabolism_Metabolism_Nucleotidemetabolism_DPA,polB1,DNApolymeraseI[EC:2.7.7.7]	2,59315E-05	2,03813E-05	7,47483E-05
K01480_ko00330_Arginineandprolinemetabolism_Metabolism_Aminoacidmetabolism_E3.5.3.11,speB,agmatinase[EC:3.5.3.11]	0,000150402	8,66207E-05	0,000182718
K01151_ko03410_Baseexcisionrepair_GeneticinformationProcessing_ReplicationandRepair_nfo,deoxyribonucleaseIV[EC:3.1.21.2]	0,000746826	0,000805063	0,000888675
K03517_ko00760_Nicotinateandnicotinamidemetabolism_Metabolism_Metabolismofcofactorsandvitamins_nadA,quinolinatesynthase[EC:2.5.1.72]	0,000466766	0,000545201	0,000390352
K13789_ko00900_Terpenoidbackbonebiosynthesis_Metabolism_Metabolismofterpenoidsandpolyketides_GGPS,geranylgeranyldiphosphatesynthase,typeII[EC:2.5.1.12.5.1.102.5.1.29]	0,000591237	0,000723537	0,000581376
K03885_ko00190_Oxidativephosphorylation_Metabolism_Energymetabolism_ndh,NADHdehydrogenase[EC:1.6.99.3]	0,000326736	0,000280243	0,000315604
K05878_ko00561_Glycerolipidmetabolism_Metabolism_Lipidmetabolism_dhaK,dihydroxyacetonekinase,N-terminaldomain[EC:2.7.1.-]	0,000134844	0,000157955	0,000174413
K01781_ko00627_Aminobenzoatedegradation_Metabolism_Xenobioticsbiodegradationandmetabolism_mdlA,mandelateracemase[EC:5.1.2.2]	6,22355E-05	5,60487E-05	2,49161E-05
K09692_ko02010_Ctransporters_Environmentalinformationprocessing_Membranetransport_tagG,teichoicacidtransportsystempermeaseprotein	0,00018152	0,000239481	0,000157802
K02843_ko00540_Lipopolysaccharidebiosynthesis_Metabolism_Glycanbiosynthesisandmetabolism_waaF,rfaF,heptosyltransferaseII[EC:2.4.-.-]	0,000264501	0,000351578	0,00032391
K01066_ko00960_Tropane,piperidineandpyridinealkaloidbiosynthesis_Metabolism_Biosynthesisofothersecondarymetabolites_E3.1.1.-,esterase/lipase[EC:3.1.1.-];K01066_ko00363_Bisphenoldegradation_Metabolism_Xenobioticsbiodegradationandmetabolism_E3	0,000523815	0,00053501	0,000456795
K03851_ko00430_Taurineandhypotaurinemetabolism_Metabolism_Metabolismofotheraminoacids_tpa,taurine-pyruvateaminotransferase[EC:2.6.1.77]	7,26081E-05	5,09533E-06	0
K02591_ko00910_Nitrogenmetabolism_Metabolism_Energymetabolism_nifK,nitrogenasemolybdenum-ironproteinbetachain[EC:1.18.6.1];K02591_ko00625_Chloroalkaneandchloroalkenedegradation_Metabolism_Xenobioticsbiodegradationandmetabolism_nifK,n	5,18629E-05	4,07627E-05	8,30537E-06
K00078_ko00040_Pentoseandglucuronateinterconversions_Metabolism_Carbohydratemetabolism_DHDH,dihydrodioldehydrogenase/D-xylose1-dehydrogenase(NADP)[EC:1.3.1.201.1.1.179];K00078_ko00980_MetabolismofxenobioticsbycytochromeP450_Metabo	4,14903E-05	6,62393E-05	0,000116275
K06920_ko00785_Lipoicacidmetabolism_Metabolism_Metabolismofcofactorsandvitamins_queC,7-cyano-7-deazaguaninesynthase[EC:6.3.4.20]	0,000347482	0,000387245	0,000315604
K07031_ko00540_Lipopolysaccharidebiosynthesis_Metabolism_Glycanbiosynthesisandmetabolism_hddA,D-glycero-alpha-D-manno-heptose-7-phosphatekinase[EC:2.7.1.168]	0,000212638	0,000107002	0,000240856
K12615_ko03018_RNAdegradation_GeneticInformationProcessing_Folding,sortinganddegradation_EDC3,enhancerofmRNA-decappingprotein3	4,14903E-05	1,5286E-05	5,81376E-05
K03336_ko00630_Glyoxylateanddicarboxylatemetabolism_Metabolism_Carbohydratemetabolism_iolD,3D-(3,5/4)-trihydroxycyclohexane-1,2-dioneacylhydrolase(decyclizing)[EC:3.7.1.22]	5,18629E-05	7,643E-05	2,49161E-05
K05284_ko00563_Glycosylphosphatidylinositol(GPI)-anchorbiosynthesis_Metabolism_Glycanbiosynthesisandmetabolism_PIGM,phosphatidylinositolglycan,classM[EC:2.4.1.-]	1,03726E-05	1,01907E-05	1,66107E-05
K01995_ko02010_Ctransporters_Environmentalinformationprocessing_Membranetransport_livG,branched-chainaminoacidtransportsystemATP-bindingprotein	0,000611982	0,000504438	0,000498322
K03474_ko00750_VitaminB6metabolism_Metabolism_Metabolismofcofactorsandvitamins_pdxJ,pyridoxine5-phosphatesynthase[EC:2.6.99.2]	0,00018152	0,000244576	0,000116275
K01844_ko00310_Lysinedegradation_Metabolism_Aminoacidmetabolism_kamD,beta-lysine5,6-aminomutasealphasubunit[EC:5.4.3.3]	5,18629E-05	4,5858E-05	3,32215E-05
K02446_ko00051_Fructoseandmannosemetabolism_Metabolism_Carbohydratemetabolism_glpX,fructose-1,6-bisphosphataseII[EC:3.1.3.11];K02446_ko00010_Glycolysis/Gluconeogenesis_Metabolism_Carbohydratemetabolism_glpX,fructose-1,6-bisphosphataseII	6,22355E-05	2,54767E-05	8,30537E-06
K01048_ko00564_Glycerophospholipidmetabolism_Metabolism_Lipidmetabolism_pldB,lysophospholipase[EC:3.1.1.5]	0,000342295	0,000356673	0,00044849
K07777_ko02020_Two-componentsystem_Environmentalinformationprocessing_Signaltrasduction_degS,two-componentsystem,NarLfamily,sensorhistidinekinaseDegS[EC:2.7.13.3]	3,11177E-05	5,09533E-06	5,81376E-05
K00882_ko00051_Fructoseandmannosemetabolism_Metabolism_Carbohydratemetabolism_fruK,1-phosphofructokinase[EC:2.7.1.56]	0,000285246	0,000295529	0,000240856
K08239_ko04142_Lysosome_CellularProcesses_Transportandcatabolism_GNPTAB,UDP-N-acetylglucosamine-lysosomal-enzyme[EC:2.7.8.17]	8,29807E-05	0,000122288	9,96645E-05
K00791_ko00908_Zeatinbiosynthesis_Metabolism_Metabolismofterpenoidsandpolyketides_miaA,TRIT1,tRNAdimethylallyltransferase[EC:2.5.1.75]	0,000985395	0,001263643	0,000963423
K00796_ko00785_Lipoicacidmetabolism_Metabolism_Metabolismofcofactorsandvitamins_folP,dihydropteroatesynthase[EC:2.5.1.15]	0,000337109	0,000519724	0,000390352
K01485_ko00330_Arginineandprolinemetabolism_Metabolism_Aminoacidmetabolism_codA,cytosinedeaminase[EC:3.5.4.1];K01485_ko00240_Pyrimidinemetabolism_Metabolism_Nucleotidemetabolism_codA,cytosinedeaminase[EC:3.5.4.1]	0,000119285	0,000224195	0,000166107
K01643_ko02020_Two-componentsystem_Environmentalinformationprocessing_Signaltrasduction_citF,citratelyasesubunitalpha/citrateCoA-transferase[EC:2.8.3.10]	0,000134844	0,000147765	0,000182718
K03786_ko00400_Phenylalanine,tyrosineandtryptophanbiosynthesis_Metabolism_Aminoacidmetabolism_aroQ,qutE,3-dehydroquinatedehydrataseII[EC:4.2.1.10];K03786_ko01230_Biosynthesisofaminoacids_Metabolism_Overview_aroQ,qutE,3-dehydroquinatede	0,000259315	0,000208909	0,000199329
K01625_ko00630_Glyoxylateanddicarboxylatemetabolism_Metabolism_Carbohydratemetabolism_eda,2-dehydro-3-deoxyphosphogluconatealdolase/(4S)-4-hydroxy-2-oxoglutaratealdolase[EC:4.1.2.144.1.3.42];K01625_ko00030_Pentosephosphatepathway_Metab	0,000446021	0,000438199	0,000415269
K02793_ko02010_Ctransporters_Environmentalinformationprocessing_Membranetransport_PTS-Man-EIIA,manX,PTSsystem,mannose-specificIIAcomponent[EC:2.7.1.69];K02793_ko00520_Aminosugarandnucleotidesugarmetabolism_Metabolism_Carbohydrateme	0,000300805	0,000183432	0,000207634
K00795_ko00900_Terpenoidbackbonebiosynthesis_Metabolism_Metabolismofterpenoidsandpolyketides_ispA,farnesyldiphosphatesynthase[EC:2.5.1.12.5.1.10]	3,6304E-05	1,01907E-05	4,15269E-05
K01761_ko00270_Cysteineandmethioninemetabolism_Metabolism_Aminoacidmetabolism_E4.4.1.11,methionine-gamma-lyase[EC:4.4.1.11];K01761_ko00450_Selenocompoundmetabolism_Metabolism_Metabolismofotheraminoacids_E4.4.1.11,methionine-gamn	7,77944E-05	8,66207E-05	3,32215E-05
K00426_ko02020_Two-componentsystem_Environmentalinformationprocessing_Signaltrasduction_cydB,cytochromedubiquinoloxidasesubunitII[EC:1.10.3.-];K00426_ko00190_Oxidativephosphorylation_Metabolism_Energymetabolism_cydB,cytochromedubiquinc	0,000560119	0,000331197	0,000265772
K14982_ko02020_Two-componentsystem_Environmentalinformationprocessing_Signaltrasduction_ciaH,two-componentsystem,OmpRfamily,sensorhistidinekinaseCiaH[EC:2.7.13.3]	5,18629E-06	2,03813E-05	6,6443E-05
K02557_ko02030_Bacterialchemotaxis_Organismalsystem_Cellmobility_motB,chemotaxisproteinMotB;K02557_ko02040_Flagellarassembly_Organismalsystem_Cellmobility_motB,chemotaxisproteinMotB	0,000648286	0,000468771	0,000490017
K00150_ko00010_Glycolysis/Gluconeogenesis_Metabolism_Carbohydratemetabolism_gap2,glyceraldehyde-3-phosphatedehydrogenase(NAD(P))[EC:1.2.1.59];K00150_ko01230_Biosynthesisofaminoacids_Metabolism_Overview_gap2,glyceraldehyde-3-phosphatec	1,55589E-05	2,54767E-05	0
K11707_ko02010_Ctransporters_Environmentalinformationprocessing_Membranetransport_troA,mntA,znuA,manganese/zinc/irontransportsystemssubstrate-bindingprotein	3,11177E-05	5,09533E-06	2,49161E-05
K10036_ko02010_Ctransporters_Environmentalinformationprocessing_Membranetransport_glnH,glutaminetransportsystemssubstrate-bindingprotein	0,00018152	0,000193623	0,000282383
K08092_ko00052_Galactosemetabolism_Metabolism_Carbohydratemetabolism_dlgD,3-dehydro-L-gulonate2-dehydrogenase[EC:1.1.1.130];K08092_ko00040_Pentoseandglucuronateinterconversions_Metabolism_Carbohydratemetabolism_dlgD,3-dehydro-L-gulo	3,6304E-05	4,07627E-05	1,66107E-05
K00175_ko00020_Citratecycle(TCAcycle)_Metabolism_Carbohydratemetabolism;K00175_ko01200_Carbonmetabolism_Metabolism_Overview;K00175_ko00194_Photosynthesisproteins_Metabolism_Energymetabolism	0,001011327	0,0007643	0,00066443
K03415_ko02020_Two-componentsystem_Environmentalinformationprocessing_Signaltrasduction_cheV,two-componentsystem,chemotaxisfamily,responseregulatorCheV;K03415_ko02030_Bacterialchemotaxis_Organismalsystem_Cellmobility_cheV,two-compon	0,000124471	0,000112097	9,96645E-05

K14558_ko03008_Ribosomebiogenesisineukaryotes_GeneticinformationProcessing_Transcription_PWP2,UTP1,periodictryptophanprotein2	2,07452E-05	2,03813E-05	4,15269E-05
K00208_ko00061_Fattyacidbiosynthesis_Metabolism_Lipidmetabolism_fabI,enoyl-[acyl-carrierprotein]reductaseI[EC:1.3.1.91.3.1.10];K00208_ko01212_Fattyacidmetabolism_Metabolism_Overview_fabI,enoyl-[acyl-carrierprotein]reductaseI[EC:1.3.1.91.3.1.10];K0(	0,000160775	0,000203813	0,000157802
K03335_ko00630_Glyoxylateanddicarboxylatemetabolism_Metabolism_Carbohydratemetabolism_iolE,inososedehydratase[EC:4.2.1.44]	0,000295619	0,000407627	0,000406963
K07644_ko02020_Two-componentsystem_Environmentalinformationprocessing_Signaltrasduction_cusS,copS,silS,two-componentsystem,OmpRfamily,heavymetalsensorhistidinekinaseCusS[EC:2.7.13.3]	4,66766E-05	7,643E-05	0,000199329
K11070_ko02010_Ctransporters_Environmentalinformationprocessing_Membranetransport_potC,spermidine/putrescinetransportsystempermeaseprotein	0,000305991	0,000397436	0,00034052
K04792_ko01053_Biosynthesisofsiderophoregroupnonribosomalpeptides_Metabolism_Metabolismofterpenoidsandpolyketides_mbtF,mycobactinpeptidesynthetaseMbtF	0	1,01907E-05	8,30537E-06
K05692_ko04520_Adherensjunction_Cellgrowthanddeath_Cellularcommunity_ACTB_G1,actinbeta/gamma1;K05692_ko04510_Focaladhesion_Cellgrowthanddeath_Cellularcommunity_ACTB_G1,actinbeta/gamma1;K05692_ko04530_Tightjunction_Cellgrowthandd	2,07452E-05	1,01907E-05	3,32215E-05
K05339_ko02020_Two-componentsystem_Environmentalinformationprocessing_Signaltrasduction_lrgB,holin-likeproteinLrgB	0,000295619	0,000361769	0,000240856
K02523_ko00900_Terpenoidbackbonebiosynthesis_Metabolism_Metabolismofterpenoidsandpolyketides_ispB,octaprenyl-diphosphatesynthase[EC:2.5.1.90]	0,000611982	0,000300625	0,000191024
K02037_ko02010_Ctransporters_Environmentalinformationprocessing_Membranetransport_pstC,phosphatetransportsystempermeaseprotein	0,00050307	0,00045858	0,000423574
K00096_ko00564_Glycerophospholipidmetabolism_Metabolism_Lipidmetabolism_araM,egsA,glycerol-1-phosphatedehydrogenase[NAD(P)+][EC:1.1.1.261]	0,000150402	0,000132479	9,96645E-05
K00934_ko00330_Arginineandprolinemetabolism_Metabolism_Aminoacidmetabolism_E2.7.3.3,argininekinase[EC:2.7.3.3]	2,07452E-05	3,56673E-05	4,98322E-05
K00226_ko00240_Pyrimidinemetabolism_Metabolism_Nucleotidemetabolism_pyrD,dihydroorotatedehydrogenase(fumarate)[EC:1.3.98.1]	0,000736453	0,000815253	0,000764094
K00836_ko00260_Glycine,serineandthreoninemetabolism_Metabolism_Aminoacidmetabolism_E2.6.1.76,ectB,diaminobutyrate-2-oxoglutaratetransaminase[EC:2.6.1.76];K00836_ko01210_Oxocarboxylicacidmetabolism_Metabolism_Overview_E2.6.1.76,ectB,diam	1,55589E-05	3,0572E-05	1,66107E-05
K01677_ko00020_Citratecycle(TCAcycle)_Metabolism_Carbohydratemetabolism_E4.2.1.2AA,fumA,fumaratehydratasesubunitalpha[EC:4.2.1.2];K01677_ko00620_Pyruvatemetabolism_Metabolism_Carbohydratemetabolism_E4.2.1.2AA,fumA,fumaratehydratasesu	0,000352668	0,000214004	0,00034052
K02586_ko00910_Nitrogenmetabolism_Metabolism_Energymetabolism_nifD,nitrogenasemolybdenum-ironproteinalphachain[EC:1.18.6.1];K02586_ko00625_Chloroalkaneandchloroalkenedegradation_Metabolism_Xenobioticsbiodegradationandmetabolism_nifD,	3,11177E-05	3,56673E-05	2,49161E-05
K00858_ko00760_Nicotinateandnicotinamidemetabolism_Metabolism_Metabolismofcofactorsandvitamins_ppnK,NADK,NAD+kinase[EC:2.7.1.23]	0,000580865	0,000820349	0,000581376
K02685_ko03030_DNAreplication_GeneticinformationProcessing_ReplicationandRepair_PRI2,DNAprimaselargesubunit[EC:2.7.7.-];K02685_ko00230_Purinemetabolism_Metabolism_Nucleotidemetabolism_PRI2,DNAprimaselargesubunit[EC:2.7.7.-];K02685_ko002	0	5,09533E-06	0
K05815_ko02010_Ctransporters_Environmentalinformationprocessing_Membranetransport_ugpE,sn-glycerol3-phosphatetransportsystempermeaseprotein	6,74218E-05	3,56673E-05	9,13591E-05
K01629_ko00051_Fructoseandmannosemetabolism_Metabolism_Carbohydratemetabolism_rhaD,rhamnulose-1-phosphatealdolase[EC:4.1.2.19];K01629_ko00040_Pentoseandglucuronateinterconversions_Metabolism_Carbohydratemetabolism_rhaD,rhamnulose	0,000243756	0,000127383	0,000240856
K07246_ko00630_Glyoxylateanddicarboxylatemetabolism_Metabolism_Carbohydratemetabolism_ttuC,dmlA,tartratedehydrogenase/decarboxylase/D-malatedehydrogenase[EC:1.1.1.934.1.1.731.1.1.83];K07246_ko00630_Glyoxylateanddicarboxylatemetabolism_I	1,55589E-05	0	2,49161E-05
K00016_ko00270_Cysteineandmethioninemetabolism_Metabolism_Aminoacidmetabolism_LDH,ldh,L-lactatedehydrogenase[EC:1.1.1.27];K00016_ko00010_Glycolysis/Gluconeogenesis_Metabolism_Carbohydratemetabolism_LDH,ldh,L-lactatedehydrogenase[EC:1	0,000674218	0,000387245	0,000506628
K00634_ko00630_Glyoxylateanddicarboxylatemetabolism_Metabolism_Carbohydratemetabolism_ptb,phosphatebutyryltransferase[EC:2.3.1.19]	0,000399344	0,000642012	0,000348826
K09698_ko00970_Aminoacyl-tRNAbiosynthesis_GeneticinformationandprocessingTranscription_gltX,nondiscriminatingglutamyl-tRNAsynthetase[EC:6.1.1.24]	0,000238569	0,00030572	0,000224245
K01425_ko05230_Centralcarbonmetabolismincancer_HumanDiseases_Cancers_glsA,GLS,glutaminase[EC:3.5.1.2];K01425_ko05206_MicroRNAsincancer_HumanDiseases_Cancers_glsA,GLS,glutaminase[EC:3.5.1.2];K01425_ko00250_Alanine,aspartateandglutamater	9,33532E-05	0,000321006	9,96645E-05
K11073_ko02010_Ctransporters_Environmentalinformationprocessing_Membranetransport_potF,putrescinetransportsystemsubstrate-bindingprotein	5,18629E-06	0	0
K02886_ko03010_Ribosome_GeneticinformationProcessing_Transcription_RP-L2,MRPL2,rplB,largesubunitribosomalproteinL2	0,001369181	0,001334977	0,001146141
K00919_ko00900_Terpenoidbackbonebiosynthesis_Metabolism_Metabolismofterpenoidsandpolyketides_ispE,4-diphosphocytidyl-2-C-methyl-D-erythritolkinase[EC:2.7.1.148]	0,004662476	0,004178174	0,005822066
K02119_ko00190_Oxidativephosphorylation_Metabolism_Energymetabolism_ATPVC,ntpC,atpC,V/A-typeH+-transportingATPasesubunitC	0,000186706	0,000107002	0,000224245
K00879_ko00051_Fructoseandmannosemetabolism_Metabolism_Carbohydratemetabolism_fucK,L-fuculokinase[EC:2.7.1.51]	8,29807E-05	7,13347E-05	0,000157802
K00645_ko00061_Fattyacidbiosynthesis_Metabolism_Lipidmetabolism_fabD,[acyl-carrier-protein]S-malonyltransferase[EC:2.3.1.39];K00645_ko01212_Fattyacidmetabolism_Metabolism_Overview_fabD,[acyl-carrier-protein]S-malonyltransferase[EC:2.3.1.39]	0,000897228	0,000601249	0,000714262
K05772_ko02010_Ctransporters_Environmentalinformationprocessing_Membranetransport_tupA,vupA,tungstatetransportsystemsubstrate-bindingprotein	4,14903E-05	2,03813E-05	3,32215E-05
K01492_ko00230_Purinemetabolism_Metabolism_Nucleotidemetabolism_E2.1.2.3,phosphoribosylaminoimidazolecarboxamideformyltransferase[EC:2.1.2.3]	7,77944E-05	7,13347E-05	9,13591E-05
K10773_ko03410_Baseexcisionrepair_GeneticinformationProcessing_ReplicationandRepair_NTH,endonucleaseIII[EC:4.2.99.18]	0,000440835	0,000657298	0,000523238
K02038_ko02010_Ctransporters_Environmentalinformationprocessing_Membranetransport_pstA,phosphatetransportsystempermeaseprotein	0,000388972	0,000300625	0,000357131
K02371_ko00061_Fattyacidbiosynthesis_Metabolism_Lipidmetabolism_fabK,enoyl-[acyl-carrierprotein]reductaseII[EC:1.3.1.9];K02371_ko01212_Fattyacidmetabolism_Metabolism_Overview_fabK,enoyl-[acyl-carrierprotein]reductaseII[EC:1.3.1.9]	0,000316364	0,000356673	0,00032391
K00127_ko00630_Glyoxylateanddicarboxylatemetabolism_Metabolism_Carbohydratemetabolism_fdoI,formatedehydrogenasesubunitgamma;K00127_ko01200_Carbonmetabolism_Metabolism_Overview_fdoI,formatedehydrogenasesubunitgamma;K00127_ko00	4,66766E-05	1,5286E-05	5,81376E-05
K10118_ko02010_Ctransporters_Environmentalinformationprocessing_Membranetransport_msmF,raffinose/stachyose/melibiosetransportsystempermeaseprotein	0,000165961	0,000295529	0,000348826
K00457_ko00360_Phenylalaninemetabolism_Metabolism_Aminoacidmetabolism_HPD,hppD,4-hydroxyphenylpyruvatedioxygenase[EC:1.13.11.27];K00457_ko00350_Tyrosinemetabolism_Metabolism_Aminoacidmetabolism_HPD,hppD,4-hydroxyphenylpyruvatedi	2,59315E-05	1,01907E-05	4,15269E-05
K02416_ko02030_Bacterialchemotaxis_Organismalsystem_Cellmobility_fliM,flagellarmotorswitchproteinFliM;K02416_ko02040_Flagellarassembly_Organismalsystem_Cellmobility_fliM,flagellarmotorswitchproteinFliM	9,33532E-05	5,60487E-05	0,000124581
K00162_ko04066_HIF-1signalingpathway_Environmentalinformationprocessing_Signaltrasduction_PDHB,pdhB,pyruvatedehydrogenaseE1componentbetasubunit[EC:1.2.4.1];K00162_ko05230_Centralcarbonmetabolismincancer_HumanDiseases_Cancers_PDHB,pd	8,8167E-05	3,56673E-05	4,15269E-05
K03800_ko00785_Lipoicacidmetabolism_Metabolism_Metabolismofcofactorsandvitamins_lplA,lipoate-proteinligaseA[EC:2.7.7.63]	0,000171148	0,000234385	0,000257467
K12294_ko02020_Two-componentsystem_Environmentalinformationprocessing_Signaltrasduction_comD,two-componentsystem,AgrAfamily,sensorhistidinekinaseComD[EC:2.7.13.-]	1,03726E-05	4,5858E-05	7,47483E-05
K10189_ko02010_Ctransporters_Environmentalinformationprocessing_Membranetransport_lacF,araP,lactose/L-arabinosetransportsystempermeaseprotein	0,00018152	0,000107002	0,000166107
K08479_ko02020_Two-componentsystem_Environmentalinformationprocessing_Signaltrasduction_sasA,two-componentsystem,OmpRfamily,clock-associatedhistidinekinaseSasA[EC:2.7.13.3]	3,6304E-05	0,000122288	3,32215E-05
K12292_ko02020_Two-componentsystem_Environmentalinformationprocessing_Signaltrasduction_ABCC-BAC.COMA,comA,ATP-bindingcassette,subfamilyC,bacterial,competencefactortransportingprotein[EC:3.4.22.-]	2,59315E-05	1,5286E-05	8,30537E-06
K01778_ko00300_Lysinebiosynthesis_Metabolism_Aminoacidmetabolism_dapF,diaminopimelateepimerase[EC:5.1.1.7];K01778_ko01230_Biosynthesisofaminoacids_Metabolism_Overview_dapF,diaminopimelateepimerase[EC:5.1.1.7]	0,000627541	0,000642012	0,000597987
K02067_ko02010_Ctransporters_Environmentalinformationprocessing_Membranetransport_mlaD,linM,phospholipid/cholesterol/gamma-HCHtransportsystemsubstrate-bindingprotein	0,000171148	0,000178337	0,000166107
K00632_ko00280_Valine,leucineandisoleucinedegradation_Metabolism_Aminoacidmetabolism_E2.3.1.16,fadA,acetyl-CoAacyltransferase[EC:2.3.1.16];K00632_ko00592_alpha-Linolenicacidmetabolism_Metabolism_Lipidmetabolism_E2.3.1.16,fadA,acetyl-CoAacyl	3,11177E-05	1,5286E-05	1,66107E-05
K02073_ko02010_Ctransporters_Environmentalinformationprocessing_Membranetransport_metQ,D-methioninetransportsystemssubstrate-bindingprotein	0,000435648	0,000295529	0,000390352
K09972_ko02010_Ctransporters_Environmentalinformationprocessing_Membranetransport_aapP,bztD,generalL-aminoacidtransportsystemATP-bindingprotein[EC:3.6.3.-]	2,59315E-05	3,56673E-05	0
K00868_ko00750_VitaminB6metabolism_Metabolism_Metabolismofcofactorsandvitamins_pdxK,pdxY,pyridoxinekinase[EC:2.7.1.35]	0,000217824	0,000463675	0,000490017
K01635_ko00052_Galactosemetabolism_Metabolism_Carbohydratemetabolism_lacD,tagatose1,6-diphosphatealdolase[EC:4.1.2.40]	9,85395E-05	0,000346483	0,000431879
K07795_ko02020_Two-componentsystem_Environmentalinformationprocessing_Signaltrasduction_tctC,putativetricarboxylictransportmembraneprotein	0,000254128	9,1716E-05	9,96645E-05
K00060_ko00260_Glycine,serineandthreoninemetabolism_Metabolism_Aminoacidmetabolism_tdh,threonine3-dehydrogenase[EC:1.1.1.103]	0,000150402	5,60487E-05	6,6443E-05
K00059_ko01040_Biosynthesisofunsaturatedfattyacids_Metabolism_Lipidmetabolism_fabG,3-oxoacyl-[acyl-carrierprotein]reductase[EC:1.1.1.100];K00059_ko00061_Fattyacidbiosynthesis_Metabolism_Lipidmetabolism_fabG,3-oxoacyl-[acyl-carrierprotein]reducta	0,002095262	0,001936227	0,002142786
K03219_ko02010_Ctransporters_Environmentalinformationprocessing_Membranetransport_yscC,sctC,typeIIIsecretionproteinC	2,07452E-05	1,5286E-05	8,30537E-06
K01083_ko00630_Glyoxylateanddicarboxylatemetabolism_Metabolism_Carbohydratemetabolism_E3.1.3.8,3-phytase[EC:3.1.3.8]	3,11177E-05	1,5286E-05	0
K11031_ko04621_NOD-likereceptorsignalingpathway_OrganismalSystems_Immunesystem_slo,thiol-activatedcytolysin	4,66766E-05	6,1144E-05	6,6443E-05
K10549_ko02010_Ctransporters_Environmentalinformationprocessing_Membranetransport_alsB,D-allosetransportsystemssubstrate-bindingprotein	2,59315E-05	3,0572E-05	6,6443E-05
K01959_ko00020_Citratecycle(TCAcycle)_Metabolism_Carbohydratemetabolism_pycA,pyruvatecarboxylasesubunitA[EC:6.4.1.1];K01959_ko00620_Pyruvatemetabolism_Metabolism_Carbohydratemetabolism_pycA,pyruvatecarboxylasesubunitA[EC:6.4.1.1];K0195	1,03726E-05	0	0
K02549_ko00130_Ubiquinoneandotherterpenoid-quinonebiosynthesis_Metabolism_Metabolismofcofactorsandvitamins_menC,O-succinylbenzoatesynthase[EC:4.2.1.113]	9,85395E-05	0,000163051	9,13591E-05
K00957_ko00920_Sulfurmetabolism_Metabolism_Energymetabolism_cysD,sulfateadenylyltransferasesubunit2[EC:2.7.7.4];K00957_ko00450_Selenocompoundmetabolism_Metabolism_Metabolismofotheraminoacids_cysD,sulfateadenylyltransferasesubunit2[EC:2	0,000155589	0,000300625	0,000207634
K10119_ko02010_Ctransporters_Environmentalinformationprocessing_Membranetransport_msmG,raffinose/stachyose/melibiosetransportsystempermeaseprotein	0,00036304	0,000606345	0,000373742
K02930_ko03010_Ribosome_GeneticinformationProcessing_Transcription_RP-L4e,RPL4,largesubunitribosomalproteinL4e	1,03726E-05	0	1,66107E-05
K00801_ko00100_Steroidbiosynthesis_Metabolism_Lipidmetabolism_FDFT1,farnesyl-diphosphatefarnesyltransferase[EC:2.5.1.21];K00801_ko00909_Sesquiterpenoidandtriterpenoidbiosynthesis_Metabolism_Metabolismofterpenoidsandpolyketides_FDFT1,farnesy	1,03726E-05	5,09533E-06	0
K01619_ko00030_Pentosephosphatepathway_Metabolism_Carbohydratemetabolism_deoC,DERA,deoxyribose-phosphatealdolase[EC:4.1.2.4]	0,000912787	0,000978304	0,000797316
K04019_ko00564_Glycerophospholipidmetabolism_Metabolism_Lipidmetabolism_eutA,ethanolamineutilizationproteinEutA	3,6304E-05	1,5286E-05	8,30537E-06
K01054_ko04723_Retrogradeendocannabinoidsignaling_Environmentalinformationprocessing_Signaltransduction_MGLL,acylglycerollipase[EC:3.1.1.23];K01054_ko00561_Glycerolipidmetabolism_Metabolism_Lipidmetabolism_MGLL,acylglycerollipase[EC:3.1.1.23	2,07452E-05	1,5286E-05	0
K01595_ko00620_Pyruvatemetabolism_Metabolism_Carbohydratemetabolism_ppc,phosphoenolpyruvatecarboxylase[EC:4.1.1.31];K01595_ko01200_Carbonmetabolism_Metabolism_Overview_ppc,phosphoenolpyruvatecarboxylase[EC:4.1.1.31];K01595_ko00194	3,6304E-05	4,07627E-05	9,96645E-05

K02747_ko02010_Ctransporters_Environmentalinformationprocessing_Membranetransport_PTS-Aga-EIID,agaE,PTSsystem,N-acetylgalactosamine-specificIIDcomponent;K02747_ko00052_Galactosemetabolism_Metabolism_Carbohydratemetabolism_PTS-Aga-EIID	3,6304E-05	4,07627E-05	2,49161E-05
K07778_ko02020_Two-componentsystem_Environmentalinformationprocessing_Signaltrasduction_desK,two-componentsystem,NarLfamily,sensorhistidinekinaseDesK[EC:2.7.13.3]	5,70492E-05	8,66207E-05	0,000157802
K01878_ko00970_Aminoacyl-tRNAbiosynthesis_Geneticinformationandprocessing_Transcription_glyQ,glycyl-tRNAsynthetasealphachain[EC:6.1.1.14]	7,26081E-05	0,00022929	0,000132886
K02220_ko04111_Cellcycle-yeast_CellularProcesses_Cellgrowthanddeath_CLB1_2,G2/mitotic-specificcyclin1/2	5,18629E-06	0	0
K01069_ko00620_Pyruvatemetabolism_Metabolism_Carbohydratemetabolism_E3.1.2.6,gloB,hydroxyacylglutathionehydrolase[EC:3.1.2.6]	0,000715708	0,000662393	0,001046477
K01902_ko00020_Citratecycle(TCAcycle)_Metabolism_Carbohydratemetabolism_sucD,succinyl-CoAsynthetasealphasubunit[EC:6.2.1.5];K01902_ko00630_Glyoxylateanddicarboxylatemetabolism_Metabolism_Carbohydratemetabolism_sucD,succinyl-CoAsynthetase	3,11177E-05	2,54767E-05	9,96645E-05
K14758_ko03008_Ribosomebiogenesisineukaryotes_GeneticinformationProcessing_Transcription_HRR25,caseinkinaselhomologHRR25[EC:2.7.11.1]	0	5,09533E-06	8,30537E-06
K08302_ko00052_Galactosemetabolism_Metabolism_Carbohydratemetabolism_gatY-kbaY,tagatose1,6-diphosphatealdolaseGatY/KbaY[EC:4.1.2.40]	0,000108912	4,5858E-05	8,30537E-05
K10193_ko02010_Ctransporters_Environmentalinformationprocessing_Membranetransport_togM,oligogalacturonidetransportsystempermeaseprotein	7,77944E-05	4,07627E-05	8,30537E-05
K03660_ko03410_Baseexcisionrepair_GeneticinformationProcessing_ReplicationandRepair_OGG1,N-glycosylase/DNAlyase[EC:3.2.2.-4.2.99.18]	0,000274873	0,00038215	0,000332215
K01142_ko03410_Baseexcisionrepair_GeneticinformationProcessing_ReplicationandRepair_E3.1.11.2,xthA,exodeoxyribonucleaseIII[EC:3.1.11.2]	0,00068459	0,000901874	0,000689346
K01591_ko00240_Pyrimidinemetabolism_Metabolism_Nucleotidemetabolism_pyrF,orotidine-5'-phosphatedecarboxylase[EC:4.1.1.23]	0,000669032	0,000835635	0,000697651
K10543_ko02010_Ctransporters_Environmentalinformationprocessing_Membranetransport_xylF,D-xylosetransportsystemsubstrate-bindingprotein	6,74218E-05	3,56673E-05	9,13591E-05
K01698_ko00830_Retinolmetabolism_Metabolism_Metabolismofcofactorsandvitamins_hemB,ALAD,porphobilinogensynthase[EC:4.2.1.24]	0,00014003	0,000193623	0,000149497
K06153_ko01005_Lipopolysaccharidebiosynthesisproteins_Metabolism_Glycanbiosynthesisandmetabolism_E3.6.1.27,bacA,undecaprenyl-diphosphatase[EC:3.6.1.27]	0,000938719	0,000937541	0,001262417
K08728_ko00240_Pyrimidinemetabolism_Metabolism_Nucleotidemetabolism_E2.4.2.6,nucleosidedeoxyribosyltransferase[EC:2.4.2.6]	2,59315E-05	4,5858E-05	1,66107E-05
K02002_ko02010_Ctransporters_Environmentalinformationprocessing_Membranetransport_proX,glycinebetaine/prolinetransportsystemsubstrate-bindingprotein	3,11177E-05	1,5286E-05	6,6443E-05
K00170_ko00020_Citratecycle(TCAcycle)_Metabolism_Carbohydratemetabolism_porB,pyruvateferredoxinoxidoreductase,betasubunit[EC:1.2.7.1];K00170_ko00010_Glycolysis/Gluconeogenesis_Metabolism_Carbohydratemetabolism_porB,pyruvateferredoxinoxid	6,22355E-05	6,1144E-05	0,000132886
K11383_ko02020_Two-componentsystem_Environmentalinformationprocessing_Signaltrasduction_kinB,two-componentsystem,NtrCfamily,sensorhistidinekinaseKinB[EC:2.7.13.3]	2,07452E-05	3,56673E-05	5,81376E-05
K03637_ko04122_Sulfurrelaysystem_GeneticInformationProcessing_Folding,sortinganddegradation_moaC,cyclicpyranopterinphosphatesynthase[EC:4.1.99.18];K03637_ko00785_Lipoicacidmetabolism_Metabolism_Metabolismofcofactorsandvitamins_moaC,cyclic	0,000160775	0,000112097	0,000174413
K00762_ko00240_Pyrimidinemetabolism_Metabolism_Nucleotidemetabolism_pyrE,orotatephosphoribosyltransferase[EC:2.4.2.10]	0,000653473	0,000713347	0,000705957
K09811_ko02010_Ctransporters_Environmentalinformationprocessing_Membranetransport_ftsX,celldivisiontransportsystempermeaseprotein	0,000596424	0,000591059	0,000506628
K03405_ko00830_Retinolmetabolism_Metabolism_Metabolismofcofactorsandvitamins_chlI,bchI,magnesiumchelatasesubunitI[EC:6.6.1.1]	1,55589E-05	0	8,30537E-06
K02189_ko00830_Retinolmetabolism_Metabolism_Metabolismofcofactorsandvitamins_cbiG,cobalt-precorrin5Ahydrolase[EC:3.7.1.12]	0,000134844	6,62393E-05	9,13591E-05
K03471_ko03030_DNAreplication_GeneticinformationProcessing_ReplicationandRepair_rnhC,ribonucleaseHIII[EC:3.1.26.4]	9,85395E-05	0,000147765	0,00021594
K00872_ko00260_Glycine,serineandthreoninemetabolism_Metabolism_Aminoacidmetabolism_thrB1,homoserinekinase[EC:2.7.1.39];K00872_ko01230_Biosynthesisofaminoacids_Metabolism_Overview_thrB1,homoserinekinase[EC:2.7.1.39]	6,74218E-05	7,13347E-05	0,000132886
K02302_ko00830_Retinolmetabolism_Metabolism_Metabolismofcofactorsandvitamins_cysG,uroporphyrin-IIIC-methyltransferase/precorrin-2dehydrogenase/sirohydrochlorinferrochelatase[EC:2.1.1.1071.3.1.764.99.1.4]	5,70492E-05	2,03813E-05	1,66107E-05
K00942_ko00230_Purinemetabolism_Metabolism_Nucleotidemetabolism_E2.7.4.8,gmk,guanylatekinase[EC:2.7.4.8]	0,00096465	0,001875083	0,001910236
K13896_ko02010_Ctransporters_Environmentalinformationprocessing_Membranetransport_yejF,microcinCtransportsystemATP-bindingprotein	5,70492E-05	8,66207E-05	9,13591E-05
K07251_ko00730_Thiaminemetabolism_Metabolism_Metabolismofcofactorsandvitamins_thiK,thiaminekinase[EC:2.7.1.89]	2,59315E-05	5,09533E-05	2,49161E-05
K02796_ko02010_Ctransporters_Environmentalinformationprocessing_Membranetransport_PTS-Man-EIID,manZ,PTSsystem,mannose-specificIIDcomponent;K02796_ko00520_Aminosugarandnucleotidesugarmetabolism_Metabolism_Carbohydratemetabolism_PT	0,000549747	0,000178337	0,000157802
K03644_ko00785_Lipoicacidmetabolism_Metabolism_Metabolismofcofactorsandvitamins_lipA,lipoicacidsynthetase[EC:2.8.1.8]	6,74218E-05	0,000254767	0,000141191
K01609_ko00400_Phenylalanine,tyrosineandtryptophanbiosynthesis_Metabolism_Aminoacidmetabolism_trpC,indole-3-glycerolphosphatesynthase[EC:4.1.1.48];K01609_ko01230_Biosynthesisofaminoacids_Metabolism_Overview_trpC,indole-3-glycerolphosphate	0,000202265	0,000224195	0,00034052
K02769_ko02010_Ctransporters_Environmentalinformationprocessing_Membranetransport_PTS-Fru-EIIB,fruA,PTSsystem,fructose-specificIIBcomponent[EC:2.7.1.69];K02769_ko00051_Fructoseandmannosemetabolism_Metabolism_Carbohydratemetabolism_PTS	8,29807E-05	4,5858E-05	9,13591E-05
K14306_ko03013_RNAtransport_GeneticinformationProcessing_Transcription_NUP62,NSP1,nuclearporecomplexproteinNup62	3,11177E-05	0	0
K09812_ko02010_Ctransporters_Environmentalinformationprocessing_Membranetransport_ftsE,celldivisiontransportsystemATP-bindingprotein	0,000710522	0,000927351	0,001137836
K00042_ko00630_Glyoxylateanddicarboxylatemetabolism_Metabolism_Carbohydratemetabolism_E1.1.1.60,garR,2-hydroxy-3-oxopropionatereductase[EC:1.1.1.60]	0,000103726	0,000117193	9,13591E-05
K00798_ko00830_Retinolmetabolism_Metabolism_Metabolismofcofactorsandvitamins_E2.5.1.17,cobO,btuR,cob(I)alaminadenosyltransferase[EC:2.5.1.17]	0,000430462	0,000468771	0,000431879
K04518_ko00400_Phenylalanine,tyrosineandtryptophanbiosynthesis_Metabolism_Aminoacidmetabolism_pheA2,prephenatedehydratase[EC:4.2.1.51];K04518_ko01230_Biosynthesisofaminoacids_Metabolism_Overview_pheA2,prephenatedehydratase[EC:4.2.1.51	0,000155589	0,000173241	0,000224245
K01457_ko00791_Atrazinedegradation_Humandiseases_Xenobioticsbiodegradationandmetabolism_E3.5.1.54,allophanatehydrolase[EC:3.5.1.54];K01457_ko00330_Arginineandprolinemetabolism_Metabolism_Aminoacidmetabolism_E3.5.1.54,allophanatehydrola	1,03726E-05	1,01907E-05	1,66107E-05
K07705_ko02020_Two-componentsystem_Environmentalinformationprocessing_Signaltrasduction_lytT,lytR,two-componentsystem,LytTfamily,responseregulatorLytT	0,000357854	0,000524819	0,000797316
K12453_ko00520_Aminosugarandnucleotidesugarmetabolism_Metabolism_Carbohydratemetabolism_rfbS,CDP-paratosesynthetase[EC:1.1.1.342]	3,6304E-05	2,54767E-05	3,32215E-05
K00963_ko00520_Aminosugarandnucleotidesugarmetabolism_Metabolism_Carbohydratemetabolism_UGP2,galU,galF,UTP--glucose-1-phosphateuridylyltransferase[EC:2.7.7.9];K00963_ko00052_Galactosemetabolism_Metabolism_Carbohydratemetabolism_UGP2	0,00042009	0,000412722	0,000357131
K05396_ko00270_Cysteineandmethioninemetabolism_Metabolism_Aminoacidmetabolism_dcyD,D-cysteinedesulfhydrase[EC:4.4.1.15]	0,000114098	8,66207E-05	0,000199329
K02419_ko02040_Flagellarassembly_Organismalsystem_Cellmobility_fliP,flagellarbiosyntheticproteinFliP	0,000160775	0,00015286	0,000224245
K02455_ko02010_Ctransporters_Environmentalinformationprocessing_Membranetransport_gspF,generalsecretionpathwayproteinF	4,14903E-05	1,01907E-05	5,81376E-05
K00878_ko00730_Thiaminemetabolism_Metabolism_Metabolismofcofactorsandvitamins_thiM,hydroxyethylthiazolekinase[EC:2.7.1.50]	0,000217824	0,00015286	0,000282383
K06013_ko00900_Terpenoidbackbonebiosynthesis_Metabolism_Metabolismofterpenoidsandpolyketides_STE24,STE24endopeptidase[EC:3.4.24.84]	6,22355E-05	3,0572E-05	0,000124581
K11071_ko02010_Ctransporters_Environmentalinformationprocessing_Membranetransport_potB,spermidine/putrescinetransportsystempermeaseprotein	0,000316364	0,000682775	0,000473406
K14083_ko01200_Carbonmetabolism_Metabolism_Overview_mttB,trimethylamine---corrinoidproteinCo-methyltransferase[EC:2.1.1.250];K14083_ko00194_Photosynthesisproteins_Metabolism_Energymetabolism_mttB,trimethylamine---corrinoidproteinCo-meth	2,07452E-05	3,0572E-05	1,66107E-05
K01661_ko00130_Ubiquinoneandotherterpenoid-quinonebiosynthesis_Metabolism_Metabolismofcofactorsandvitamins_menB,naphthoatesynthase[EC:4.1.3.36]	0,000311177	0,000173241	0,000282383
K03082_ko00040_Pentoseandglucuronateinterconversions_Metabolism_Carbohydratemetabolism_sgbU,hexulose-6-phosphateisomerase[EC:5.-.-.-]	4,66766E-05	4,5858E-05	9,13591E-05
K02417_ko02030_Bacterialchemotaxis_Organismalsystem_Cellmobility_fliNY,fliN,flagellarmotorswitchproteinFliN/FliY;K02417_ko02040_Flagellarassembly_Organismalsystem_Cellmobility_fliNY,fliN,flagellarmotorswitchproteinFliN/FliY	0,000150402	0,000122288	0,000191024
K02936_ko03010_Ribosome_GeneticinformationProcessing_Transcription_RP-L7Ae,RPL7A,largesubunitribosomalproteinL7Ae	7,77944E-05	0,000300625	0,000207634
K02435_ko00970_Aminoacyl-tRNAbiosynthesis_Geneticinformationandprocessing_Transcription_gatC,GATC,aspartyl-tRNA(Asn)/glutamyl-tRNA(Gln)amidotransferasesubunitC[EC:6.3.5.66.3.5.7]	0,000202265	9,1716E-05	0,000141191
K14327_ko03015_mRNAsurveillancepathway_GeneticinformationProcessing_Transcription_UPF2,RENT2,regulatorofnonsensetranscripts2;K14327_ko03013_RNAtransport_GeneticinformationProcessing_Transcription_UPF2,RENT2,regulatorofnonsensetranscripts2	5,18629E-06	2,54767E-05	0
K01808_ko00051_Fructoseandmannosemetabolism_Metabolism_Carbohydratemetabolism_rpiB,ribose5-phosphateisomeraseB[EC:5.3.1.6];K01808_ko00030_Pentosephosphatepathway_Metabolism_Carbohydratemetabolism_rpiB,ribose5-phosphateisomeraseB[	0,000508257	0,000448389	0,000490017
K02020_ko02010_Ctransporters_Environmentalinformationprocessing_Membranetransport_modA,molybdatetransportsystemsubstrate-bindingprotein	0,000217824	0,000173241	0,000199329
K00891_ko00400_Phenylalanine,tyrosineandtryptophanbiosynthesis_Metabolism_Aminoacidmetabolism_E2.7.1.71,aroK,aroL,shikimatekinase[EC:2.7.1.71];K00891_ko01230_Biosynthesisofaminoacids_Metabolism_Overview_E2.7.1.71,aroK,aroL,shikimatekinase[E	0,000446021	0,000448389	0,000498322
K01968_ko00280_Valine,leucineandisoleucinedegradation_Metabolism_Aminoacidmetabolism_E6.4.1.4A,3-methylcrotonyl-CoAcarboxylasealphasubunit[EC:6.4.1.4]	1,03726E-05	3,0572E-05	1,66107E-05
K00867_ko00770_PantothenateandCoABiosynthesis_Metabolism_Metabolismofcofactorsandvitamins_coaA,typelpantothenatekinase[EC:2.7.1.33]	6,74218E-05	4,07627E-05	2,49161E-05
K00603_ko00340_Histidinemetabolism_Metabolism_Aminoacidmetabolism_fctD,glutamateformiminotransferase[EC:2.1.2.5];K00603_ko00670_Onecarbonpoolbyfolate_Metabolism_Metabolismofcofactorsandvitamins_fctD,glutamateformiminotransferase[EC:2.1	7,77944E-05	0,000122288	0,000199329
K02414_ko02040_Flagellarassembly_Organismalsystem_Cellmobility_fliK,flagellarhook-lengthcontrolproteinFliK	4,14903E-05	7,13347E-05	9,96645E-05
K00015_ko00630_Glyoxylateanddicarboxylatemetabolism_Metabolism_Carbohydratemetabolism_gyaR,glyoxylatereductase[EC:1.1.1.26]	0,000150402	0,000147765	0,000166107
K01433_ko00630_Glyoxylateanddicarboxylatemetabolism_Metabolism_Carbohydratemetabolism_purU,formyltetrahydrofolatedeformylase[EC:3.5.1.10];K01433_ko00670_Onecarbonpoolbyfolate_Metabolism_Metabolismofcofactorsandvitamins_purU,formyltetr	3,11177E-05	0,000117193	8,30537E-05
K04561_ko00910_Nitrogenmetabolism_Metabolism_Energymetabolism_norB,nitricoxidereductasesubunitB[EC:1.7.2.5]	1,03726E-05	0	8,30537E-06
K10941_ko02020_Two-componentsystem_Environmentalinformationprocessing_Signaltrasduction_flrA,sigma-54specifictranscriptionalregulator,flagellarregulatoryproteinA;K10941_ko05111_Vibriocholeraepathogeniccycle_HumanDiseases_Infectiousdiseases_flr	9,33532E-05	8,15253E-05	0,000116275
K01426_ko00330_Arginineandprolinemetabolism_Metabolism_Aminoacidmetabolism_E3.5.1.4,amiE,amidase[EC:3.5.1.4];K01426_ko00360_Phenylalaninemetabolism_Metabolism_Aminoacidmetabolism_E3.5.1.4,amiE,amidase[EC:3.5.1.4];K01426_ko00380_Tryp	0,000108912	7,13347E-05	0,000141191
K13953_ko00350_Tyrosinemetabolism_Metabolism_Aminoacidmetabolism_adhP,alcoholdehydrogenase,propanol-preferring[EC:1.1.1.1];K13953_ko00010_Glycolysis/Gluconeogenesis_Metabolism_Carbohydratemetabolism_adhP,alcoholdehydrogenase,propanol	0,000202265	6,1144E-05	7,47483E-05
K00930_ko00330_Arginineandprolinemetabolism_Metabolism_Aminoacidmetabolism_argB,acetylglutamatekinase[EC:2.7.2.8];K00930_ko01210_Oxocarboxylicacidmetabolism_Metabolism_Overview_argB,acetylglutamatekinase[EC:2.7.2.8];K00930_ko01230_Bios	0,000435648	0,000468771	0,000390352

K01963_ko00630_Glyoxylateanddicarboxylatemetabolism_Metabolism_Carbohydratemetabolism_accD,acetyl-CoAcarboxylasecarboxyltransferasesubunitbeta[EC:6.4.1.2];K01963_ko00620_Pyruvatemetabolism_Metabolism_Carbohydratemetabolism_accD,acetyl-	0,000269687	0,000198718	0,000382047
K12251_ko00330_Arginineandprolinemetabolism_Metabolism_Aminoacidmetabolism_aguB,N-carbamoylputrescineamidase[EC:3.5.1.53]	0,000404531	0,000545201	0,000481712
K00606_ko00770_PantothenateandCoAbiosynthesis_Metabolism_Metabolismofcofactorsandvitamins_panB,3-methyl-2-oxobutanoatehydroxymethyltransferase[EC:2.1.2.11]	0,000570492	0,000321006	0,000141191
K00101_ko00620_Pyruvatemetabolism_Metabolism_Carbohydratemetabolism_E1.1.2.3,lldD,L-lactatedehydrogenase(cytochrome)[EC:1.1.2.3]	3,6304E-05	5,09533E-06	3,32215E-05
K00286_ko00330_Arginineandprolinemetabolism_Metabolism_Aminoacidmetabolism_E1.5.1.2,proC,pyrroline-5-carboxylatereductase[EC:1.5.1.2];K00286_ko01230_Biosynthesisofaminoacids_Metabolism_Overview_E1.5.1.2,proC,pyrroline-5-carboxylatereductas	0,00036304	0,000356673	0,000282383
K01753_ko00260_Glycine,serineandthreoninemetabolism_Metabolism_Aminoacidmetabolism_dsdA,D-serinedehydratase[EC:4.3.1.18]	8,8167E-05	2,54767E-05	6,6443E-05
K02065_ko02010_Ctransporters_Environmentalinformationprocessing_Membranetransport_mlaF,linL,mkl,phospholipid/cholesterol/gamma-HCHtransportsystemATP-bindingprotein	0,000404531	0,000280243	0,000257467
K14205_ko05150_Staphylococcusaureusinfection_HumanDiseases_Infectiousdiseases_mprF,fmtC,phosphatidylglycerollysyltransferase[EC:2.3.2.3]	7,77944E-05	5,60487E-05	6,6443E-05
K10201_ko02010_Ctransporters_Environmentalinformationprocessing_Membranetransport_ABC.NGC.P,N-acetylglucosaminetransportsystempermeaseprotein	2,07452E-05	4,07627E-05	0
K02008_ko02010_Ctransporters_Environmentalinformationprocessing_Membranetransport_cbiQ,cobalt/nickeltransportsystempermeaseprotein	0,001166916	0,001013971	0,000946812
K15146_ko04919_Thyroidhormonesignalingpathway_Organismalsystem_Endocrinsystem_MED4,mediatorofRNApolymeraseIItranscriptionsubunit4	1,03726E-05	0	0
K03527_ko00900_Terpenoidbackbonebiosynthesis_Metabolism_Metabolismofterpenoidsandpolyketides_ispH,lytB,4-hydroxy-3-methylbut-2-enyldiphosphatereductase[EC:1.17.1.2]	0,000477139	0,000662393	0,000597987
K03783_ko00760_Nicotinateandnicotinamidemetabolism_Metabolism_Metabolismofcofactorsandvitamins_punA,purine-nucleosidephosphorylase[EC:2.4.2.1];K03783_ko00230_Purinemetabolism_Metabolism_Nucleotidemetabolism_punA,purine-nucleosidephos	0,000757199	0,000779586	0,000539849
K00981_ko04066_HIF-1signalingpathway_Environmentalinformationprocessing_Signaltrasduction_E2.7.7.41,CDS1,CDS2,cdsA,phosphatidatecytidylyltransferase[EC:2.7.7.41];K00981_ko00564_Glycerophospholipidmetabolism_Metabolism_Lipidmetabolism_E2.7.7	0,000580865	0,000713347	0,000514933
K03182_ko00130_Ubiquinoneandotherterpenoid-quinonebiosynthesis_Metabolism_Metabolismofcofactorsandvitamins_ubiD,3-octaprenyl-4-hydroxybenzoatecarboxy-lyaseUbiD[EC:4.1.1.-]	7,77944E-05	4,5858E-05	7,47483E-05
K02169_ko00780_Biotinmetabolism_Metabolism_Metabolismofcofactorsandvitamins_bioC,malonyl-CoAO-methyltransferase[EC:2.1.1.197]	0,000155589	0,000280243	0,000207634
K00161_ko04066_HIF-1signalingpathway_Environmentalinformationprocessing_Signaltrasduction_PDHA,pdhA,pyruvatedehydrogenaseE1componentalphasubunit[EC:1.2.4.1];K00161_ko05230_Centralcarbonmetabolismincancer_HumanDiseases_Cancers_PDHA,p	0,000223011	0,000107002	0,000174413
K00385_ko00920_Sulfurmetabolism_Metabolism_Energymetabolism_asrC,anaerobicsulfitereductasesubunitC	0,000145216	8,15253E-05	7,47483E-05
K05966_ko02020_Two-componentsystem_Environmentalinformationprocessing_Signaltrasduction_citG,triphosphoribosyl-dephospho-CoAsynthase[EC:2.4.2.52]	1,55589E-05	2,54767E-05	7,47483E-05
K13602_ko00830_Retinolmetabolism_Metabolism_Metabolismofcofactorsandvitamins_bchR,bacteriochlorophyllC12methyltransferase[EC:2.1.1.-]	3,6304E-05	3,0572E-05	2,49161E-05
K02304_ko00830_Retinolmetabolism_Metabolism_Metabolismofcofactorsandvitamins_MET8,precorrin-2dehydrogenase/sirohydrochlorinferrochelatase[EC:1.3.1.764.99.1.4]	9,33532E-05	0,000219099	0,000149497
K07668_ko02020_Two-componentsystem_Environmentalinformationprocessing_Signaltrasduction_vicR,two-componentsystem,OmpRfamily,responseregulatorVicR	0,001078749	0,001385931	0,001137836
K12820_ko03040_Spliceosome_GeneticinformationProcessing_Transcription_DHX15,PRP43,pre-mRNA-splicingfactorATP-dependentRNAhelicaseDHX15/PRP43[EC:3.6.4.13]	4,66766E-05	1,5286E-05	1,66107E-05
K01623_ko00051_Fructoseandmannosemetabolism_Metabolism_Carbohydratemetabolism_ALDO,fructose-bisphosphatealdolase,classI[EC:4.1.2.13];K01623_ko00010_Glycolysis/Gluconeogenesis_Metabolism_Carbohydratemetabolism_ALDO,fructose-bisphospha	6,22355E-05	6,62393E-05	0,00010797
K09816_ko02010_Ctransporters_Environmentalinformationprocessing_Membranetransport_znuB,zinctransportsystempermeaseprotein	0,000347482	0,000519724	0,000656124
K00806_ko00900_Terpenoidbackbonebiosynthesis_Metabolism_Metabolismofterpenoidsandpolyketides_uppS,undecaprenyldiphosphatesynthase[EC:2.5.1.31]	0,000793503	0,000850921	0,0007724
K05363_ko01005_Lipopolysaccharidebiosynthesisproteins_Metabolism_Glycanbiosynthesisandmetabolism_murM,serine/alanineaddingenzyme[EC:2.3.2.10]	6,74218E-05	8,15253E-05	9,96645E-05
K12554_ko01005_Lipopolysaccharidebiosynthesisproteins_Metabolism_Glycanbiosynthesisandmetabolism_murN,alanineaddingenzyme[EC:2.3.2.-]	2,59315E-05	5,09533E-05	7,47483E-05
K02428_ko00230_Purinemetabolism_Metabolism_Nucleotidemetabolism_rdgB,XTP/dITPdiphosphohydrolase[EC:3.6.1.66]	0,000326736	0,000524819	0,000390352
K02841_ko00540_Lipopolysaccharidebiosynthesis_Metabolism_Glycanbiosynthesisandmetabolism_waaC,rfaC,heptosyltransferaseI[EC:2.4.-.-]	3,11177E-05	3,56673E-05	8,30537E-06
K09680_ko00770_PantothenateandCoAbiosynthesis_Metabolism_Metabolismofcofactorsandvitamins_coaW,typeIIpantothenatekinase[EC:2.7.1.33]	7,26081E-05	0,000157955	9,13591E-05
K02042_ko02010_Ctransporters_Environmentalinformationprocessing_Membranetransport_phnE,phosphonatetransportsystempermeaseprotein	0,000124471	0,000127383	0,00023255
K06879_ko00785_Lipoicacidmetabolism_Metabolism_Metabolismofcofactorsandvitamins_queF,7-cyano-7-deazaguaninereductase[EC:1.7.1.13]	4,14903E-05	1,01907E-05	3,32215E-05
K02115_ko00190_Oxidativephosphorylation_Metabolism_Energymetabolism_ATPF1G,atpG,F-typeH+-transportingATPasesubunitgamma;K02115_ko00195_Photosynthesis_Metabolism_Energymetabolism_ATPF1G,atpG,F-typeH+-transportingATPasesubunitgamma	0,000622355	0,000677679	0,000506628
K00720_ko00600_Sphingolipidmetabolism_Metabolism_Lipidmetabolism_UGCG,ceramideglucosyltransferase[EC:2.4.1.80]	0	1,5286E-05	0
K06861_ko02010_Ctransporters_Environmentalinformationprocessing_Membranetransport_lptB,lipopolysaccharideexportsystemATP-bindingprotein[EC:3.6.3.-]	0,000446021	0,000591059	0,000564765
K10560_ko02010_Ctransporters_Environmentalinformationprocessing_Membranetransport_rhaP,rhamnosetransportsystempermeaseprotein	1,03726E-05	0	1,66107E-05
K00998_ko00260_Glycine,serineandthreoninemetabolism_Metabolism_Aminoacidmetabolism_pssA,CDP-diacylglycerol---serineO-phosphatidyltransferase[EC:2.7.8.8];K00998_ko00564_Glycerophospholipidmetabolism_Metabolism_Lipidmetabolism_pssA,CDP-dia	0,000311177	0,000259862	0,000207634
K02795_ko02010_Ctransporters_Environmentalinformationprocessing_Membranetransport_PTS-Man-EIIC,manY,PTSsystem,mannose-specificIICcomponent;K02795_ko00520_Aminosugarandnucleotidesugarmetabolism_Metabolism_Carbohydratemetabolism_PT	0,000497884	0,000285339	0,000282383
K00074_ko00360_Phenylalaninemetabolism_Metabolism_Aminoacidmetabolism_paaH,hbd,fadB,mmgB,3-hydroxybutyryl-CoAdehydrogenase[EC:1.1.1.157];K00074_ko00630_Glyoxylateanddicarboxylatemetabolism_Metabolism_Carbohydratemetabolism_paaH,h	0,000435648	0,000290434	0,000348826
K10918_ko05111_Vibriocholeraepathogeniccycle_HumanDiseases_Infectiousdiseases_aphB,LysRfamilytranscriptionalregulator,transcriptionalactivatorAphB	0,000165961	0,000112097	0,000124581
K06215_ko00750_VitaminB6metabolism_Metabolism_Metabolismofcofactorsandvitamins_pdxS,pdx1,pyridoxal5'-phosphatesynthasepdxSsubunit[EC:4.3.3.6]	0,000238569	0,000107002	0,000116275
K00337_ko00190_Oxidativephosphorylation_Metabolism_Energymetabolism_nuoH,NADH-quinoneoxidoreductasesubunitH[EC:1.6.5.3]	0,000809061	0,00038215	0,00032391
K11041_ko05150_Staphylococcusaureusinfection_HumanDiseases_Infectiousdiseases_eta,exfoliativetoxinA/B	0,000108912	7,643E-05	3,32215E-05
K03525_ko00770_PantothenateandCoAbiosynthesis_Metabolism_Metabolismofcofactorsandvitamins_coaX,typeIIIpantothenatekinase[EC:2.7.1.33]	0,000399344	0,000371959	0,000282383
K10563_ko03410_Baseexcisionrepair_GeneticinformationProcessing_ReplicationandRepair_mutM,fpg,formamidopyrimidine-DNAglycosylase[EC:3.2.2.234.2.99.18]	0,000155589	0,000117193	0,000199329
K05936_ko00830_Retinolmetabolism_Metabolism_Metabolismofcofactorsandvitamins_cobM,cbiF,precorrin-4/cobalt-precorrin-4C11-methyltransferase[EC:2.1.1.1332.1.1.271]	0,000233383	0,000254767	0,000249161
K01611_ko00330_Arginineandprolinemetabolism_Metabolism_Aminoacidmetabolism_speD,AMD1,S-adenosylmethioninedecarboxylase[EC:4.1.1.50];K01611_ko00270_Cysteineandmethioninemetabolism_Metabolism_Aminoacidmetabolism_speD,AMD1,S-adeno	0,000108912	4,5858E-05	9,96645E-05
K00767_ko00760_Nicotinateandnicotinamidemetabolism_Metabolism_Metabolismofcofactorsandvitamins_nadC,QPRT,nicotinate-nucleotidepyrophosphorylase(carboxylating)[EC:2.4.2.19]	0,00046158	0,000545201	0,000398658
K10110_ko02010_Ctransporters_Environmentalinformationprocessing_Membranetransport_malG,maltose/maltodextrintransportsystempermeaseprotein	0,000150402	0,000112097	0,00010797
K01062_ko00564_Glycerophospholipidmetabolism_Metabolism_Lipidmetabolism_PAFAH,platelet-activatingfactoracetylhydrolase[EC:3.1.1.47]	0,000145216	0,000193623	9,96645E-05
K14455_ko00250_Alanine,aspartateandglutamatemetabolism_Metabolism_Aminoacidmetabolism_GOT2,aspartateaminotransferase,mitochondrial[EC:2.6.1.1];K14455_ko00330_Arginineandprolinemetabolism_Metabolism_Aminoacidmetabolism_GOT2,aspartate	1,03726E-05	0	0
K01501_ko00380_Tryptophanmetabolism_Metabolism_Aminoacidmetabolism_E3.5.5.1,nitrilase[EC:3.5.5.1];K01501_ko00910_Nitrogenmetabolism_Metabolism_Energymetabolism_E3.5.5.1,nitrilase[EC:3.5.5.1];K01501_ko00460_Cyanoaminoacidmetabolism_Met	9,33532E-05	3,56673E-05	0,000116275
K01905_ko00010_Glycolysis/Gluconeogenesis_Metabolism_Carbohydratemetabolism_E6.2.1.13,acetyl-CoAsynthetase(ADP-forming)[EC:6.2.1.13];K01905_ko00630_Glyoxylateanddicarboxylatemetabolism_Metabolism_Carbohydratemetabolism_E6.2.1.13,acetyl-(	0	2,03813E-05	1,66107E-05
K02489_ko02020_Two-componentsystem_Environmentalinformationprocessing_Signaltrasduction_hk1,two-componentsystem,glyceroluptakeandutilizationsensorkinase[EC:2.7.13.3]	5,18629E-06	0	0
K02517_ko00540_Lipopolysaccharidebiosynthesis_Metabolism_Glycanbiosynthesisandmetabolism_htrB,lipidAbiosynthesislauroylacyltransferase[EC:2.3.1.-]	0,000202265	0,000239481	0,000182718
K07699_ko02020_Two-componentsystem_Environmentalinformationprocessing_Signaltrasduction_spo0A,two-componentsystem,responseregulator,stage0sporulationproteinA	0,000596424	0,000601249	0,000465101
K00529_ko00360_Phenylalaninemetabolism_Metabolism_Aminoacidmetabolism_hcaD,3-phenylpropionate/trans-cinnamatedioxygenaseferredoxinreductasesubunit[EC:1.18.1.3];K00529_ko00071_Fattyaciddegradation_Metabolism_Lipidmetabolism_hcaD,3-phen	0,000108912	0,000270053	0,000116275
K07308_ko00920_Sulfurmetabolism_Metabolism_Energymetabolism_dmsC,anaerobicdimethylsulfoxidereductasesubunitC(DMSOreductaseanchorsubunit)	0	5,09533E-05	1,66107E-05
K00037_ko00120_Primarybileacidbiosynthesis_Metabolism_Lipidmetabolism_E1.1.1.50,3-alpha-hydroxysteroiddehydrogenase[EC:1.1.1.50];K00037_ko00140_Steroidhormonebiosynthesis_Metabolism_Lipidmetabolism_E1.1.1.50,3-alpha-hydroxysteroiddehydrog	1,03726E-05	1,5286E-05	8,30537E-06
K08094_ko00030_Pentosephosphatepathway_Metabolism_Carbohydratemetabolism_hxlB,6-phospho-3-hexuloisomerase[EC:5.3.1.27];K08094_ko01230_Biosynthesisofaminoacids_Metabolism_Overview_hxlB,6-phospho-3-hexuloisomerase[EC:5.3.1.27];K08094_k	8,29807E-05	6,1144E-05	7,47483E-05
K05306_ko00440_Phosphonateandphosphinatemetabolism_Metabolismofotheraminoacids_phnX,phosphonoacetaldehydehydrolase[EC:3.11.1.1]	6,22355E-05	7,643E-05	0,000132886
K07673_ko02020_Two-componentsystem_Environmentalinformationprocessing_Signaltrasduction_narX,two-componentsystem,NarLfamily,nitrate/nitritesensorhistidinekinaseNarX[EC:2.7.13.3]	3,6304E-05	1,5286E-05	3,32215E-05
K01749_ko00830_Retinolmetabolism_Metabolism_Metabolismofcofactorsandvitamins_hemC,HMBS,hydroxymethylbilanesynthase[EC:2.5.1.61]	0,000129657	0,000259862	0,00021594
K00065_ko00040_Pentoseandglucuronateinterconversions_Metabolism_Carbohydratemetabolism_kduD,2-deoxy-D-gluconate3-dehydrogenase[EC:1.1.1.125]	0,000129657	9,1716E-05	9,13591E-05
K01644_ko02020_Two-componentsystem_Environmentalinformationprocessing_Signaltrasduction_citE,citratelyasesubunitbeta/citryl-CoAlyase[EC:4.1.3.34]	0,000186706	0,000163051	0,000124581
K03196_ko02010_Ctransporters_Environmentalinformationprocessing_Membranetransport_virB11,lvhB11,typeIVsecretionsystemproteinVirB11;K03196_ko05120_EpithelialcellsignalinginHelicobacterpyloriinfection_HumanDiseases_Infectiousdiseases_virB11,lvhE	5,18629E-05	1,01907E-05	3,32215E-05
K00979_ko00540_Lipopolysaccharidebiosynthesis_Metabolism_Glycanbiosynthesisandmetabolism_kdsB,3-deoxy-manno-octulosonatecytidylyltransferase(CMP-KDOsynthetase)[EC:2.7.7.38]	0,000269687	0,000280243	0,000274077
K01838_ko00500_Starchandsucrosemetabolism_Metabolism_Carbohydratemetabolism_pgmB,beta-phosphoglucomutase[EC:5.4.2.6]	0,000663845	0,000621631	0,000581376
K10227_ko02010_Ctransporters_Environmentalinformationprocessing_Membranetransport_smoE,mtlE,sorbitol/mannitoltransportsystemsubstrate-bindingprotein	0	0	8,30537E-06

K03183_ko00130_Ubiquinoneandotherterpenoid-quinonebiosynthesis_Metabolism_Metabolismofcofactorsandvitamins_ubiE,ubiquinone/menaquinonebiosynthesismethyltransferase[EC:2.1.1.1632.1.1.201]	0,00050307	0,000361769	0,00032391
K07674_ko02020_Two-componentsystem_Environmentalinformationprocessing_Signaltrasduction_narQ,two-componentsystem,NarLfamily,nitrate/nitritesensorhistidinekinaseNarQ[EC:2.7.13.3]	5,18629E-06	2,03813E-05	1,66107E-05
K02588_ko00910_Nitrogenmetabolism_Metabolism_Energymetabolism_nifH,nitrogenaseironproteinNifH[EC:1.18.6.1];K02588_ko00625_Chloroalkaneandchloroalkenedegradation_Metabolism_Xenobioticsbiodegradationandmetabolism_nifH,nitrogenaseironprot	8,29807E-05	7,643E-05	0,000166107
K03584_ko03440_Homologousrecombination_GeneticinformationProcessing_ReplicationandRepair_recO,DNArepairproteinRecO(recombinationproteinO)	0,000311177	0,000524819	0,000705957
K01803_ko00051_Fructoseandmannosemetabolism_Metabolism_Carbohydratemetabolism_TPI,tpiA,triosephosphateisomerase(TIM)[EC:5.3.1.1];K01803_ko00010_Glycolysis/Gluconeogenesis_Metabolism_Carbohydratemetabolism_TPI,tpiA,triosephosphateisome	0,001125425	0,001054734	0,000955118
K12343_ko00140_Steroidhormonebiosynthesis_Metabolism_Lipidmetabolism_SRD5A1,3-oxo-5-alpha-steroid4-dehydrogenase1[EC:1.3.1.22]	0,000103726	0,000127383	4,98322E-05
K12344_ko05215_Prostatecancer_HumanDiseases_Cancers_SRD5A2,3-oxo-5-alpha-steroid4-dehydrogenase2[EC:1.3.1.22];K12344_ko00140_Steroidhormonebiosynthesis_Metabolism_Lipidmetabolism_SRD5A2,3-oxo-5-alpha-steroid4-dehydrogenase2[EC:1.3.1.22	3,6304E-05	2,54767E-05	0,00010797
K02823_ko00240_Pyrimidinemetabolism_Metabolism_Nucleotidemetabolism_pyrDII,dihydroorotatedehydrogenaseelectrontransfersubunit	0,000264501	0,000341387	0,000456795
K01776_ko00471_D-GlutamineandD-glutamatemetabolism_Metabolism_Metabolismofotheraminoacids_murI,glutamateracemase[EC:5.1.1.3]	0,000814248	0,000876397	0,000747483
K01820_ko00040_Pentoseandglucuronateinterconversions_Metabolism_Carbohydratemetabolism_E5.3.1.-,[EC:5.3.1.-]	9,85395E-05	0,000101907	0,000141191
K11214_ko00194_Photosynthesisproteins_Metabolism_Energymetabolism_SHPK,sedoheptulokinase[EC:2.7.1.14]	4,14903E-05	3,0572E-05	6,6443E-05
K10557_ko02010_Ctransporters_Environmentalinformationprocessing_Membranetransport_IsrD,AI-2transportsystempermeaseprotein	1,55589E-05	1,01907E-05	0
K09817_ko02010_Ctransporters_Environmentalinformationprocessing_Membranetransport_znuC,zinctransportsystemATP-bindingprotein[EC:3.6.3.-]	0,000368227	0,00045858	0,000382047
K00559_ko00100_Steroidbiosynthesis_Metabolism_Lipidmetabolism_E2.1.1.41,SMT1,ERG6,sterol24-C-methyltransferase[EC:2.1.1.41]	1,03726E-05	1,5286E-05	8,30537E-06
K01715_ko00630_Glyoxylateanddicarboxylatemetabolism_Metabolism_Carbohydratemetabolism_crt,enoyl-CoAhydratase[EC:4.2.1.17];K01715_ko01200_Carbonmetabolism_Metabolism_Overview_crt,enoyl-CoAhydratase[EC:4.2.1.17];K01715_ko00194_Photosyr	0,00028006	0,000280243	0,000257467
K01071_ko00061_Fattyacidbiosynthesis_Metabolism_Lipidmetabolism_MCH,medium-chainacyl-[acyl-carrier-protein]hydrolase[EC:3.1.2.21]	0,000347482	0,000504438	0,00034052
K01708_ko00052_Galactosemetabolism_Metabolism_Carbohydratemetabolism_garD,galactaratedehydratase[EC:4.2.1.42]	1,55589E-05	4,5858E-05	8,30537E-06
K01241_ko00230_Purinemetabolism_Metabolism_Nucleotidemetabolism_amn,AMPnucleosidase[EC:3.2.2.4]	4,14903E-05	0,000198718	0,000116275
K11176_ko00230_Purinemetabolism_Metabolism_Nucleotidemetabolism_purO,IMPcyclohydrolase[EC:3.5.4.10]	0,000259315	0,000234385	0,000166107
K01826_ko00350_Tyrosinemetabolism_Metabolism_Aminoacidmetabolism_hpaF,hpcD,5-carboxymethyl-2-hydroxymuconateisomerase[EC:5.3.3.10];K01826_ko01220_Degradationofaromaticcompounds_Metabolism_Overview_hpaF,hpcD,5-carboxymethyl-2-hydı	6,74218E-05	4,07627E-05	8,30537E-05
K06164_ko00440_Phosphonateandphosphinatemetabolism_Metabolism_Metabolismofotheraminoacids_phnI,alpha-D-ribose1-methylphosphonate5-triphosphatesynthasesubunitPhnI[EC:2.7.8.37]	2,07452E-05	2,03813E-05	1,66107E-05
K03648_ko03410_Baseexcisionrepair_GeneticinformationProcessing_ReplicationandRepair_UNG,UDG,uracil-DNAglycosylase[EC:3.2.2.27];K03648_ko05340_Primaryimmunodeficiency_Humandiseases_Immunediseases_UNG,UDG,uracil-DNAglycosylase[EC:3.2.2.2	0,000591237	0,000642012	0,000597987
K02411_ko02040_Flagellarassembly_Organismalsystem_Cellmobility_fliH,flagellarassemblyproteinFliH	8,29807E-05	7,13347E-05	8,30537E-05
K03736_ko00564_Glycerophospholipidmetabolism_Metabolism_Lipidmetabolism_eutC,ethanolamineammonia-lyasesmallsubunit[EC:4.3.1.7]	2,59315E-05	5,09533E-05	1,66107E-05
K07658_ko02020_Two-componentsystem_Environmentalinformationprocessing_Signaltrasduction_phoB1,phoP,two-componentsystem,OmpRfamily,alkalinephosphatasesynthesisresponseregulatorPhoP	0,001135798	0,000932446	0,000880369
K07776_ko02020_Two-componentsystem_Environmentalinformationprocessing_Signaltrasduction_regX3,two-componentsystem,OmpRfamily,responseregulatorRegX3	0,00046158	0,000295529	0,000290688
K00616_ko00030_Pentosephosphatepathway_Metabolism_Carbohydratemetabolism_E2.2.1.2,talA,talB,transaldolase[EC:2.2.1.2];K00616_ko01230_Biosynthesisofaminoacids_Metabolism_Overview_E2.2.1.2,talA,talB,transaldolase[EC:2.2.1.2];K00616_ko01200_Ca	0,000223011	0,00038215	0,000332215
K01695_ko00260_Glycine,serineandthreoninemetabolism_Metabolism_Aminoacidmetabolism_trpA,tryptophansynthasealphachain[EC:4.2.1.20];K01695_ko00400_Phenylalanine,tyrosineandtryptophanbiosynthesis_Metabolism_Aminoacidmetabolism_trpA,trypto	0,000243756	0,000188527	0,000240856
K01058_ko00592_alpha-Linolenicacidmetabolism_Metabolism_Lipidmetabolism_pldA,phospholipaseA1[EC:3.1.1.323.1.1.4];K01058_ko00590_Arachidonicacidmetabolism_Metabolism_Lipidmetabolism_pldA,phospholipaseA1[EC:3.1.1.323.1.1.4];K01058_ko00564	0,00042009	0,000107002	0,000141191
K01489_ko00240_Pyrimidinemetabolism_Metabolism_Nucleotidemetabolism_cdd,CDA,cytidinedeaminase[EC:3.5.4.5];K01489_ko00983_Drugmetabolism-otherenzymes_Metabolism_Xenobioticsbiodegradationandmetabolism_cdd,CDA,cytidinedeaminase[EC:3.5	0,000451207	0,00045858	0,000473406
K00176_ko00020_Citratecycle(TCAcycle)_Metabolism_Carbohydratemetabolism;K00176_ko01200_Carbonmetabolism_Metabolism_Overview;K00176_ko00194_Photosynthesisproteins_Metabolism_Energymetabolism	0,000155589	0,000183432	0,000132886
K11751_ko00760_Nicotinateandnicotinamidemetabolism_Metabolism_Metabolismofcofactorsandvitamins_ushA,5'-nucleotidase/UDP-sugardiphosphatase[EC:3.1.3.53.6.1.45];K11751_ko00230_Purinemetabolism_Metabolism_Nucleotidemetabolism_ushA,5'-nuc	9,85395E-05	0,000147765	8,30537E-05
K03784_ko00760_Nicotinateandnicotinamidemetabolism_Metabolism_Metabolismofcofactorsandvitamins_deoD,purine-nucleosidephosphorylase[EC:2.4.2.1];K03784_ko00230_Purinemetabolism_Metabolism_Nucleotidemetabolism_deoD,purine-nucleosidepho	0,000243756	0,000264957	0,000240856
K09690_ko02010_Ctransporters_Environmentalinformationprocessing_Membranetransport_ABC-2.LPSE.P,lipopolysaccharidetransportsystempermeaseprotein	0,000368227	0,000377055	0,000739178
K00068_ko00051_Fructoseandmannosemetabolism_Metabolism_Carbohydratemetabolism_srlD,sorbitol-6-phosphate2-dehydrogenase[EC:1.1.1.140]	3,11177E-05	5,60487E-05	5,81376E-05
K07701_ko02020_Two-componentsystem_Environmentalinformationprocessing_Signaltrasduction_dcuS,two-componentsystem,CitBfamily,sensorhistidinekinaseDcuS[EC:2.7.13.3]	5,18629E-06	5,09533E-06	4,98322E-05
K03787_ko00760_Nicotinateandnicotinamidemetabolism_Metabolism_Metabolismofcofactorsandvitamins_surE,5'-nucleotidase[EC:3.1.3.5];K03787_ko00230_Purinemetabolism_Metabolism_Nucleotidemetabolism_surE,5'-nucleotidase[EC:3.1.3.5];K03787_ko002	0,000285246	0,000315911	0,000382047
K03337_ko00630_Glyoxylateanddicarboxylatemetabolism_Metabolism_Carbohydratemetabolism_iolB,5-deoxy-glucuronateisomerase[EC:5.3.1.30]	4,14903E-05	3,56673E-05	6,6443E-05
K02066_ko02010_Ctransporters_Environmentalinformationprocessing_Membranetransport_mlaE,linK,phospholipid/cholesterol/gamma-HCHtransportsystempermeaseprotein	0,00028006	0,000280243	0,00023255
K07130_ko00380_Tryptophanmetabolism_Metabolism_Aminoacidmetabolism_kynB,arylformamidase[EC:3.5.1.9];K07130_ko00630_Glyoxylateanddicarboxylatemetabolism_Metabolism_Carbohydratemetabolism_kynB,arylformamidase[EC:3.5.1.9]	0,000160775	0,000122288	0,000157802
K11606_ko02010_Ctransporters_Environmentalinformationprocessing_Membranetransport_sitD,manganese/irontransportsystempermeaseprotein	1,03726E-05	5,09533E-06	3,32215E-05
K09007_ko00785_Lipoicacidmetabolism_Metabolism_Metabolismofcofactorsandvitamins_GCH4,folE,GTPcyclohydrolaseI[EC:3.5.4.16]	2,07452E-05	2,54767E-05	4,98322E-05
K00978_ko00520_Aminosugarandnucleotidesugarmetabolism_Metabolism_Carbohydratemetabolism_rfbF,glucose-1-phosphatecytidylyltransferase[EC:2.7.7.33];K00978_ko00500_Starchandsucrosemetabolism_Metabolism_Carbohydratemetabolism_rfbF,glucose	0,000207452	0,000310815	0,000307299
K00641_ko00270_Cysteineandmethioninemetabolism_Metabolism_Aminoacidmetabolism_metX,homoserineO-acetyltransferase[EC:2.3.1.31]	6,22355E-05	0,000122288	4,15269E-05
K03118_ko02010_Ctransporters_Environmentalinformationprocessing_Membranetransport_tatC,sec-independentproteintranslocaseproteinTatC;K03118_ko04120_Ubiquitinmediatedproteolysis_GeneticInformationProcessing_Folding,sortinganddegradation_tatC	0,000176334	0,000371959	0,00032391
K00677_ko00540_Lipopolysaccharidebiosynthesis_Metabolism_Glycanbiosynthesisandmetabolism_lpxA,UDP-N-acetylglucosamineacyltransferase[EC:2.3.1.129]	0,000456394	0,000433103	0,000365436
K07667_ko02020_Two-componentsystem_Environmentalinformationprocessing_Signaltrasduction_kdpE,two-componentsystem,OmpRfamily,KDPoperonresponseregulatorKdpE	0,000305991	0,000326101	0,000249161
K03470_ko03030_DNAreplication_GeneticinformationProcessing_ReplicationandRepair_rnhB,ribonucleaseHII[EC:3.1.26.4]	0,000544561	0,000703156	0,000672735
K01101_ko00627_Aminobenzoatedegradation_Metabolism_Xenobioticsbiodegradationandmetabolism_E3.1.3.41,4-nitrophenylphosphatase[EC:3.1.3.41]	7,26081E-05	9,68113E-05	6,6443E-05
K10190_ko02010_Ctransporters_Environmentalinformationprocessing_Membranetransport_lacG,araQ,lactose/L-arabinosetransportsystempermeaseprotein	0,000186706	0,000178337	0,000282383
K01589_ko00230_Purinemetabolism_Metabolism_Nucleotidemetabolism_purK,5-(carboxyamino)imidazoleribonucleotidesynthase[EC:6.3.4.18]	5,18629E-05	4,07627E-05	9,13591E-05
K09810_ko02010_Ctransporters_Environmentalinformationprocessing_Membranetransport_ABC.LPT.A,lolD,lipoprotein-releasingsystemATP-bindingprotein[EC:3.6.3.-]	0,000285246	0,000275148	0,000465101
K07686_ko02020_Two-componentsystem_Environmentalinformationprocessing_Signaltrasduction_uhpA,two-componentsystem,NarLfamily,uhpToperonresponseregulatorUhpA	1,55589E-05	0	0
K03785_ko00400_Phenylalanine,tyrosineandtryptophanbiosynthesis_Metabolism_Aminoacidmetabolism_aroD,3-dehydroquinatedehydrataseI[EC:4.2.1.10];K03785_ko01230_Biosynthesisofaminoacids_Metabolism_Overview_aroD,3-dehydroquinatedehydrataseI[	0,00014003	0,000122288	0,000174413
K03823_ko00440_Phosphonateandphosphinatemetabolism_Metabolism_Metabolismofotheraminoacids_pat,phosphinothricinacetyltransferase[EC:2.3.1.183]	0,000217824	0,000122288	9,96645E-05
K01692_ko00310_Lysinedegradation_Metabolism_Aminoacidmetabolism_paaF,echA,enoyl-CoAhydratase[EC:4.2.1.17];K01692_ko00360_Phenylalaninemetabolism_Metabolism_Aminoacidmetabolism_paaF,echA,enoyl-CoAhydratase[EC:4.2.1.17];K01692_ko0038(	0,00014003	6,1144E-05	3,32215E-05
K00020_ko00280_Valine,leucineandisoleucinedegradation_Metabolism_Aminoacidmetabolism_E1.1.1.31,mmsB,3-hydroxyisobutyratedehydrogenase[EC:1.1.1.31]	7,26081E-05	6,1144E-05	8,30537E-05
K02668_ko02020_Two-componentsystem_Environmentalinformationprocessing_Signaltrasduction_pilS,two-componentsystem,NtrCfamily,sensorhistidinekinasePilS[EC:2.7.13.3]	5,18629E-06	3,56673E-05	3,32215E-05
K03274_ko00540_Lipopolysaccharidebiosynthesis_Metabolism_Glycanbiosynthesisandmetabolism_gmhD,rfaD,ADP-L-glycero-D-manno-heptose6-epimerase[EC:5.1.3.20]	7,77944E-05	3,56673E-05	6,6443E-05
K10014_ko02010_Ctransporters_Environmentalinformationprocessing_Membranetransport_hisJ,histidinetransportsystemsubstrate-bindingprotein	0	0	1,66107E-05
K02041_ko02010_Ctransporters_Environmentalinformationprocessing_Membranetransport_phnC,phosphonatetransportsystemATP-bindingprotein[EC:3.6.3.28]	0,000134844	0,000219099	0,000207634
K02999_ko03020_RNApolymerase_GeneticinformationProcessing_Transcription_RPA1,POLR1A,DNA-directedRNApolymerasIsubunitRPA1[EC:2.7.7.6];K02999_ko00230_Purinemetabolism_Metabolism_Nucleotidemetabolism_RPA1,POLR1A,DNA-directedRNApoly	1,03726E-05	5,09533E-06	2,49161E-05
K00050_ko00260_Glycine,serineandthreoninemetabolism_Metabolism_Aminoacidmetabolism_ttuD,hydroxypyruvatereductase[EC:1.1.1.81];K00050_ko00630_Glyoxylateanddicarboxylatemetabolism_Metabolism_Carbohydratemetabolism_ttuD,hydroxypyruvater	6,74218E-05	5,60487E-05	4,15269E-05
K00674_ko00300_Lysinebiosynthesis_Metabolism_Aminoacidmetabolism_dapD,2,3,4,5-tetrahydropyridine-2-carboxylateN-succinyltransferase[EC:2.3.1.117];K00674_ko01230_Biosynthesisofaminoacids_Metabolism_Overview_dapD,2,3,4,5-tetrahydropyridine-2-c	0,000129657	7,643E-05	5,81376E-05
K06133_ko00770_PantothenateandCoABiosynthesis_Metabolism_Metabolismofcofactorsandvitamins_LYS5,acpT,4'-phosphopantetheinyltransferase[EC:2.7.8.-]	0,00014003	0,000183432	0,000406963
K03732_ko03018_RNAdegradation_GeneticInformationProcessing_Folding,sortinganddegradation_rhlB,ATP-dependentRNAhelicaseRhlB[EC:3.6.4.13]	0	1,01907E-05	0
K02392_ko02040_Flagellarassembly_Organismalsystem_Cellmobility_flgG,flagellarbasal-bodyrodproteinFlgG	0,000155589	9,1716E-05	0,000132886
K10041_ko02010_Ctransporters_Environmentalinformationprocessing_Membranetransport_ABC.GLN1.A,putativeglutaminetransportsystemATP-bindingprotein[EC:3.6.3.-]	0,000108912	6,62393E-05	4,15269E-05
K09697_ko02010_Ctransporters_Environmentalinformationprocessing_Membranetransport_natA,sodiumtransportsystemATP-bindingprotein;K09697_ko02020_Two-componentsystem_Environmentalinformationprocessing_Signaltrasduction_natA,sodiumtranspo	3,11177E-05	5,60487E-05	5,81376E-05
K00813_ko00250_Alanine,aspartateandglutamatemetabolism_Metabolism_Aminoacidmetabolism_aspC,aspartateaminotransferase[EC:2.6.1.1];K00813_ko00330_Arginineandprolinemetabolism_Metabolism_Aminoacidmetabolism_aspC,aspartateaminotransferas	1,03726E-05	0	3,32215E-05

K01040_ko00630_Glyoxylateanddicarboxylatemetabolism_Metabolism_Carbohydratemetabolism_gctB,glutaconateCoA-transferase,subunitB[EC:2.8.3.12];K01040_ko00643_Styrenedegradation_Metabolism_Xenobioticsbiodegradationandmetabolism_gctB,glutacc	2,59315E-05	4,07627E-05	3,32215E-05
K07657_ko02020_Two-componentsystem_Environmentalinformationprocessing_Signaltrasduction_phoB,two-componentsystem,OmpRfamily,phosphateregulonresponseregulatorPhoB	0,000949091	0,000749014	0,000523238
K02233_ko00830_Retinolmetabolism_Metabolism_Metabolismofcofactorsandvitamins_E2.7.8.26,cobS,cobV,adenosylcobinamide-GDPribazoletransferase[EC:2.7.8.26]	0,000259315	0,000428008	0,000290688
K01627_ko00540_Lipopolysaccharidebiosynthesis_Metabolism_Glycanbiosynthesisandmetabolism_kdsA,2-dehydro-3-deoxyphosphooctonatealdolase(KDO8-Psynthase)[EC:2.5.1.55]	0,000456394	0,000254767	0,000282383
K03389_ko01200_Carbonmetabolism_Metabolism_Overview_hdrB,heterodisulfidereductasesubunitB[EC:1.8.98.1];K03389_ko00194_Photosynthesisproteins_Metabolism_Energymetabolism_hdrB,heterodisulfidereductasesubunitB[EC:1.8.98.1]	3,11177E-05	7,643E-05	9,96645E-05
K04751_ko02020_Two-componentsystem_Environmentalinformationprocessing_Signaltrasduction_glnB,nitrogenregulatoryproteinP-II1	0,000124471	5,60487E-05	5,81376E-05
K09882_ko00830_Retinolmetabolism_Metabolismofcofactorsandvitamins_cobS,cobaltochelataseCobS[EC:6.6.1.2]	6,74218E-05	7,13347E-05	6,6443E-05
K09789_ko00780_Biotinmetabolism_Metabolism_Metabolismofcofactorsandvitamins_bioG,biotinsynthesisproteinBioG	5,18629E-05	0,000132479	7,47483E-05
K03146_ko00730_Thiaminemetabolism_Metabolism_Metabolismofcofactorsandvitamins_THI4,THI1,thiaminethiazolesynthase	3,11177E-05	2,54767E-05	3,32215E-05
K07669_ko02020_Two-componentsystem_Environmentalinformationprocessing_Signaltrasduction_mprA,two-componentsystem,OmpRfamily,responseregulatorMprA	9,33532E-05	4,07627E-05	4,15269E-05
K07675_ko02020_Two-componentsystem_Environmentalinformationprocessing_Signaltrasduction_uhpB,two-componentsystem,NarLfamily,sensorhistidinekinaseUhpB[EC:2.7.13.3]	4,66766E-05	2,03813E-05	4,98322E-05
K10004_ko02010_Ctransporters_Environmentalinformationprocessing_Membranetransport_gltL,aatP,glutamate/aspartatetransportsystemATP-bindingprotein[EC:3.6.3.-];K10004_ko02020_Two-componentsystem_Environmentalinformationprocessing_Signaltrasc	1,55589E-05	2,03813E-05	8,30537E-06
K02106_ko02020_Two-componentsystem_Environmentalinformationprocessing_Signaltrasduction_atoE,short-chainfattyacidstransporter	2,59315E-05	3,0572E-05	1,66107E-05
K07665_ko02020_Two-componentsystem_Environmentalinformationprocessing_Signaltrasduction_cusR,copR,silR,two-componentsystem,OmpRfamily,copperresistancephosphateregulonresponseregulatorCusR	0,000451207	0,000443294	0,000498322
K14983_ko02020_Two-componentsystem_Environmentalinformationprocessing_Signaltrasduction_ciaR,two-componentsystem,OmpRfamily,responseregulatorCiaR	7,26081E-05	0,000122288	9,96645E-05
K08358_ko02020_Two-componentsystem_Environmentalinformationprocessing_Signaltrasduction_ttrB,tetrathionatereductasesubunitB;K08358_ko00920_Sulfurmetabolism_Metabolism_Energymetabolism_ttrB,tetrathionatereductasesubunitB	2,07452E-05	1,01907E-05	1,66107E-05
K00011_ko00051_Fructoseandmannosemetabolism_Metabolism_Carbohydratemetabolism_E1.1.1.21,AKR1,aldehydereductase[EC:1.1.1.21];K00011_ko00052_Galactosemetabolism_Metabolism_Carbohydratemetabolism_E1.1.1.21,AKR1,aldehydereductase[EC:1.	5,18629E-06	0	0
K08591_ko00561_Glycerolipidmetabolism_Metabolism_Lipidmetabolism_plsY,glycerol-3-phosphateacyltransferasePlsY[EC:2.3.1.15];K08591_ko00564_Glycerophospholipidmetabolism_Metabolism_Lipidmetabolism_plsY,glycerol-3-phosphateacyltransferasePlsY[E	0,000295619	0,000321006	0,000307299
K11915_ko02010_Ctransporters_Environmentalinformationprocessing_Membranetransport_stp1,pppA,serine/threonineproteinphosphataseStp1[EC:3.1.3.16]	0	1,01907E-05	0
K04032_ko00830_Retinolmetabolism_Metabolismofcofactorsandvitamins_eutT,ethanolamineutilizationcobalaminadenosyltransferase[EC:2.5.1.17]	3,6304E-05	3,0572E-05	2,49161E-05
K12972_ko00260_Glycine,serineandthreoninemetabolism_Metabolism_Aminoacidmetabolism_ghrA,gyoxylate/hydroxypyruvatereductaseA[EC:1.1.1.791.1.1.81];K12972_ko00630_Glyoxylateanddicarboxylatemetabolism_Metabolism_Carbohydratemetabolism_gh	4,14903E-05	0	0
K03739_ko05150_Staphylococcusaureusinfection_HumanDiseases_Infectiousdiseases_dltB,membraneproteininvolvedinD-alanineexport	5,18629E-05	5,60487E-05	9,13591E-05
K05776_ko02010_Ctransporters_Environmentalinformationprocessing_Membranetransport_modF,molybdatetransportsystemATP-bindingprotein	8,29807E-05	0,000198718	0,000132886
K05846_ko02010_Ctransporters_Environmentalinformationprocessing_Membranetransport_opuBD,osmoprotectanttransportsystempermeaseprotein	4,14903E-05	4,07627E-05	6,6443E-05
K00844_ko04066_HIF-1signalingpathway_Environmentalinformationprocessing_Signaltrasduction_HK,hexokinase[EC:2.7.1.1];K00844_ko05230_Centralcarbonmetabolismincancer_HumanDiseases_Cancers_HK,hexokinase[EC:2.7.1.1];K00844_ko04930_Typelldiabe	2,07452E-05	3,56673E-05	6,6443E-05
K10986_ko02010_Ctransporters_Environmentalinformationprocessing_Membranetransport_PTS-Gam-EIID,agaD,PTSsystem,galactosamine-specificIIDcomponent;K10986_ko00052_Galactosemetabolism_Metabolism_Carbohydratemetabolism_PTS-Gam-EIID,agaD	0	0	2,49161E-05
K01092_ko04066_HIF-1signalingpathway_Environmentalinformationprocessing_Signaltrasduction_E3.1.3.25,IMPA,suhB,myo-inositol-1(or4)-monophosphatase[EC:3.1.3.25];K01092_ko00521_Streptomycinbiosynthesis_Metabolism_Biosynthesisofothersecondarym	0,000373413	0,000321006	0,000365436
K02746_ko02010_Ctransporters_Environmentalinformationprocessing_Membranetransport_PTS-Aga-EIIC,agaW,PTSsystem,N-acetylgalactosamine-specificIICcomponent;K02746_ko00052_Galactosemetabolism_Metabolism_Carbohydratemetabolism_PTS-Aga-EIIC	6,22355E-05	2,03813E-05	3,32215E-05
K01697_ko00270_Cysteineandmethioninemetabolism_Metabolism_Aminoacidmetabolism_E4.2.1.22,CBS,cystathioninebeta-synthase[EC:4.2.1.22];K01697_ko00260_Glycine,serineandthreoninemetabolism_Metabolism_Aminoacidmetabolism_E4.2.1.22,CBS,cysta	6,74218E-05	2,54767E-05	2,49161E-05
K00338_ko00190_Oxidativephosphorylation_Metabolism_Energymetabolism_nuoI,NADH-quinoneoxidoreductasesubunitI[EC:1.6.5.3]	0,000316364	0,000285339	0,000207634
K10601_ko04141_Proteinprocessinginendoplasmicreticulum_GeneticInformationProcessing_Folding,sortinganddegradation_SYVN1,HRD1,E3ubiquitin-proteinligasesynoviolin[EC:6.3.2.19];K10601_ko04120_Ubiquitinmediatedproteolysis_GeneticInformationProces	0	0	8,30537E-06
K10866_ko03440_Homologousrecombination_GeneticinformationProcessing_ReplicationandRepair_RAD50,DNArepairproteinRAD50[EC:3.6.-.-];K10866_ko03450_non-homologousend-joining_GeneticinformationProcessing_ReplicationandRepair_RAD50,DNArepa	2,59315E-05	0	8,30537E-06
K00210_ko00400_Phenylalanine,tyrosineandtryptophanbiosynthesis_Metabolism_Aminoacidmetabolism_E1.3.1.12,prephenatedehydrogenase[EC:1.3.1.12];K00210_ko00401_Novobiocinbiosynthesis_Metabolism_Biosynthesisofothersecondarymetabolites_E1.3.1	7,26081E-05	0,000203813	0,000116275
K00450_ko00350_Tyrosinemetabolism_Metabolism_Aminoacidmetabolism_E1.13.11.4,gentisate1,2-dioxygenase[EC:1.13.11.4]	5,18629E-06	5,09533E-06	0
K06167_ko00440_Phosphonateandphosphinatemetabolism_Metabolism_Metabolismofotheraminoacids_phnP,phosphoribosyl1,2-cyclicphosphatephosphodiesterase[EC:3.1.4.55]	0,000150402	0,000142669	0,000207634
K03149_ko00730_Thiaminemetabolism_Metabolism_Metabolismofcofactorsandvitamins_thiG,thiazolesynthase[EC:2.8.1.10]	0,000274873	0,000168146	9,96645E-05
K14654_ko00740_Riboflavinmetabolism_Metabolism_Metabolismofcofactorsandvitamins_RIB7,arfC,2,5-diamino-6-(ribosylamino)-4(3H)-pyrimidinone5'-phosphatereductase[EC:1.1.1.302]	2,07452E-05	4,07627E-05	1,66107E-05
K00658_ko00310_Lysinedegradation_Metabolism_Aminoacidmetabolism_DLST,sucB,2-oxoglutaratedehydrogenaseE2component(dihydrolipoamidesuccinyltransferase)[EC:2.3.1.61];K00658_ko00020_Citratecycle(TCAcycle)_Metabolism_Carbohydratemetabolism_	5,18629E-05	5,09533E-06	4,98322E-05
K02858_ko00740_Riboflavinmetabolism_Metabolism_Metabolismofcofactorsandvitamins_ribB,RIB3,3,4-dihydroxy2-butanone4-phosphatesynthase[EC:4.1.99.12]	1,03726E-05	3,56673E-05	8,30537E-05
K00113_ko00564_Glycerophospholipidmetabolism_Metabolism_Lipidmetabolism_glpC,glycerol-3-phosphatedehydrogenasesubunitC[EC:1.1.5.3]	0,000223011	5,60487E-05	0,000141191
K02405_ko02020_Two-componentsystem_Environmentalinformationprocessing_Signaltrasduction_fliA,RNApolymerasesigmafactorforflagellaroperonFliA;K02405_ko05111_Vibriocholeraepathogeniccycle_HumanDiseases_Infectiousdiseases_fliA,RNApolymerasesi	9,33532E-05	1,5286E-05	8,30537E-05
K05884_ko00194_Photosynthesisproteins_Metabolism_Energymetabolism_comC,L-2-hydroxycarboxylatedehydrogenase(NAD+)[EC:1.1.1.337]	2,07452E-05	7,13347E-05	9,96645E-05
K00355_ko00130_Ubiquinoneandotherterpenoid-quinonebiosynthesis_Metabolism_Metabolismofcofactorsandvitamins_NQO1,NAD(P)Hdehydrogenase(quinone)[EC:1.6.5.2]	3,11177E-05	1,5286E-05	8,30537E-06
K09903_ko00240_Pyrimidinemetabolism_Metabolism_Nucleotidemetabolism_pyrH,uridylatekinase[EC:2.7.4.22]	0,001115053	0,000799967	0,000656124
K03550_ko03440_Homologousrecombination_GeneticinformationProcessing_ReplicationandRepair_ruvA,hollidayjunctionDNAhelicaseRuvA[EC:3.6.4.12]	0,000487511	0,000580868	0,000548155
K10026_ko00785_Lipoicacidmetabolism_Metabolism_Metabolismofcofactorsandvitamins_queE,7-carboxy-7-deazaguaninesynthase[EC:4.3.99.3]	0,000207452	0,000178337	0,000307299
K02421_ko02040_Flagellarassembly_Organismalsystem_Cellmobility_fliR,flagellarbiosyntheticproteinFliR	9,33532E-05	0,000142669	6,6443E-05
K03476_ko00052_Galactosemetabolism_Metabolism_Carbohydratemetabolism_ulaG,L-ascorbate6-phosphatelactonase[EC:3.1.1.-]	0,000134844	6,62393E-05	5,81376E-05
K10010_ko02010_Ctransporters_Environmentalinformationprocessing_Membranetransport_ABC.CYST.A,cystinetransportsystemATP-bindingprotein[EC:3.6.3.-]	8,29807E-05	9,1716E-05	6,6443E-05
K01044_ko00983_Drugmetabolism-otherenzymes_Metabolism_Xenobioticsbiodegradationandmetabolism_CES1,carboxylesterase1[EC:3.1.1.1]	5,18629E-05	5,09533E-05	6,6443E-05
K13288_ko03008_Ribosomebiogenesisineukaryotes_GeneticinformationProcessing_Transcription_orn,REX2,REXO2,oligoribonuclease[EC:3.1.-.-]	5,18629E-06	1,01907E-05	8,30537E-06
K00991_ko00900_Terpenoidbackbonebiosynthesis_Metabolism_Metabolismofterpenoidsandpolyketides_ispD,2-C-methyl-D-erythritol4-phosphatecytidylyltransferase[EC:2.7.7.60]	0,000492698	0,000759205	0,000656124
K02500_ko00340_Histidinemetabolism_Metabolism_Aminoacidmetabolism_hisF,cyclase[EC:4.1.3.-];K02500_ko01230_Biosynthesisofaminoacids_Metabolism_Overview_hisF,cyclase[EC:4.1.3.-]	0,000471953	0,000341387	0,000265772
K02906_ko03010_Ribosome_GeneticinformationProcessing_Transcription_RP-L3,MRPL3,rplC,largesubunitribosomalproteinL3	0,001166916	0,000856016	0,00078901
K00943_ko00240_Pyrimidinemetabolism_Metabolism_Nucleotidemetabolism_tmk,DTYMK,dTMPkinase[EC:2.7.4.9]	0,000274873	0,000519724	0,000548155
K03801_ko00785_Lipoicacidmetabolism_Metabolism_Metabolismofcofactorsandvitamins_lipB,lipoyl(octanoyl)transferase[EC:2.3.1.181]	9,85395E-05	0,000122288	4,98322E-05
K00851_ko00030_Pentosephosphatepathway_Metabolism_Carbohydratemetabolism_E2.7.1.12,gntK,idnK,gluconokinase[EC:2.7.1.12];K00851_ko01200_Carbonmetabolism_Metabolism_Overview_E2.7.1.12,gntK,idnK,gluconokinase[EC:2.7.1.12]	3,6304E-05	2,54767E-05	1,66107E-05
K02170_ko00780_Biotinmetabolism_Metabolism_Metabolismofcofactorsandvitamins_bioH,pimeloyl-[acyl-carrierprotein]methylesteresterase[EC:3.1.1.85]	3,6304E-05	3,56673E-05	1,66107E-05
K08097_ko00194_Photosynthesisproteins_Metabolism_Energymetabolism_E4.4.1.19,comA,phosphosulfolactatesynthase[EC:4.4.1.19]	0	0	8,30537E-06
K00824_ko00330_Arginineandprolinemetabolism_Metabolism_Aminoacidmetabolism_dat,D-alaninetransaminase[EC:2.6.1.21];K00824_ko00310_Lysinedegradation_Metabolism_Aminoacidmetabolism_dat,D-alaninetransaminase[EC:2.6.1.21];K00824_ko00360_P	7,77944E-05	4,5858E-05	4,98322E-05
K10003_ko02010_Ctransporters_Environmentalinformationprocessing_Membranetransport_gltJ,aatQ,glutamate/aspartatetransportsystempermeaseprotein;K10003_ko02020_Two-componentsystem_Environmentalinformationprocessing_Signaltrasduction_gltJ,a	1,55589E-05	0	8,30537E-06
K08083_ko02020_Two-componentsystem_Environmentalinformationprocessing_Signaltrasduction_algR,two-componentsystem,LytTfamily,responseregulatorAlgR	0,000228197	0,000336292	0,000373742
K01560_ko00625_Chloroalkaneandchloroalkenedegradation_Metabolism_Xenobioticsbiodegradationandmetabolism_E3.8.1.2,2-haloaciddehalogenase[EC:3.8.1.2];K01560_ko00361_Chlorocyclohexaneandchlorobenzenedegradation_Metabolism_Xenobioticsbiode	0,00014003	0,000101907	9,13591E-05
K01817_ko00400_Phenylalanine,tyrosineandtryptophanbiosynthesis_Metabolism_Aminoacidmetabolism_trpF,phosphoribosylanthranilateisomerase[EC:5.3.1.24];K01817_ko01230_Biosynthesisofaminoacids_Metabolism_Overview_trpF,phosphoribosylanthranilat	0,000160775	0,000214004	0,000315604
K05351_ko00040_Pentoseandglucuronateinterconversions_Metabolism_Carbohydratemetabolism_E1.1.1.9,D-xylulosereductase[EC:1.1.1.9]	0	5,09533E-06	1,66107E-05
K07660_ko02020_Two-componentsystem_Environmentalinformationprocessing_Signaltrasduction_phoP,two-componentsystem,OmpRfamily,responseregulatorPhoP	2,07452E-05	0	1,66107E-05
K00881_ko00051_Fructoseandmannosemetabolism_Metabolism_Carbohydratemetabolism_alsK,allosekinase[EC:2.7.1.55]	2,07452E-05	1,5286E-05	8,30537E-06
K07707_ko02020_Two-componentsystem_Environmentalinformationprocessing_Signaltrasduction_agrA,two-componentsystem,AgrAfamily,responseregulatorAgrA	0,000150402	0,000183432	0,000132886
K07770_ko02020_Two-componentsystem_Environmentalinformationprocessing_Signaltrasduction_cssR,two-componentsystem,OmpRfamily,responseregulatorCssR	9,85395E-05	0,000117193	5,81376E-05
K13894_ko02010_Ctransporters_Environmentalinformationprocessing_Membranetransport_yejB,microcinCtransportsystempermeaseprotein	2,07452E-05	2,03813E-05	1,66107E-05

K00038_ko00140_Steroidhormonebiosynthesis_Metabolism_Lipidmetabolism_E1.1.1.53,3alpha(or20beta)-hydroxysteroiddehydrogenase[EC:1.1.1.53]	2,59315E-05	1,01907E-05	0
K00158_ko00620_Pyruvatemetabolism_Metabolism_Carbohydratemetabolism_E1.2.3.3,poxL,pyruvateoxidase[EC:1.2.3.3]	4,66766E-05	3,56673E-05	3,32215E-05
K03533_ko02020_Two-componentsystem_Environmentalinformationprocessing_Signaltrasduction_torD,TorAspecificchaperone	1,03726E-05	0	1,66107E-05
K02047_ko02010_Ctransporters_Environmentalinformationprocessing_Membranetransport_cysW,sulfatetransportsystempermeaseprotein;K02047_ko00920_Sulfurmetabolism_Metabolism_Energymetabolism_cysW,sulfatetransportsystempermeaseprotein	3,6304E-05	4,07627E-05	1,66107E-05
K01788_ko00520_Aminosugarandnucleotidesugarmetabolism_Metabolism_Carbohydratemetabolism_nanE,N-acylglucosamine-6-phosphate2-epimerase[EC:5.1.3.9]	0,000186706	0,000208909	0,000332215
K09420_ko04151_PI3K-Aktsignalingpathway_Environmentalinformationprocessing_Signaltrasduction_MYB,mybproto-oncogeneprotein;K09420_ko05166_HTLV-Iinfection_HumanDiseases_Infectiousdiseases_MYB,mybproto-oncogeneprotein	0	0	8,30537E-06
K01658_ko00400_Phenylalanine,tyrosineandtryptophanbiosynthesis_Metabolism_Aminoacidmetabolism_trpG,anthranilatesynthasecomponentII[EC:4.1.3.27];K01658_ko01230_Biosynthesisofaminoacids_Metabolism_Overview_trpG,anthranilatesynthasecomponen	0,000145216	0,000163051	0,00023255
K01807_ko00030_Pentosephosphatepathway_Metabolism_Carbohydratemetabolism_rpiA,ribose5-phosphateisomeraseA[EC:5.3.1.6];K01807_ko01230_Biosynthesisofaminoacids_Metabolism_Overview_rpiA,ribose5-phosphateisomeraseA[EC:5.3.1.6];K01807_ko0	9,33532E-05	9,1716E-05	0,000116275
K02120_ko00190_Oxidativephosphorylation_Metabolism_Energymetabolism_ATPVD,ntpD,atpD,V/A-typeH+-transportingATPasesubunitD	0,000347482	0,000371959	0,000415269
K03469_ko03030_DNAreplication_GeneticinformationProcessing_ReplicationandRepair_E3.1.26.4A,RNASEH1,rnhA,ribonucleaseHI[EC:3.1.26.4]	0,000669032	0,000631821	0,000739178
K01916_ko00760_Nicotinateandnicotinamidemetabolism_Metabolism_Metabolismofcofactorsandvitamins_nadE,NAD+synthase[EC:6.3.1.5]	0,000160775	0,000127383	0,000207634
K07664_ko02020_Two-componentsystem_Environmentalinformationprocessing_Signaltrasduction_baeR,smeR,two-componentsystem,OmpRfamily,responseregulatorBaeR	0,000492698	0,000315911	0,000431879
K11329_ko02020_Two-componentsystem_Environmentalinformationprocessing_Signaltrasduction_rpaB,two-componentsystem,OmpRfamily,responseregulatorRpaB	6,22355E-05	0,000101907	6,6443E-05
K05712_ko00360_Phenylalaninemetabolism_Metabolism_Aminoacidmetabolism_mhpA,3-(3-hydroxy-phenyl)propionatehydroxylase[EC:1.14.13.127];K05712_ko01220_Degradationofaromaticcompounds_Metabolism_Overview_mhpA,3-(3-hydroxy-phenyl)propio	5,18629E-06	0	0
K07670_ko02020_Two-componentsystem_Environmentalinformationprocessing_Signaltrasduction_mtrA,two-componentsystem,OmpRfamily,responseregulatorMtrA	0,00014003	0,000208909	0,000124581
K02863_ko03010_Ribosome_GeneticinformationProcessing_Transcription_RP-L1,MRPL1,rplA,largesubunitribosomalproteinL1	0,001369181	0,001171927	0,000797316
K00737_ko00513_VariaustypesofN-glycanbiosynthesis_Metabolism_Glycanbiosynthesisandmetabolism_MGAT3,beta-1,4-mannosyl-glycoproteinbeta-1,4-N-acetylglucosaminyltransferase[EC:2.4.1.144]	1,55589E-05	1,01907E-05	2,49161E-05
K07441_ko00513_VariaustypesofN-glycanbiosynthesis_Metabolism_Glycanbiosynthesisandmetabolism_ALG14,beta-1,4-N-acetylglucosaminyltransferase[EC:2.4.1.141];K07441_ko00513_VariaustypesofN-glycanbiosynthesis_Metabolism_Glycanbiosynthesisandme	0,000114098	0,000132479	0,000166107
K00240_ko00020_Citratecycle(TCAcycle)_Metabolism_Carbohydratemetabolism_sdhB,succinatedehydrogenaseiron-sulfursubunit[EC:1.3.5.1];K00240_ko00630_Glyoxylateanddicarboxylatemetabolism_Metabolism_Carbohydratemetabolism_sdhB,succinatedehydr	0,000736453	0,000682775	0,00044849
K02288_ko00195_Photosynthesis_Metabolism_Energymetabolism_cpcE,phycocyanobilinlyasealphasubunit[EC:4.-.-.-]	1,03726E-05	2,54767E-05	0
K00793_ko00740_Riboflavinmetabolism_Metabolism_Metabolismofcofactorsandvitamins_ribE,RIB5,riboflavinsynthase[EC:2.5.1.9]	0,00046158	0,00045858	0,000182718
K09021_ko00240_Pyrimidinemetabolism_Metabolism_Nucleotidemetabolism_rutC,aminoacrylateperacidreductase	8,29807E-05	0,000122288	1,66107E-05
K01719_ko00830_Retinolmetabolism_Metabolism_Metabolismofcofactorsandvitamins_hemD,UROS,uroporphyrinogen-IIIsynthase[EC:4.2.1.75]	0,000440835	0,000494247	0,000290688
K03707_ko00730_Thiaminemetabolism_Metabolism_Metabolismofcofactorsandvitamins_tenA,thiaminase(transcriptionalactivatorTenA)[EC:3.5.99.2]	5,70492E-05	3,56673E-05	3,32215E-05
K00761_ko00240_Pyrimidinemetabolism_Metabolism_Nucleotidemetabolism_upp,UPRT,uracilphosphoribosyltransferase[EC:2.4.2.9]	0,000679404	0,000703156	0,000548155
K07692_ko02020_Two-componentsystem_Environmentalinformationprocessing_Signaltrasduction_degU,two-componentsystem,NarLfamily,responseregulatorDegU	3,11177E-05	8,66207E-05	5,81376E-05
K01574_ko00630_Glyoxylateanddicarboxylatemetabolism_Metabolism_Carbohydratemetabolism_adc,acetoacetatedecarboxylase[EC:4.1.1.4];K01574_ko00071_Fattyaciddegradation_Metabolism_Lipidmetabolism_adc,acetoacetatedecarboxylase[EC:4.1.1.4]	1,03726E-05	0	8,30537E-06
K01996_ko02010_Ctransporters_Environmentalinformationprocessing_Membranetransport_livF,branched-chainaminoacidtransportsystemATP-bindingprotein	0,000331923	0,000341387	0,000257467
K01790_ko00521_Streptomycinbiosynthesis_Metabolism_Biosynthesisofothersecondarymetabolites_rfbC,rmlC,dTDP-4-dehydrorhamnose3,5-epimerase[EC:5.1.3.13];K01790_ko00523_Polyketidesugarunitbiosynthesis_Metabolism_Metabolismofterpenoidsandpol	0,00068459	0,000529915	0,000597987
K01935_ko00780_Biotinmetabolism_Metabolism_Metabolismofcofactorsandvitamins_bioD,dethiobiotinsynthetase[EC:6.3.3.3]	0,000134844	0,000219099	0,000166107
K07816_ko00230_Purinemetabolism_Metabolism_Nucleotidemetabolism_E2.7.6.5X,putativeGTPpyrophosphokinase[EC:2.7.6.5]	0,000119285	0,000224195	0,000149497
K00939_ko00230_Purinemetabolism_Metabolism_Nucleotidemetabolism_adk,AK,adenylatekinase[EC:2.7.4.3]	0,000793503	0,000754109	0,000639514
K01055_ko01220_Degradationofaromaticcompounds_Metabolism_Overview_pcaD,3-oxoadipateenol-lactonase[EC:3.1.1.24];K01055_ko00362_Benzoatedegradation_Metabolism_Xenobioticsbiodegradationandmetabolism_pcaD,3-oxoadipateenol-lactonase[EC:3.	4,14903E-05	0,000163051	5,81376E-05
K04708_ko00600_Sphingolipidmetabolism_Metabolism_Lipidmetabolism_E1.1.1.102,3-dehydrosphinganinereductase[EC:1.1.1.102]	0	1,01907E-05	0
K03148_ko04122_Sulfurrelaysystem_GeneticInformationProcessing_Folding,sortinganddegradation_thiF,sulfurcarrierproteinThiSadenylyltransferase[EC:2.7.7.73];K03148_ko00730_Thiaminemetabolism_Metabolism_Metabolismofcofactorsandvitamins_thiF,sulfur	0,000150402	0,000137574	0,000166107
K07638_ko02020_Two-componentsystem_Environmentalinformationprocessing_Signaltrasduction_envZ,two-componentsystem,OmpRfamily,osmolaritysensorhistidinekinaseEnvZ[EC:2.7.13.3]	1,55589E-05	3,56673E-05	2,49161E-05
K02556_ko02020_Two-componentsystem_Environmentalinformationprocessing_Signaltrasduction_motA,chemotaxisproteinMotA;K02556_ko02030_Bacterialchemotaxis_Organismalsystem_Cellmobility_motA,chemotaxisproteinMotA;K02556_ko02040_Flagellara	7,26081E-05	5,60487E-05	6,6443E-05
K04091_ko00920_Sulfurmetabolism_Metabolism_Energymetabolism_ssuD,alkanesulfonatemonooxygenase[EC:1.14.14.5]	5,18629E-06	5,09533E-06	3,32215E-05
K01884_ko00970_Aminoacyl-tRNAbiosynthesis_Geneticinformationandprocessing_Transcription_cysS1,cysteinyl-tRNAsynthetase,unknownclass[EC:6.1.1.16]	2,59315E-05	2,03813E-05	8,30537E-06
K02848_ko00540_Lipopolysaccharidebiosynthesis_Metabolism_Glycanbiosynthesisandmetabolism_waaP,rfaP,heptose(I)phosphotransferase[EC:2.7.1.-]	5,18629E-06	5,09533E-06	3,32215E-05
K01786_ko00040_Pentoseandglucuronateinterconversions_Metabolism_Carbohydratemetabolism_araD,L-ribulose-5-phosphate4-epimerase[EC:5.1.3.4]	0,000254128	0,000234385	0,000199329
K07684_ko02020_Two-componentsystem_Environmentalinformationprocessing_Signaltrasduction_narL,two-componentsystem,NarLfamily,nitrate/nitriteresponseregulatorNarL	7,26081E-05	3,0572E-05	0,000157802
K10538_ko02010_Ctransporters_Environmentalinformationprocessing_Membranetransport_araH,L-arabinosetransportsystempermeaseprotein	1,03726E-05	5,09533E-06	3,32215E-05
K05824_ko00300_Lysinebiosynthesis_Metabolism_Aminoacidmetabolism_LYS12,homoisocitratedehydrogenase[EC:1.1.1.87];K05824_ko01210_Oxocarboxylicacidmetabolism_Metabolism_Overview_LYS12,homoisocitratedehydrogenase[EC:1.1.1.87];K05824_ko01	5,18629E-06	0	0
K01135_ko04142_Lysosome_CellularProcesses_Transportandcatabolism_ARSB,arylsulfataseB[EC:3.1.6.12];K01135_ko00531_Glycosaminoglycandegradation_Metabolism_Glycanbiosynthesisandmetabolism_ARSB,arylsulfataseB[EC:3.1.6.12]	1,55589E-05	2,54767E-05	3,32215E-05
K08682_ko00770_PantothenateandCoAbiosynthesis_Metabolism_Metabolismofcofactorsandvitamins_acpH,acylcarrierproteinphosphodiesterase[EC:3.1.4.14]	0	0,000122288	0
K03002_ko03020_RNApolymerase_GeneticinformationProcessing_Transcription_RPA2,POLR1B,DNA-directedRNApolymerasIsubunitRPA2[EC:2.7.7.6];K03002_ko00230_Purinemetabolism_Metabolism_Nucleotidemetabolism_RPA2,POLR1B,DNA-directedRNApoly	5,18629E-06	0	0
K02651_ko04112_Cellcycle-Caulobacter_CellularProcesses_Cellgrowthanddeath_flp,pilA,pilusassemblyproteinFlp/PilA	2,07452E-05	0,000107002	4,98322E-05
K07046_ko00051_Fructoseandmannosemetabolism_Metabolism_Carbohydratemetabolism_K07046,L-fuconolactonase[EC:3.1.1.-]	2,59315E-05	1,01907E-05	2,49161E-05
K06187_ko03440_Homologousrecombination_GeneticinformationProcessing_ReplicationandRepair_recR,recombinationproteinRecR	0,000518629	0,00053501	0,000490017
K08681_ko00750_VitaminB6metabolism_Metabolism_Metabolismofcofactorsandvitamins_pdxT,pdx2,5'-phosphatesynthasepdxTsubunit[EC:4.3.3.6]	8,29807E-05	6,1144E-05	4,15269E-05
K02982_ko03010_Ribosome_GeneticinformationProcessing_Transcription_RP-S3,rpsC,smallsubunitribosomalproteinS3	0,001312132	0,001309501	0,001079698
K00760_ko00230_Purinemetabolism_Metabolism_Nucleotidemetabolism_hprT,hpt,HPRT1,hypoxanthinephosphoribosyltransferase[EC:2.4.2.8];K00760_ko00983_Drugmetabolism-otherenzymes_Metabolism_Xenobioticsbiodegradationandmetabolism_hprT,hpt,H	0,00042009	0,000738823	0,000764094
K08680_ko00130_Ubiquinoneandotherterpenoid-quinonebiosynthesis_Metabolism_Metabolismofcofactorsandvitamins_menH,2-succinyl-6-hydroxy-2,4-cyclohexadiene-1-carboxylatesynthase[EC:4.2.99.20]	4,66766E-05	5,09533E-05	4,15269E-05
K10697_ko02020_Two-componentsystem_Environmentalinformationprocessing_Signaltrasduction_rpaA,two-componentsystem,OmpRfamily,responseregulatorRpaA	5,18629E-06	3,56673E-05	3,32215E-05
K02552_ko00130_Ubiquinoneandotherterpenoid-quinonebiosynthesis_Metabolism_Metabolismofcofactorsandvitamins_menF,menaquinone-specificisochorismatesynthase[EC:5.4.4.2];K02552_ko01053_Biosynthesisofsiderophoregroupnonribosomalpeptides_Me	2,59315E-05	0	1,66107E-05
K04564_ko04146_Peroxisome_CellularProcesses_Transportandcatabolism_SOD2,superoxidedismutase,Fe-Mnfamily[EC:1.15.1.1];K04564_ko04066_HIF-1signalingpathway_Environmentalinformationprocessing_Signaltrasduction_SOD2,superoxidedismutase,Fe-Mr	0,000285246	0,000326101	0,00034052
K07693_ko02020_Two-componentsystem_Environmentalinformationprocessing_Signaltrasduction_desR,two-componentsystem,NarLfamily,responseregulatorDesR	2,59315E-05	1,5286E-05	8,30537E-06
K00949_ko00730_Thiaminemetabolism_Metabolism_Metabolismofcofactorsandvitamins_thiN,TPK1,THI80,thiaminepyrophosphokinase[EC:2.7.6.2]	0,000414903	0,000412722	0,000415269
K10537_ko02010_Ctransporters_Environmentalinformationprocessing_Membranetransport_araF,L-arabinosetransportsystemsubstrate-bindingprotein	3,11177E-05	1,01907E-05	1,66107E-05
K03394_ko00830_Retinolmetabolism_Metabolism_Metabolismofcofactorsandvitamins_cobI-cbiL,precorrin-2/cobalt-factor-2C20-methyltransferase[EC:2.1.1.1302.1.1.151]	0,000134844	0,000132479	0,000149497
K11630_ko02020_Two-componentsystem_Environmentalinformationprocessing_Signaltrasduction_bceR,two-componentsystem,OmpRfamily,bacitracinresistanceresponseregulatorBceR	0,000145216	0,000163051	0,000265772
K03111_ko03030_DNAreplication_GeneticinformationProcessing_ReplicationandRepair_ssb,single-strandDNA-bindingprotein;K03111_ko03440_Homologousrecombination_GeneticinformationProcessing_ReplicationandRepair_ssb,single-strandDNA-bindingprotei	0,001255083	0,001365549	0,001137836
K13581_ko04112_Cellcycle-Caulobacter_CellularProcesses_Cellgrowthanddeath_ccrM,modificationmethylase[EC:2.1.1.72]	0,000114098	0,000147765	0,000199329
K01057_ko00030_Pentosephosphatepathway_Metabolism_Carbohydratemetabolism_PGLS,pgl,devB,6-phosphogluconolactonase[EC:3.1.1.31];K01057_ko01200_Carbonmetabolism_Metabolism_Overview_PGLS,pgl,devB,6-phosphogluconolactonase[EC:3.1.1.31]	3,6304E-05	0,000188527	0,000124581
K12483_ko04144_Endocytosis_CellularProcesses_Transportandcatabolism_EHD1,EHdomain-containingprotein1	1,55589E-05	0	8,30537E-06
K02226_ko00830_Retinolmetabolism_Metabolism_Metabolismofcofactorsandvitamins_cobC2,cobC,phpB,alpha-ribazolephosphatase[EC:3.1.3.73]	0,000134844	0,000259862	0,000157802
K02787_ko02010_Ctransporters_Environmentalinformationprocessing_Membranetransport_PTS-Lac-EIIB,lacE,PTSsystem,lactose-specificIIBcomponent[EC:2.7.1.69];K02787_ko00052_Galactosemetabolism_Metabolism_Carbohydratemetabolism_PTS-Lac-EIIB,lacE	5,18629E-05	8,15253E-05	9,96645E-05
K00997_ko00770_PantothenateandCoAbiosynthesis_Metabolism_Metabolismofcofactorsandvitamins_acpS,holo-[acyl-carrierprotein]synthase[EC:2.7.8.7]	9,85395E-05	9,68113E-05	0,000141191
K00859_ko00770_PantothenateandCoAbiosynthesis_Metabolism_Metabolismofcofactorsandvitamins_coaE,dephospho-CoAkinase[EC:2.7.1.24]	0,00036304	0,000463675	0,000390352

K07659_ko02020_Two-componentsystem_Environmentalinformationprocessing_Signaltrasduction_ompR,two-componentsystem,OmpRfamily,phosphateregulonresponseregulatorOmpR	3,11177E-05	1,5286E-05	1,66107E-05
K11689_ko02020_Two-componentsystem_Environmentalinformationprocessing_Signaltrasduction_dctQ,C4-dicarboxylatetransporter,DctQsubunit	0,000197079	0,000254767	0,000265772
K10979_ko03450_non-homologousend-joining_GeneticinformationProcessing_ReplicationandRepair_ku,DNAend-bindingproteinKu	4,14903E-05	1,5286E-05	6,6443E-05
K12858_ko03040_Spliceosome_GeneticinformationProcessing_Transcription_DDX23,PRP28,ATP-dependentRNAhelicaseDDX23/PRP28[EC:3.6.4.13]	2,07452E-05	0	0
K00483_ko00350_Tyrosinemetabolism_Metabolism_Aminoacidmetabolism_hpaB,4-hydroxyphenylacetate3-monooxygenase[EC:1.14.14.9];K00483_ko01220_Degradationofaromaticcompounds_Metabolism_Overview_hpaB,4-hydroxyphenylacetate3-monooxyger	2,59315E-05	0	1,66107E-05
K00079_ko05204_Chemicalcarcinogenesis_HumanDiseases_Cancers_CBR1,carbonylreductase1[EC:1.1.1.1841.1.1.1891.1.1.197];K00079_ko00590_Arachidonicacidmetabolism_Metabolism_Lipidmetabolism_CBR1,carbonylreductase1[EC:1.1.1.1841.1.1.1891.1.1.19	5,18629E-06	1,01907E-05	0,000116275
K00587_ko00900_Terpenoidbackbonebiosynthesis_Metabolism_Metabolismofterpenoidsandpolyketides_ICMT,STE14,protein-S-isoprenylcysteineO-methyltransferase[EC:2.1.1.100]	1,55589E-05	2,54767E-05	3,32215E-05
K07694_ko02020_Two-componentsystem_Environmentalinformationprocessing_Signaltrasduction_vraR,two-componentsystem,NarLfamily,vancomycinresistanceassociatedresponseregulatorVraR	4,66766E-05	6,62393E-05	4,98322E-05
K07696_ko02020_Two-componentsystem_Environmentalinformationprocessing_Signaltrasduction_nreC,two-componentsystem,NarLfamily,responseregulatorNreC	4,14903E-05	3,56673E-05	4,98322E-05
K03519_ko01200_Carbonmetabolism_Metabolism_Overview_coxM,cutM,carbon-monoxidedehydrogenasemediumsubunit[EC:1.2.99.2];K03519_ko00633_Nitrotoluenedegradation_Metabolism_Xenobioticsbiodegradationandmetabolism_coxM,cutM,carbon-mon	4,66766E-05	2,54767E-05	3,32215E-05
K10218_ko00630_Glyoxylateanddicarboxylatemetabolism_Metabolism_Carbohydratemetabolism_ligK,galC,4-hydroxy-4-methyl-2-oxoglutaratealdolase[EC:4.1.3.17];K10218_ko00362_Benzoatedegradation_Metabolism_Xenobioticsbiodegradationandmetabolism_	9,85395E-05	8,66207E-05	4,98322E-05
K11175_ko00670_Onecarbonpoolbyfolate_Metabolism_Metabolismofcofactorsandvitamins_purN,phosphoribosylglycinamideformyltransferase1[EC:2.1.2.2];K11175_ko00230_Purinemetabolism_Metabolism_Nucleotidemetabolism_purN,phosphoribosylglycinam	0,000342295	0,000504438	0,000406963
K02045_ko02010_Ctransporters_Environmentalinformationprocessing_Membranetransport_cysA,sulfatetransportsystemATP-bindingprotein[EC:3.6.3.25];K02045_ko00920_Sulfurmetabolism_Metabolism_Energymetabolism_cysA,sulfatetransportsystemATP-bindi	7,77944E-05	4,5858E-05	0,000157802
K05873_ko00230_Purinemetabolism_Metabolism_Nucleotidemetabolism_E4.6.1.1B,cyaB,adenylatecyclase,class2[EC:4.6.1.1]	7,77944E-05	8,15253E-05	8,30537E-05
K01087_ko00500_Starchandsucrosemetabolism_Metabolism_Carbohydratemetabolism_otsB,trehalose6-phosphatephosphatase[EC:3.1.3.12]	1,03726E-05	0	1,66107E-05
K03816_ko00230_Purinemetabolism_Metabolism_Nucleotidemetabolism_xpt,xanthinephosphoribosyltransferase[EC:2.4.2.22]	0,000285246	0,000244576	0,000290688
K13566_ko00250_Alanine,aspartateandglutamatemetabolism_Metabolism_Aminoacidmetabolism_NIT2,omega-amidase[EC:3.5.1.3]	4,66766E-05	3,0572E-05	8,30537E-05
K02635_ko00195_Photosynthesis_Metabolism_Energymetabolism_petB,cytochromeb6	0	0	4,15269E-05
K00202_ko01200_Carbonmetabolism_Metabolism_Overview_fwdC,fmdC,formylmethanofurandehydrogenasesubunitC[EC:1.2.99.5];K00202_ko00194_Photosynthesisproteins_Metabolism_Energymetabolism_fwdC,fmdC,formylmethanofurandehydrogenasesubun	4,14903E-05	2,54767E-05	1,66107E-05
K10040_ko02010_Ctransporters_Environmentalinformationprocessing_Membranetransport_ABC.GLN1.P,putativeglutaminetransportsystempermeaseprotein	7,77944E-05	3,0572E-05	4,98322E-05
K01673_ko00910_Nitrogenmetabolism_Metabolism_Energymetabolism_cynT,can,carbonicanhydrase[EC:4.2.1.1]	0,000342295	0,000224195	0,000298993
K01783_ko00040_Pentoseandglucuronateinterconversions_Metabolism_Carbohydratemetabolism_rpe,RPE,ribulose-phosphate3-epimerase[EC:5.1.3.1];K01783_ko00030_Pentosephosphatepathway_Metabolism_Carbohydratemetabolism_rpe,RPE,ribulose-phosp	0,000658659	0,000682775	0,000606292
K10016_ko02010_Ctransporters_Environmentalinformationprocessing_Membranetransport_hisQ,histidinetransportsystempermeaseprotein	0	2,03813E-05	8,30537E-06
K09970_ko02010_Ctransporters_Environmentalinformationprocessing_Membranetransport_aapQ,bztB,generalL-aminoacidtransportsystempermeaseprotein	2,07452E-05	1,01907E-05	3,32215E-05
K02424_ko02010_Ctransporters_Environmentalinformationprocessing_Membranetransport_fliY,cystinetransportsystemsubstrate-bindingprotein	2,07452E-05	5,09533E-06	2,49161E-05
K14084_ko01200_Carbonmetabolism_Metabolism_Overview_mttC,trimethylaminecorrinoidprotein;K14084_ko00194_Photosynthesisproteins_Metabolism_Energymetabolism_mttC,trimethylaminecorrinoidprotein	2,59315E-05	4,5858E-05	3,32215E-05
K07794_ko02020_Two-componentsystem_Environmentalinformationprocessing_Signaltrasduction_tctB,putativetricarboxylictransportmembraneprotein	4,14903E-05	9,68113E-05	3,32215E-05
K03077_ko00052_Galactosemetabolism_Metabolism_Carbohydratemetabolism_ulaF,sgaE,L-ribulose-5-phosphate4-epimerase[EC:5.1.3.4]	0,000243756	0,000168146	8,30537E-05
K07703_ko02020_Two-componentsystem_Environmentalinformationprocessing_Signaltrasduction_dcuR,two-componentsystem,CitBfamily,responseregulatorDcuR	1,03726E-05	0	0
K06209_ko00400_Phenylalanine,tyrosineandtryptophanbiosynthesis_Metabolism_Aminoacidmetabolism_pheB,chorismatemutase[EC:5.4.99.5];K06209_ko01230_Biosynthesisofaminoacids_Metabolism_Overview_pheB,chorismatemutase[EC:5.4.99.5]	0,000176334	0,000112097	4,15269E-05
K05822_ko00300_Lysinebiosynthesis_Metabolism_Aminoacidmetabolism_dapH,dapD,tetrahydrodipicolinateN-acetyltransferase[EC:2.3.1.89];K05822_ko01230_Biosynthesisofaminoacids_Metabolism_Overview_dapH,dapD,tetrahydrodipicolinateN-acetyltransfera	3,11177E-05	5,09533E-06	2,49161E-05
K02948_ko03010_Ribosome_GeneticinformationProcessing_Transcription_RP-S11,MRPS11,rpsK,smallsubunitribosomalproteinS11	0,000845366	0,000682775	0,000531544
K07813_ko02020_Two-componentsystem_Environmentalinformationprocessing_Signaltrasduction_agrB,accessorygeneregulatorB	0,000243756	0,000280243	0,000589681
K01034_ko02020_Two-componentsystem_Environmentalinformationprocessing_Signaltrasduction_atoD,acetateCoA/acetoacetateCoA-transferasealphasubunit[EC:2.8.3.82.8.3.9];K01034_ko00310_Lysinedegradation_Metabolism_Aminoacidmetabolism_atoD,ace	1,55589E-05	1,5286E-05	1,66107E-05
K05895_ko00830_Retinolmetabolism_Metabolismofcofactorsandvitamins_cobK-cbiJ,precorrin-6A/cobalt-precorrin-6Areductase[EC:1.3.1.541.3.1.106]	3,11177E-05	2,54767E-05	1,66107E-05
K00759_ko00230_Purinemetabolism_Metabolism_Nucleotidemetabolism_APRT,apt,adeninephosphoribosyltransferase[EC:2.4.2.7]	0,000435648	0,00068787	0,000597987
K05814_ko02010_Ctransporters_Environmentalinformationprocessing_Membranetransport_ugpA,sn-glycerol3-phosphatetransportsystempermeaseprotein	6,22355E-05	7,13347E-05	6,6443E-05
K03270_ko00540_Lipopolysaccharidebiosynthesis_Metabolism_Glycanbiosynthesisandmetabolism_kdsC,3-deoxy-D-manno-octulosonate8-phosphatephosphatase(KDO8-Pphosphatase)[EC:3.1.3.45]	8,8167E-05	0,000168146	0,000116275
K02535_ko00540_Lipopolysaccharidebiosynthesis_Metabolism_Glycanbiosynthesisandmetabolism_lpxC,UDP-3-O-[3-hydroxymyristoyl]N-acetylglucosaminedeacetylase[EC:3.5.1.108]	1,55589E-05	3,0572E-05	6,6443E-05
K12815_ko03040_Spliceosome_GeneticinformationProcessing_Transcription_DHX38,PRP16,pre-mRNA-splicingfactorATP-dependentRNAhelicaseDHX38/PRP16[EC:3.6.4.13]	1,55589E-05	1,01907E-05	0
K07789_ko02020_Two-componentsystem_Environmentalinformationprocessing_Signaltrasduction_mdtC,RNDsuperfamily,multidrugtransportproteinMdtC	3,6304E-05	0	0
K07173_ko05111_Vibriocholeraepathogeniccycle_HumanDiseases_Infectiousdiseases_luxS,S-ribosylhomocysteinelyase[EC:4.4.1.21];K07173_ko00270_Cysteineandmethioninemetabolism_Metabolism_Aminoacidmetabolism_luxS,S-ribosylhomocysteinelyase[EC:4.	0,000285246	0,000448389	0,000182718
K15024_ko00630_Glyoxylateanddicarboxylatemetabolism_Metabolism_Carbohydratemetabolism_K15024,putativephosphotransacetylase[EC:2.3.1.8];K15024_ko00620_Pyruvatemetabolism_Metabolism_Carbohydratemetabolism_K15024,putativephosphotransac	0,000155589	0,000264957	0,000132886
K02959_ko03010_Ribosome_GeneticinformationProcessing_Transcription_RP-S16,MRPS16,rpsP,smallsubunitribosomalproteinS16	0,000985395	0,001655983	0,001926846
K08679_ko00520_Aminosugarandnucleotidesugarmetabolism_Metabolism_Carbohydratemetabolism_E5.1.3.6,UDP-glucuronate4-epimerase[EC:5.1.3.6];K08679_ko00500_Starchandsucrosemetabolism_Metabolism_Carbohydratemetabolism_E5.1.3.6,UDP-glucur	0	0	8,30537E-06
K06446_ko00930_Caprolactamdegradation_Metabolism_Xenobioticsbiodegradationandmetabolism_DCAA,acyl-CoAdehydrogenase[EC:1.3.99.-]	1,03726E-05	3,0572E-05	1,66107E-05
K02393_ko02040_Flagellarassembly_Organismalsystem_Cellmobility_flgH,flagellarL-ringproteinprecursorFlgH	1,55589E-05	1,01907E-05	0
K01495_ko00785_Lipoicacidmetabolism_Metabolism_Metabolismofcofactorsandvitamins_GCH1,folE,GTPcyclohydrolaseI[EC:3.5.4.16]	0,000295619	0,000295529	0,000382047
K00492_ko00340_Histidinemetabolism_Metabolism_Aminoacidmetabolism_E1.14.13.-,[EC:1.14.13.-];K00492_ko00903_Limoneneandpinenedegradation_Metabolism_Metabolismofterpenoidsandpolyketides_E1.14.13.-,[EC:1.14.13.-];K00492_ko00627_Aminobenz	0,000114098	0,000101907	0,000207634
K02941_ko03010_Ribosome_GeneticinformationProcessing_Transcription_RP-LP0,RPLP0,largesubunitribosomalproteinLP0	4,66766E-05	2,54767E-05	5,81376E-05
K01563_ko00625_Chloroalkaneandchloroalkenedegradation_Metabolism_Xenobioticsbiodegradationandmetabolism_dhaA,haloalkanedehalogenase[EC:3.8.1.5];K01563_ko00361_Chlorocyclohexaneandchlorobenzenedegradation_Metabolism_Xenobioticsbiodegr	2,59315E-05	5,09533E-06	3,32215E-05
K00287_ko00785_Lipoicacidmetabolism_Metabolism_Metabolismofcofactorsandvitamins_folA,dihydrofolatereductase[EC:1.5.1.3];K00287_ko00670_Onecarbonpoolbyfolate_Metabolism_Metabolismofcofactorsandvitamins_folA,dihydrofolatereductase[EC:1.5.1.:	0,000425276	0,000321006	0,000498322
K02988_ko03010_Ribosome_GeneticinformationProcessing_Transcription_RP-S5,MRPS5,rpsE,smallsubunitribosomalproteinS5	0,001006141	0,000718442	0,000722567
K03101_ko04120_Ubiquitinmediatedproteolysis_GeneticInformationProcessing_Folding,sortinganddegradation_lspA,signalpeptidaseII[EC:3.4.23.36]	0,000669032	0,000601249	0,000822232
K10008_ko02010_Ctransporters_Environmentalinformationprocessing_Membranetransport_gluA,glutamatetransportsystemATP-bindingprotein[EC:3.6.3.-]	2,07452E-05	0	0
K02986_ko03010_Ribosome_GeneticinformationProcessing_Transcription_RP-S4,rpsD,smallsubunitribosomalproteinS4	0,001135798	0,001085306	0,000647819
K00331_ko00190_Oxidativephosphorylation_Metabolism_Energymetabolism_nuoB,NADH-quinoneoxidoreductasesubunitB[EC:1.6.5.3]	0,000456394	0,000397436	0,000257467
K03779_ko00630_Glyoxylateanddicarboxylatemetabolism_Metabolism_Carbohydratemetabolism_ttdA,L(+)-tartratedehydratasealphasubunit[EC:4.2.1.32]	3,6304E-05	2,03813E-05	2,49161E-05
K10678_ko00633_Nitrotoluenedegradation_Metabolism_Xenobioticsbiodegradationandmetabolism_nfsA,nitroreductase[EC:1.-.-.-]	3,6304E-05	1,01907E-05	1,66107E-05
K02756_ko02010_Ctransporters_Environmentalinformationprocessing_Membranetransport_PTS-Bgl-EIIB,bglF,PTSsystem,beta-glucosides-specificIIBcomponent[EC:2.7.1.69]	4,14903E-05	5,09533E-05	0,000124581
K01653_ko00290_Valine,leucineandisoleucinebiosynthesis_Metabolism_Aminoacidmetabolism_E2.2.1.6S,ilvH,ilvN,acetolactatesynthasel/IIIsmallsubunit[EC:2.2.1.6];K01653_ko00630_Glyoxylateanddicarboxylatemetabolism_Metabolism_Carbohydratemetabolism	0,000331923	0,000244576	0,000249161
K01799_ko00630_Glyoxylateanddicarboxylatemetabolism_Metabolism_Carbohydratemetabolism_nicE,maiA,maleateisomerase[EC:5.2.1.1];K01799_ko00760_Nicotinateandnicotinamidemetabolism_Metabolism_Metabolismofcofactorsandvitamins_nicE,maiA,mal	3,11177E-05	4,5858E-05	5,81376E-05
K01096_ko00564_Glycerophospholipidmetabolism_Metabolism_Lipidmetabolism_pgpB,phosphatidylglycerophosphataseB[EC:3.1.3.273.1.3.813.1.3.43.6.1.27]	9,85395E-05	0,000142669	0,000116275
K01704_ko00290_Valine,leucineandisoleucinebiosynthesis_Metabolism_Aminoacidmetabolism_leuD,3-isopropylmalate/(R)-2-methylmalatedehydratasesmallsubunit[EC:4.2.1.334.2.1.35];K01704_ko00630_Glyoxylateanddicarboxylatemetabolism_Metabolism_Car	0,000425276	0,000310815	0,000240856
K02926_ko03010_Ribosome_GeneticinformationProcessing_Transcription_RP-L4,MRPL4,rplD,largesubunitribosomalproteinL4	0,000762385	0,000749014	0,00055646
K03649_ko03410_Baseexcisionrepair_GeneticinformationProcessing_ReplicationandRepair_MUG,TDG,TDG/mugDNAglycosylasefamilyprotein[EC:3.2.2.-]	0,000160775	0,000249671	0,000298993
K03780_ko00630_Glyoxylateanddicarboxylatemetabolism_Metabolism_Carbohydratemetabolism_ttdB,L(+)-tartratedehydratasebetasubunit[EC:4.2.1.32]	4,14903E-05	4,07627E-05	2,49161E-05
K03204_ko02010_Ctransporters_Environmentalinformationprocessing_Membranetransport_virB9,lvhB9,typeIVsecretionsystemproteinVirB9	6,74218E-05	2,54767E-05	7,47483E-05
K14977_ko00230_Purinemetabolism_Metabolism_Nucleotidemetabolism_ylbA,UGHY,(S)-ureidoglycineaminohydrolase[EC:3.5.3.26]	2,07452E-05	1,5286E-05	2,49161E-05
K00995_ko00564_Glycerophospholipidmetabolism_Metabolism_Lipidmetabolism_pgsA,PGS1,CDP-diacylglycerol--glycerol-3-phosphate3-phosphatidyltransferase[EC:2.7.8.5]	0,000430462	0,000550296	0,000597987

K01556_ko00380_Tryptophanmetabolism_Metabolism_Aminoacidmetabolism_KYNU,kynU,kynureninase[EC:3.7.1.3]	1,03726E-05	0	0
K01770_ko00900_Terpenoidbackbonebiosynthesis_Metabolism_Metabolismofterpenoidsandpolyketides_ispF,2-C-methyl-D-erythritol2,4-cyclodiphosphatesynthase[EC:4.6.1.12]	0,000523815	0,000361769	0,000265772
K07661_ko02020_Two-componentsystem_Environmentalinformationprocessing_Signaltrasduction_rstA,two-componentsystem,OmpRfamily,responseregulatorRstA	2,59315E-05	2,03813E-05	8,30537E-06
K07666_ko02020_Two-componentsystem_Environmentalinformationprocessing_Signaltrasduction_qseB,two-componentsystem,OmpRfamily,responseregulatorQseB	3,11177E-05	0	4,15269E-05
K11731_ko00281_Geranioldegradation_Metabolism_Metabolismofterpenoidsandpolyketides_atuD,citronellyl-CoAdehydrogenase[EC:1.3.99.-]	1,03726E-05	0	0
K12295_ko02020_Two-componentsystem_Environmentalinformationprocessing_Signaltrasduction_comE,two-componentsystem,AgrAfamily,responseregulatorComE	0	5,09533E-06	8,30537E-06
K13041_ko02020_Two-componentsystem_Environmentalinformationprocessing_Signaltrasduction_ttrR,two-componentsystem,LuxRfamily,responseregulatorTtrR	5,18629E-06	2,03813E-05	0
K02501_ko00340_Histidinemetabolism_Metabolism_Aminoacidmetabolism_hisH,glutamineamidotransferase[EC:2.4.2.-];K02501_ko01230_Biosynthesisofaminoacids_Metabolism_Overview_hisH,glutamineamidotransferase[EC:2.4.2.-]	0,000243756	0,000203813	0,000166107
K00772_ko00270_Cysteineandmethioninemetabolism_Metabolism_Aminoacidmetabolism_E2.4.2.28,mtaP,5'-methylthioadenosinephosphorylase[EC:2.4.2.28]	5,18629E-05	1,5286E-05	8,30537E-05
K01746_ko00670_Onecarbonpoolbyfolate_Metabolism_Metabolismofcofactorsandvitamins_E4.3.1.4,formiminotetrahydrofolatecyclodeaminase[EC:4.3.1.4]	0,000165961	0,000137574	0,000149497
K00275_ko00750_VitaminB6metabolism_Metabolism_Metabolismofcofactorsandvitamins_pdxH,PNPO,pyridoxamine5'-phosphateoxidase[EC:1.4.3.5]	3,6304E-05	1,5286E-05	2,49161E-05
K00857_ko00240_Pyrimidinemetabolism_Metabolism_Nucleotidemetabolism_tdk,TK,thymidinekinase[EC:2.7.1.21];K00857_ko00983_Drugmetabolism-otherenzymes_Metabolism_Xenobioticsbiodegradationandmetabolism_tdk,TK,thymidinekinase[EC:2.7.1.21]	0,000357854	0,000397436	0,000257467
K05929_ko00564_Glycerophospholipidmetabolism_Metabolism_Lipidmetabolism_E2.1.1.103,NMT,phosphoethanolamineN-methyltransferase[EC:2.1.1.103]	4,14903E-05	0,000132479	0,000174413
K02510_ko00350_Tyrosinemetabolism_Metabolism_Aminoacidmetabolism_hpaI,hpcH,4-hydroxy-2-oxoheptanedioatealdolase[EC:4.1.2.52]	7,26081E-05	6,1144E-05	3,32215E-05
K01548_ko02020_Two-componentsystem_Environmentalinformationprocessing_Signaltrasduction_kdpC,K+-transportingATPaseATPaseCchain[EC:3.6.3.12]	0,000108912	7,643E-05	8,30537E-05
K02897_ko03010_Ribosome_GeneticinformationProcessing_Transcription_RP-L25,rplY,largesubunitribosomalproteinL25	0,000471953	0,000290434	0,000332215
K08281_ko00760_Nicotinateandnicotinamidemetabolism_Metabolism_Metabolismofcofactorsandvitamins_pncA,nicotinamidase/pyrazinamidase[EC:3.5.1.193.5.1.-]	0,000207452	7,13347E-05	5,81376E-05
K08866_ko04111_Cellcycle-yeast_CellularProcesses_Cellgrowthanddeath_TTK,MPS1,serine/threonine-proteinkinaseTTK/MPS1[EC:2.7.12.1];K08866_ko04110_Cellcycle_CellularProcesses_Cellgrowthanddeath_TTK,MPS1,serine/threonine-proteinkinaseTTK/MPS1[E	2,07452E-05	0	0
K06162_ko00440_Phosphonateandphosphinatemetabolism_Metabolism_Metabolismofotheraminoacids_phnM,alpha-D-ribose1-methylphosphonate5-triphosphatediphosphatase[EC:3.6.1.63]	3,11177E-05	2,03813E-05	0
K01575_ko00630_Glyoxylateanddicarboxylatemetabolism_Metabolism_Carbohydratemetabolism_E4.1.1.5,alsD,acetolactatedecarboxylase[EC:4.1.1.5];K01575_ko00630_Glyoxylateanddicarboxylatemetabolism_Metabolism_Carbohydratemetabolism_E4.1.1.5,alsD	3,11177E-05	2,03813E-05	1,66107E-05
K09457_ko00785_Lipoicacidmetabolism_Metabolism_Metabolismofcofactorsandvitamins_queF,7-cyano-7-deazaguaninereductase[EC:1.7.1.13]	0,000285246	0,000234385	0,00021594
K01617_ko01220_Degradationofaromaticcompounds_Metabolism_Overview_dmpH,xylI,nahK,2-oxo-3-hexenedioatedecarboxylase[EC:4.1.1.77];K01617_ko00362_Benzoatedegradation_Metabolism_Xenobioticsbiodegradationandmetabolism_dmpH,xylI,nahK,2-ox	2,07452E-05	0	0
K01525_ko00230_Purinemetabolism_Metabolism_Nucleotidemetabolism_apaH,bis(5'-nucleosyl)-tetraphosphatase(symmetrical)[EC:3.6.1.41]	0	1,01907E-05	1,66107E-05
K10037_ko02010_Ctransporters_Environmentalinformationprocessing_Membranetransport_glnP,glutaminetransportsystempermeaseprotein	0	2,03813E-05	8,30537E-06
K12810_ko05130_PathogenicEscherichiacoliinfection_HumanDiseases_Infectiousdiseases_bfpA,majorstructuralsubunitofbundle-formingpilus	5,18629E-06	5,09533E-06	8,30537E-06
K13831_ko00030_Pentosephosphatepathway_Metabolism_Carbohydratemetabolism_hps-phi,3-hexulose-6-phosphatesynthase/6-phospho-3-hexuloisomerase[EC:4.1.2.435.3.1.27];K13831_ko01230_Biosynthesisofaminoacids_Metabolism_Overview_hps-phi,3-hex	0	2,54767E-05	2,49161E-05
K02121_ko00190_Oxidativephosphorylation_Metabolism_Energymetabolism_ATPVE,ntpE,atpE,V/A-typeH+-transportingATPasesubunitE	0,000223011	0,000244576	0,000365436
K11718_ko04141_Proteinprocessinginendoplasmicreticulum_GeneticInformationProcessing_Folding,sortinganddegradation_HUGT,UDP-glucose:glycoproteinglucosyltransferase[EC:2.4.1.-]	0	0	8,30537E-06
K00799_ko05204_Chemicalcarcinogenesis_HumanDiseases_Cancers_GST,gst,glutathioneS-transferase[EC:2.5.1.18];K00799_ko00480_Glutathionemetabolism_Metabolism_Metabolismofotheraminoacids_GST,gst,glutathioneS-transferase[EC:2.5.1.18];K00799_ko0	2,59315E-05	5,60487E-05	9,13591E-05
K02864_ko03010_Ribosome_GeneticinformationProcessing_Transcription_RP-L10,MRPL10,rplJ,largesubunitribosomalproteinL10	0,000674218	0,000774491	0,000689346
K02990_ko03010_Ribosome_GeneticinformationProcessing_Transcription_RP-S6,MRPS6,rpsF,smallsubunitribosomalproteinS6	0,000679404	0,000570677	0,000531544
K01664_ko00785_Lipoicacidmetabolism_Metabolism_Metabolismofcofactorsandvitamins_pabA,para-aminobenzoatesynthetasecomponentII[EC:2.6.1.85]	5,18629E-05	0,000122288	0,000149497
K10551_ko02010_Ctransporters_Environmentalinformationprocessing_Membranetransport_alsA,D-allosetransportsystemATP-bindingprotein[EC:3.6.3.17]	1,03726E-05	2,03813E-05	0
K01693_ko00340_Histidinemetabolism_Metabolism_Aminoacidmetabolism_hisB,imidazoleglycerol-phosphatedehydratase[EC:4.2.1.19];K01693_ko01230_Biosynthesisofaminoacids_Metabolism_Overview_hisB,imidazoleglycerol-phosphatedehydratase[EC:4.2.1.1	0,000171148	0,000147765	0,000191024
K02825_ko00240_Pyrimidinemetabolism_Metabolism_Nucleotidemetabolism_pyrR,pyrimidineoperonattenuationprotein/uracilphosphoribosyltransferase[EC:2.4.2.9]	6,22355E-05	0,000137574	7,47483E-05
K01494_ko00240_Pyrimidinemetabolism_Metabolism_Nucleotidemetabolism_dcd,dCTPdeaminase[EC:3.5.4.13]	9,85395E-05	7,13347E-05	9,96645E-05
K11022_ko05134_Legionellosis_HumanDiseases_Infectiousdiseases_rtxA1,rtxA,structuraltoxinprotein(hemagglutinin/hemolysin)RtxA	8,29807E-05	0,000168146	0,000116275
K00034_ko00030_Pentosephosphatepathway_Metabolism_Carbohydratemetabolism_gdh,glucose1-dehydrogenase[EC:1.1.1.47];K00034_ko01200_Carbonmetabolism_Metabolism_Overview_gdh,glucose1-dehydrogenase[EC:1.1.1.47]	6,22355E-05	6,62393E-05	7,47483E-05
K11407_ko05203_Viralcarcinogenesis_HumanDiseases_Cancers_HDAC6,histonedeacetylase6[EC:3.5.1.98];K11407_ko05034_Alcoholism_HumanDiseases_SubstanceDependence_HDAC6,histonedeacetylase6[EC:3.5.1.98]	1,55589E-05	5,09533E-06	0
K00406_ko02020_Two-componentsystem_Environmentalinformationprocessing_Signaltrasduction_ccoP,cytochromecoxidasecbb3-typesubunitIII;K00406_ko00190_Oxidativephosphorylation_Metabolism_Energymetabolism_ccoP,cytochromecoxidasecbb3-typesu	5,18629E-06	0	0
K02231_ko00830_Retinolmetabolism_Metabolism_Metabolismofcofactorsandvitamins_cobP,cobU,adenosylcobinamidekinase/adenosylcobinamide-phosphateguanylyltransferase[EC:2.7.1.1562.7.7.62]	0,000119285	0,00022929	0,000282383
K01588_ko00230_Purinemetabolism_Metabolism_Nucleotidemetabolism_purE,5-(carboxyamino)imidazoleribonucleotidemutase[EC:5.4.99.18]	0,000606796	0,000509533	0,00034052
K11004_ko02010_Ctransporters_Environmentalinformationprocessing_Membranetransport_hlyB,cyaB,ATP-bindingcassette,subfamilyB,bacterialHlyB/CyaB;K11004_ko02010_Ctransporters_Environmentalinformationprocessing_Membranetransport_hlyB,cyaB,ATI	3,11177E-05	3,56673E-05	6,6443E-05
K01934_ko00670_Onecarbonpoolbyfolate_Metabolism_Metabolismofcofactorsandvitamins_E6.3.3.2,5-formyltetrahydrofolatecyclo-ligase[EC:6.3.3.2]	0,000285246	0,000346483	0,000431879
K06046_ko02020_Two-componentsystem_Environmentalinformationprocessing_Signaltrasduction_luxE,long-chain-fatty-acid---luciferin-componentligase[EC:6.2.1.19]	7,77944E-05	4,5858E-05	9,96645E-05
K02950_ko03010_Ribosome_GeneticinformationProcessing_Transcription_RP-S12,MRPS12,rpsL,smallsubunitribosomalproteinS12	0,00092316	0,000652203	0,000564765
K03399_ko00830_Retinolmetabolism_Metabolism_Metabolismofcofactorsandvitamins_cbiE,cobalt-precorrin-7(C5)-methyltransferase[EC:2.1.1.289]	1,55589E-05	2,54767E-05	3,32215E-05
K03079_ko00052_Galactosemetabolism_Metabolism_Carbohydratemetabolism_ulaE,sgaU,L-ribulose-5-phosphate3-epimerase[EC:5.1.3.22]	2,59315E-05	4,5858E-05	6,6443E-05
K02806_ko02010_Ctransporters_Environmentalinformationprocessing_Membranetransport_PTS-Ntr-EIIA,ptsN,PTSsystem,nitrogenregulatoryIIAcomponent[EC:2.7.1.69]	2,07452E-05	3,0572E-05	3,32215E-05
K01655_ko00300_Lysinebiosynthesis_Metabolism_Aminoacidmetabolism_LYS21,LYS20,homocitratesynthase[EC:2.3.3.14];K01655_ko00620_Pyruvatemetabolism_Metabolism_Carbohydratemetabolism_LYS21,LYS20,homocitratesynthase[EC:2.3.3.14];K01655_ko01	6,22355E-05	1,5286E-05	4,98322E-05
K11584_ko04113_Meiosis-yeast_CellularProcesses_Cellgrowthanddeath_PPP2R5,serine/threonine-proteinphosphatase2AregulatorysubunitB';K11584_ko04114_Oocytemeiosis_CellularProcesses_Cellgrowthanddeath_PPP2R5,serine/threonine-proteinphosphatase	1,03726E-05	5,09533E-06	0
K03843_ko00513_VarioustypesofN-glycanbiosynthesis_Metabolism_Glycanbiosynthesisandmetabolism_ALG2,alpha-1,3/alpha-1,6-mannosyltransferase[EC:2.4.1.1322.4.1.257];K03843_ko00513_VarioustypesofN-glycanbiosynthesis_Metabolism_Glycanbiosynthesis	1,03726E-05	0	3,32215E-05
K10682_ko02020_Two-componentsystem_Environmentalinformationprocessing_Signaltrasduction_saeR,two-componentsystem,OmpRfamily,responseregulatorSaeR	5,18629E-05	1,5286E-05	4,98322E-05
K02619_ko00785_Lipoicacidmetabolism_Metabolism_Metabolismofcofactorsandvitamins_pabC,4-amino-4-deoxychorismatelyase[EC:4.1.3.38]	8,8167E-05	0,000239481	0,000182718
K05784_ko01220_Degradationofaromaticcompounds_Metabolism_Overview_benC-xylZ,benzoate/toluate1,2-dioxygenasereductasesubunit[EC:1.18.1.-];K05784_ko00362_Benzoatedegradation_Metabolism_Xenobioticsbiodegradationandmetabolism_benC-xylZ,be	1,03726E-05	0	0
K01965_ko00280_Valine,leucineandisoleucinedegradation_Metabolism_Aminoacidmetabolism_PCCA,pccA,propionyl-CoAcarboxylasealphachain[EC:6.4.1.3];K01965_ko00630_Glyoxylateanddicarboxylatemetabolism_Metabolism_Carbohydratemetabolism_PCCA,p	3,11177E-05	5,60487E-05	8,30537E-06
K03428_ko00830_Retinolmetabolism_Metabolism_Metabolismofcofactorsandvitamins_E2.1.1.11,chlM,bchM,magnesium-protoporphyrinO-methyltransferase[EC:2.1.1.11]	0	0	1,66107E-05
K11180_ko00920_Sulfurmetabolism_Metabolism_Energymetabolism_dsrA,sulfitereductasealphasubunit[EC:1.8.99.31.8.99.1];K11180_ko00633_Nitrotoluenedegradation_Metabolism_Xenobioticsbiodegradationandmetabolism_dsrA,sulfitereductasealphasubunit[	4,14903E-05	1,01907E-05	1,66107E-05
K12529_ko00450_Selenocompoundmetabolism_Metabolism_Metabolismofotheraminoacids_ygfM,putativeselenatereductaseFAD-bindingsubunit	4,66766E-05	3,0572E-05	4,15269E-05
K00167_ko00280_Valine,leucineandisoleucinedegradation_Metabolism_Aminoacidmetabolism_BCKDHB,bkdA2,2-oxoisovaleratedehydrogenaseE1componentbetasubunit[EC:1.2.4.4]	5,18629E-06	0	0
K03652_ko03410_Baseexcisionrepair_GeneticinformationProcessing_ReplicationandRepair_MPG,DNA-3-methyladenineglycosylase[EC:3.2.2.21]	1,55589E-05	0,000193623	6,6443E-05
K02931_ko03010_Ribosome_GeneticinformationProcessing_Transcription_RP-L5,MRPL5,rplE,largesubunitribosomalproteinL5	0,00120322	0,000835635	0,000631208
K01825_ko00310_Lysinedegradation_Metabolism_Aminoacidmetabolism_fadB,3-hydroxyacyl-CoAdehydrogenase/enoyl-CoAhydratase/3-hydroxybutyryl-CoAepimerase/enoyl-CoAisomerase[EC:1.1.1.354.2.1.175.1.2.35.3.3.8];K01825_ko00380_Tryptophanmetabo	1,03726E-05	1,5286E-05	1,66107E-05
K00073_ko00230_Purinemetabolism_Metabolism_Nucleotidemetabolism_allD,ureidoglycolatedehydrogenase(NAD+)[EC:1.1.1.350]	5,18629E-06	3,0572E-05	2,49161E-05
K01792_ko00010_Glycolysis/Gluconeogenesis_Metabolism_Carbohydratemetabolism_E5.1.3.15,glucose-6-phosphate1-epimerase[EC:5.1.3.15]	1,03726E-05	5,09533E-06	4,15269E-05
K04058_ko02010_Ctransporters_Environmentalinformationprocessing_Membranetransport_yscW,sctW,typeIIIsecretionproteinW	1,55589E-05	0	0
K12107_ko05120_EpithelialcellsignalinginHelicobacterpyloriinfection_HumanDiseases_Infectiousdiseases_cag22,cagpathogenicityislandprotein22	5,18629E-06	0	4,98322E-05
K02328_ko03410_Baseexcisionrepair_GeneticinformationProcessing_ReplicationandRepair_POLD2,DNApolymerasedeltasubunit2;K02328_ko03030_DNAreplication_GeneticinformationProcessing_ReplicationandRepair_POLD2,DNApolymerasedeltasubunit2;K023	0	1,5286E-05	0
K01678_ko00020_Citratecycle(TCAcycle)_Metabolism_Carbohydratemetabolism_E4.2.1.2AB,fumB,fumaratehydratasesubunitbeta[EC:4.2.1.2];K01678_ko00620_Pyruvatemetabolism_Metabolism_Carbohydratemetabolism_E4.2.1.2AB,fumB,fumaratehydratasesub	0,000171148	0,000132479	0,000182718
K05879_ko00561_Glycerolipidmetabolism_Metabolism_Lipidmetabolism_dhaL,dihydroxyacetonekinase,C-terminaldomain[EC:2.7.1.-]	0,000114098	5,09533E-05	0,000149497

K14986_ko02020_Two-componentsystem_Environmentalinformationprocessing_Signaltrasduction_fixL,two-componentsystem,LuxRfamily,sensorkinaseFixL[EC:2.7.13.3]	2,59315E-05	1,01907E-05	1,66107E-05
K00657_ko00330_Arginineandprolinemetabolism_Metabolism_Aminoacidmetabolism_E2.3.1.57,speG,diamineN-acetyltransferase[EC:2.3.1.57]	0,000171148	0,00015286	0,000141191
K14539_ko03008_Ribosomebiogenesisineukaryotes_GeneticinformationProcessing_Transcription_LSG1,largesubunitGTPase1[EC:3.6.1.-]	1,03726E-05	1,01907E-05	0
K03411_ko02030_Bacterialchemotaxis_Organismalsystem_Cellmobility_cheD,chemotaxisproteinCheD[EC:3.5.1.44]	3,6304E-05	3,56673E-05	2,49161E-05
K00823_ko00250_Alanine,aspartateandglutamatemetabolism_Metabolism_Aminoacidmetabolism_puuE,4-aminobutyrateaminotransferase[EC:2.6.1.19];K00823_ko00630_Glyoxylateanddicarboxylatemetabolism_Metabolism_Carbohydratemetabolism_puuE,4-an	7,77944E-05	6,62393E-05	7,47483E-05
K13895_ko02010_Ctransporters_Environmentalinformationprocessing_Membranetransport_yejE,microcinCtransportsystempermeaseprotein	5,70492E-05	5,09533E-05	0,000124581
K03523_ko02010_Ctransporters_Environmentalinformationprocessing_Membranetransport_bioY,biotintransportsystemsubstrate-specificcomponent	0,000269687	0,000346483	0,000290688
K01823_ko00900_Terpenoidbackbonebiosynthesis_Metabolism_Metabolismofterpenoidsandpolyketides_idi,IDI,isopentenyl-diphosphatedelta-isomerase[EC:5.3.3.2]	9,85395E-05	4,5858E-05	4,15269E-05
K11694_ko01005_Lipopolysaccharidebiosynthesisproteins_Metabolism_Glycanbiosynthesisandmetabolism_femA,peptidoglycanpentaglycineglycinetransferase(thesecondandthirdglycine)[EC:2.3.2.17]	9,33532E-05	9,68113E-05	0,000174413
K01103_ko04066_HIF-1signalingpathway_Environmentalinformationprocessing_Signaltrasduction_PFKFB,6-phosphofructo-2-kinase/fructose-2,6-bisphosphatase[EC:2.7.1.1053.1.3.46];K01103_ko04151_PI3K-Aktsignalingpathway_Environmentalinformationproces	0	0	8,30537E-06
K14292_ko03013_RNAtransport_GeneticinformationProcessing_Transcription_TGS1,trimethylguanosinesynthase[EC:2.1.1.-]	0	1,01907E-05	0
K01521_ko00564_Glycerophospholipidmetabolism_Metabolism_Lipidmetabolism_cdh,CDP-diacylglycerolpyrophosphatase[EC:3.6.1.26]	0	1,5286E-05	3,32215E-05
K03936_ko05010_Alzheimer'sdisease_HumanDiseases_Degenerativediseases_NDUFS3,NADHdehydrogenase(ubiquinone)Fe-Sprotein3[EC:1.6.5.31.6.99.3];K03936_ko05016_Huntington'sdisease_HumanDiseases_Degenerativediseases_NDUFS3,NADHdehydrogenas	0	1,01907E-05	1,66107E-05
K01497_ko00740_Riboflavinmetabolism_Metabolism_Metabolismofcofactorsandvitamins_ribA,RIB1,GTPcyclohydrolaseII[EC:3.5.4.25]	1,03726E-05	1,5286E-05	0
K02771_ko02010_Ctransporters_Environmentalinformationprocessing_Membranetransport_PTS-Fru1-EIID,levG,PTSsystem,fructose-specificIIDcomponent;K02771_ko00520_Aminosugarandnucleotidesugarmetabolism_Metabolism_Carbohydratemetabolism_PTS-	7,77944E-05	3,0572E-05	3,32215E-05
K12455_ko00520_Aminosugarandnucleotidesugarmetabolism_Metabolism_Carbohydratemetabolism_rfbJ,CDP-abequosesynthase[EC:1.1.1.341]	5,18629E-06	0	8,30537E-06
K03186_ko00130_Ubiquinoneandotherterpenoid-quinonebiosynthesis_Metabolism_Metabolismofcofactorsandvitamins_ubiX,3-octaprenyl-4-hydroxybenzoatecarboxy-lyaseUbiX[EC:4.1.1.-]	6,74218E-05	1,01907E-05	6,6443E-05
K00805_ko00900_Terpenoidbackbonebiosynthesis_Metabolism_Metabolismofterpenoidsandpolyketides_hepST,heptaprenyldiphosphatesynthase[EC:2.5.1.30]	0,000399344	0,000672584	0,000755789
K03350_ko04111_Cellcycle-yeast_CellularProcesses_Cellgrowthanddeath_APC3,CDC27,anaphase-promotingcomplexsubunit3;K03350_ko04110_Cellcycle_CellularProcesses_Cellgrowthanddeath_APC3,CDC27,anaphase-promotingcomplexsubunit3;K03350_ko0411	0	2,03813E-05	8,30537E-06
K03210_ko02010_Ctransporters_Environmentalinformationprocessing_Membranetransport_yajC,preproteintranslocasesubunitYajC;K03210_ko04120_Ubiquitinmediatedproteolysis_GeneticInformationProcessing_Folding,sortinganddegradation_yajC,preproteintr	0,000446021	0,000361769	0,000415269
K00177_ko00020_Citratecycle(TCAcycle)_Metabolism_Carbohydratemetabolism;K00177_ko01200_Carbonmetabolism_Metabolism_Overview;K00177_ko00194_Photosynthesisproteins_Metabolism_Energymetabolism	0,00036304	0,000321006	0,000282383
K00172_ko00020_Citratecycle(TCAcycle)_Metabolism_Carbohydratemetabolism_porG,pyruvateferredoxinoxidoreductase,gammasubunit[EC:1.2.7.1];K00172_ko00010_Glycolysis/Gluconeogenesis_Metabolism_Carbohydratemetabolism_porG,pyruvateferredoxinc	0,000119285	3,56673E-05	0,00010797
K01816_ko00630_Glyoxylateanddicarboxylatemetabolism_Metabolism_Carbohydratemetabolism_E5.3.1.22,gip,hydroxypyruvateisomerase[EC:5.3.1.22]	6,22355E-05	6,62393E-05	8,30537E-05
K02705_ko00195_Photosynthesis_Metabolism_Energymetabolism_psbC,photosystemIICP43chlorophyllaproprotein	2,59315E-05	0	8,30537E-06
K01518_ko00230_Purinemetabolism_Metabolism_Nucleotidemetabolism_NUDT2,bis(5'-nucleosidyl)-tetraphosphataseEC:3.6.1.17];K01518_ko00240_Pyrimidinemetabolism_Metabolism_Nucleotidemetabolism_NUDT2,bis(5'-nucleosidyl)-tetraphosphataseEC:3.6	3,6304E-05	1,01907E-05	1,66107E-05
K01734_ko00630_Glyoxylateanddicarboxylatemetabolism_Metabolism_Carbohydratemetabolism_mgsA,methylglyoxalsynthase[EC:4.2.3.3]	0,000425276	0,000448389	0,000174413
K05915_ko00363_Bisphenoldegradation_Metabolism_Xenobioticsbiodegradationandmetabolism_E1.13.-.-,[EC:1.13.-.-];K05915_ko00626_Naphthalenedegradation_Metabolism_Xenobioticsbiodegradationandmetabolism_E1.13.-.-,[EC:1.13.-.-]	1,03726E-05	1,5286E-05	1,66107E-05
K03392_ko00380_Tryptophanmetabolism_Metabolism_Aminoacidmetabolism_ACMSD,aminocarboxymuconate-semialdehydedecarboxylase[EC:4.1.1.45]	0	1,01907E-05	4,15269E-05
K02933_ko03010_Ribosome_GeneticinformationProcessing_Transcription_RP-L6,MRPL6,rplF,largesubunitribosomalproteinL6	0,000949091	0,001054734	0,000639514
K06859_ko00520_Aminosugarandnucleotidesugarmetabolism_Metabolism_Carbohydratemetabolism_pgi1,glucose-6-phosphateisomerase,archaeal[EC:5.3.1.9];K06859_ko00010_Glycolysis/Gluconeogenesis_Metabolism_Carbohydratemetabolism_pgi1,glucose-6-	5,18629E-05	1,5286E-05	1,66107E-05
K02879_ko03010_Ribosome_GeneticinformationProcessing_Transcription_RP-L17,MRPL17,rplQ,largesubunitribosomalproteinL17	0,000980209	0,000392341	0,000589681
K01070_ko01200_Carbonmetabolism_Metabolism_Overview_frmB,ESD,fghA,S-formylglutathionehydrolase[EC:3.1.2.12];K01070_ko00194_Photosynthesisproteins_Metabolism_Energymetabolism_frmB,ESD,fghA,S-formylglutathionehydrolase[EC:3.1.2.12]	0,000103726	0,000132479	0,000257467
K00588_ko00360_Phenylalaninemetabolism_Metabolism_Aminoacidmetabolism_E2.1.1.104,caffeoyl-CoAO-methyltransferase[EC:2.1.1.104];K00588_ko00941_Flavonoidbiosynthesis_Metabolism_Biosynthesisofothersecondarymetabolites_E2.1.1.104,caffeoyl-CoA	0,000160775	0,00015286	5,81376E-05
K02113_ko00190_Oxidativephosphorylation_Metabolism_Energymetabolism_ATPF1D,atpH,F-typeH+-transportingATPasesubunitdelta;K02113_ko00195_Photosynthesis_Metabolism_Energymetabolism_ATPF1D,atpH,F-typeH+-transportingATPasesubunitdelta	0,000331923	0,000341387	0,000390352
K10554_ko02010_Ctransporters_Environmentalinformationprocessing_Membranetransport_frcA,fructosetransportsystemATP-bindingprotein	2,07452E-05	0	0
K05606_ko00280_Valine,leucineandisoleucinedegradation_Metabolism_Aminoacidmetabolism_MCEE,epi,methylmalonyl-CoA/ethylmalonyl-CoAepimerase[EC:5.1.99.1];K05606_ko00630_Glyoxylateanddicarboxylatemetabolism_Metabolism_Carbohydratemetabo	0,000243756	0,000244576	0,000141191
K01479_ko00340_Histidinemetabolism_Metabolism_Aminoacidmetabolism_hutG,formiminoglutamase[EC:3.5.3.8]	0	2,54767E-05	4,98322E-05
K00339_ko00190_Oxidativephosphorylation_Metabolism_Energymetabolism_nuoJ,NADH-quinoneoxidoreductasesubunitJ[EC:1.6.5.3]	0,000238569	0,000193623	9,96645E-05
K02884_ko03010_Ribosome_GeneticinformationProcessing_Transcription_RP-L19,MRPL19,rplS,largesubunitribosomalproteinL19	0,000663845	0,000545201	0,000514933
K13891_ko02010_Ctransporters_Environmentalinformationprocessing_Membranetransport_gsiD,glutathionetransportsystempermeaseprotein	2,59315E-05	1,01907E-05	0
K00432_ko00590_Arachidonicacidmetabolism_Metabolism_Lipidmetabolism_E1.11.1.9,glutathioneperoxidase[EC:1.11.1.9];K00432_ko00480_Glutathionemetabolism_Metabolism_Metabolismofotheraminoacids_E1.11.1.9,glutathioneperoxidase[EC:1.11.1.9];K00	2,07452E-05	3,0572E-05	9,96645E-05
K00794_ko00740_Riboflavinmetabolism_Metabolism_Metabolismofcofactorsandvitamins_ribH,RIB4,6,7-dimethyl-8-ribityllumazinesynthase[EC:2.5.1.78]	0,000191893	0,000244576	0,000199329
K04565_ko04146_Peroxisome_CellularProcesses_Transportandcatabolism_SOD1,superoxidedismutase,Cu-Znfamily[EC:1.15.1.1];K04565_ko05014_Amyotrophiclateralsclerosis(ALS)_HumanDiseases_Degenerativediseases_SOD1,superoxidedismutase,Cu-Znfamily[E	4,14903E-05	7,13347E-05	5,81376E-05
K10679_ko00633_Nitrotoluenedegradation_Metabolism_Xenobioticsbiodegradationandmetabolism_nfnB,nfsB,nitroreductase/dihydropteridinereductase[EC:1.-.-.-1.5.1.34]	2,07452E-05	0	4,15269E-05
K11621_ko02020_Two-componentsystem_Environmentalinformationprocessing_Signaltrasduction_liaG,liaoperonproteinLiaG	5,18629E-06	1,5286E-05	0
K02794_ko02010_Ctransporters_Environmentalinformationprocessing_Membranetransport_PTS-Man-EIIB,manX,PTSsystem,mannose-specificIIBcomponent[EC:2.7.1.69];K02794_ko00520_Aminosugarandnucleotidesugarmetabolism_Metabolism_Carbohydrateme	0,000217824	0,000178337	0,000224245
K11634_ko02020_Two-componentsystem_Environmentalinformationprocessing_Signaltrasduction_yxdJ,two-componentsystem,OmpRfamily,responseregulatorYxdJ	0	1,5286E-05	0
K12555_ko00312_beta-Lactamresistance_HumanDiseases_Drugresistance_pbp2A,penicillin-bindingprotein2A[EC:2.4.1.1292.3.2.-];K12555_ko01005_Lipopolysaccharidebiosynthesisproteins_Metabolism_Glycanbiosynthesisandmetabolism_pbp2A,penicillin-binding	4,14903E-05	1,01907E-05	7,47483E-05
K05964_ko02020_Two-componentsystem_Environmentalinformationprocessing_Signaltrasduction_citX,holo-ACPsynthase[EC:2.7.7.61]	3,6304E-05	3,0572E-05	2,49161E-05
K12661_ko00051_Fructoseandmannosemetabolism_Metabolism_Carbohydratemetabolism_LRA3,yfaW,L-rhamnonatedehydratase[EC:4.2.1.90]	1,03726E-05	5,09533E-06	1,66107E-05
K02994_ko03010_Ribosome_GeneticinformationProcessing_Transcription_RP-S8,rpsH,smallsubunitribosomalproteinS8	0,000757199	0,000631821	0,00055646
K03179_ko00130_Ubiquinoneandotherterpenoid-quinonebiosynthesis_Metabolism_Metabolismofcofactorsandvitamins_ubiA,4-hydroxybenzoateoctaprenyltransferase[EC:2.5.1.-]	1,55589E-05	5,09533E-06	3,32215E-05
K01630_ko00052_Galactosemetabolism_Metabolism_Carbohydratemetabolism_garL,2-dehydro-3-deoxyglucarateraldolase[EC:4.1.2.20]	4,14903E-05	3,0572E-05	5,81376E-05
K02203_ko00260_Glycine,serineandthreoninemetabolism_Metabolism_Aminoacidmetabolism_thrH,phosphoserine/homoserinephosphotransferase[EC:3.1.3.32.7.1.39];K02203_ko01230_Biosynthesisofaminoacids_Metabolism_Overview_thrH,phosphoserine/hon	0,000155589	0,000178337	0,000240856
K00230_ko00830_Retinolmetabolism_Metabolism_Metabolismofcofactorsandvitamins_hemG,menaquinone-dependentprotoporphyrinogenoxidase[EC:1.3.5.3]	2,59315E-05	1,5286E-05	5,81376E-05
K02109_ko00190_Oxidativephosphorylation_Metabolism_Energymetabolism_ATPF0B,atpF,F-typeH+-transportingATPasesubunitb;K02109_ko00195_Photosynthesis_Metabolism_Energymetabolism_ATPF0B,atpF,F-typeH+-transportingATPasesubunitb	0,000534188	0,00061144	0,000539849
K02339_ko03030_DNAreplication_GeneticinformationProcessing_ReplicationandRepair_DPO3C,holC,DNApolymeraseIIIsubunitchi[EC:2.7.7.7];K02339_ko03440_Homologousrecombination_GeneticinformationProcessing_ReplicationandRepair_DPO3C,holC,DNApc	1,55589E-05	1,01907E-05	0
K13993_ko04141_Proteinprocessinginendoplasmicreticulum_GeneticInformationProcessing_Folding,sortinganddegradation_HSP20,HSP20familyprotein	0,000394158	0,000341387	0,000639514
K13018_ko00520_Aminosugarandnucleotidesugarmetabolism_Metabolism_Carbohydratemetabolism_wbpD,wlbB,UDP-2-acetamido-3-amino-2,3-dideoxy-glucuronateN-acetyltransferase[EC:2.3.1.201]	2,59315E-05	3,0572E-05	7,47483E-05
K10934_ko05110_Vibriocholeraeinfection_HumanDiseases_Infectiousdiseases_tcpE,toxinco-regulatedpilusbiosynthesisproteinE;K10934_ko05111_Vibriocholeraepathogeniccycle_HumanDiseases_Infectiousdiseases_tcpE,toxinco-regulatedpilusbiosynthesisproteinI	1,03726E-05	1,5286E-05	1,66107E-05
K00899_ko00270_Cysteineandmethioninemetabolism_Metabolism_Aminoacidmetabolism_mtnK,5-methylthioribosekinase[EC:2.7.1.100]	6,22355E-05	3,0572E-05	5,81376E-05
K00954_ko00770_PantothenateandCoABiosynthesis_Metabolism_Metabolismofcofactorsandvitamins_E2.7.7.3A,coaD,kdtB,pantetheine-phosphateadenylyltransferase[EC:2.7.7.3]	0,000316364	0,000387245	0,000240856
K07774_ko02020_Two-componentsystem_Environmentalinformationprocessing_Signaltrasduction_tctD,two-componentsystem,OmpRfamily,responseregulatorTctD	1,03726E-05	5,09533E-06	9,96645E-05
K00856_ko00230_Purinemetabolism_Metabolism_Nucleotidemetabolism_E2.7.1.20,ADK,adenosinekinase[EC:2.7.1.20]	9,33532E-05	1,01907E-05	8,30537E-05
K03021_ko03020_RNApolymerase_GeneticinformationProcessing_Transcription_RPC2,POLR3B,DNA-directedRNApolymeraseIIIsubunitRPC2[EC:2.7.7.6];K03021_ko05169_Epstein-Barrvirusinfection_HumanDiseases_Infectiousdiseases_RPC2,POLR3B,DNA-directedF	1,03726E-05	0	0
K02895_ko03010_Ribosome_GeneticinformationProcessing_Transcription_RP-L24,MRPL24,rplX,largesubunitribosomalproteinL24	0,000648286	0,000468771	0,000274077
K00371_ko02020_Two-componentsystem_Environmentalinformationprocessing_Signaltrasduction_narH,nitratereductasebetasubunit[EC:1.7.99.4];K00371_ko00910_Nitrogenmetabolism_Metabolism_Energymetabolism_narH,nitratereductasebetasubunit[EC:1.7.	2,59315E-05	3,0572E-05	1,66107E-05
K02184_ko04320_Dorso-ventralaxisformation_Organismalsystem_Development_FMN2,formin2	0	0	1,66107E-05
K07689_ko02020_Two-componentsystem_Environmentalinformationprocessing_Signaltrasduction_uvrY,two-componentsystem,NarLfamily,invasionresponseregulatorUvrY	5,18629E-06	5,09533E-06	3,32215E-05
K03666_ko03018_RNAdegradation_GeneticInformationProcessing_Folding,sortinganddegradation_hfq,hostfactor-Iprotein	3,6304E-05	3,56673E-05	3,32215E-05

K03269_ko00540_Lipopolysaccharidebiosynthesis_Metabolism_Glycanbiosynthesisandmetabolism_lpxH,UDP-2,3-diacylglucosaminehydrolase[EC:3.6.1.54]	0,000129657	0,000132479	0,00010797
K15036_ko00280_Valine,leucineandisoleucinedegradation_Metabolism_Aminoacidmetabolism_K15036,acetyl-CoA/propionyl-CoAcarboxylase[EC:6.4.1.2 6.4.1.3];K15036_ko00630_Glyoxylateanddicarboxylatemetabolism_Metabolism_Carbohydratemetabolism_K1	1,03726E-05	0	2,49161E-05
K04936_ko04024_cAMPsignalingpathway_Environmentalinformationprocessing_Signaltrasduction_KCNMA1,potassiumlargeconductancecalcium-activatedchannelsubfamilyMalphamember1;K04936_ko04260_Cardiacmusclecontraction_Organismalsystem_Circula	3,6304E-05	3,0572E-05	8,30537E-05
K14559_ko03008_Ribosomebiogenesisineukaryotes_GeneticinformationProcessing_Transcription_MPP10,U3smallnucleolarRNA-associatedproteinMPP10	4,14903E-05	0	1,66107E-05
K02150_ko04145_Phagosome_CellularProcesses_Transportandcatabolism_ATPeV1E,ATP6E,V-typeH+-transportingATPasesubunitE;K02150_ko04721_Synapticvesiclecycle_Environmentalinformationprocessing_Signaltransduction_ATPeV1E,ATP6E,V-typeH+-transpo	1,03726E-05	1,01907E-05	1,66107E-05
K03200_ko02010_Ctransporters_Environmentalinformationprocessing_Membranetransport_virB5,lvhB5,typeIVsecretionsystemproteinVirB5	3,6304E-05	1,01907E-05	5,81376E-05
K01095_ko00564_Glycerophospholipidmetabolism_Metabolism_Lipidmetabolism_pgpA,phosphatidylglycerophosphataseA[EC:3.1.3.27]	5,70492E-05	6,62393E-05	5,81376E-05
K06989_ko00760_Nicotinateandnicotinamidemetabolism_Metabolism_Metabolismofcofactorsandvitamins_nadX,aspartatedehydrogenase[EC:1.4.1.21]	2,59315E-05	2,54767E-05	0,00010797
K00373_ko02020_Two-componentsystem_Environmentalinformationprocessing_Signaltrasduction_narJ,nitratereductasedeltasubunit;K00373_ko00910_Nitrogenmetabolism_Metabolism_Energymetabolism_narJ,nitratereductasedeltasubunit	0	1,01907E-05	3,32215E-05
K10213_ko00230_Purinemetabolism_Metabolism_Nucleotidemetabolism_rihB,ribosylpyrimidinenucleosidase[EC:3.2.2.8];K10213_ko00240_Pyrimidinemetabolism_Metabolism_Nucleotidemetabolism_rihB,ribosylpyrimidinenucleosidase[EC:3.2.2.8]	1,03726E-05	5,09533E-06	0
K00071_ko00140_Steroidhormonebiosynthesis_Metabolism_Lipidmetabolism_HSD11B2,corticosteroid11-beta-dehydrogenaseisozyme2[EC:1.1.1.-];K00071_ko04960_Aldosterone-regulatedsodiumreabsorption_Organismalsystem_Excretorysystem_HSD11B2,cortic	1,55589E-05	0	3,32215E-05
K02992_ko03010_Ribosome_GeneticinformationProcessing_Transcription_RP-S7,MRPS7,rpsG,smallsubunitribosomalproteinS7	0,000990582	0,00084073	0,000564765
K00950_ko00785_Lipoicacidmetabolism_Metabolism_Metabolismofcofactorsandvitamins_folK,2-amino-4-hydroxy-6-hydroxymethyldihydropteridinediphosphokinase[EC:2.7.6.3]	9,85395E-05	0,000224195	0,000240856
K06211_ko00760_Nicotinateandnicotinamidemetabolism_Metabolism_Metabolismofcofactorsandvitamins_nadR,HipBfamilytranscriptionalregulator,transcriptionalrepressorofNADbiosynthesisgenes[EC:2.7.7.12 7.1.22]	1,03726E-05	1,01907E-05	2,49161E-05
K10038_ko02010_Ctransporters_Environmentalinformationprocessing_Membranetransport_glnQ,glutaminetransportsystemATP-bindingprotein[EC:3.6.3.-]	1,03726E-05	2,03813E-05	4,15269E-05
K03594_ko00830_Retinolmetabolism_Metabolism_Metabolismofcofactorsandvitamins_bfr,bacterioferritin[EC1.16.3.1]	0,000108912	0,000101907	7,47483E-05
K02744_ko02010_Ctransporters_Environmentalinformationprocessing_Membranetransport_PTS-Aga-EIIA,agaF,PTSsystem,N-acetylgalactosamine-specificIIAcomponent[EC:2.7.1.69];K02744_ko00052_Galactosemetabolism_Metabolism_Carbohydratemetabolism_	2,07452E-05	6,62393E-05	4,15269E-05
K01737_ko00785_Lipoicacidmetabolism_Metabolism_Metabolismofcofactorsandvitamins_queD,ptpS,PTS,6-pyruvoyltetrahydropterin/6-carboxytetrahydropterinsynthase[EC:4.2.3.124.1.2.50]	0,000176334	0,000183432	0,000157802
K06445_ko00071_Fattyaciddegradation_Metabolism_Lipidmetabolism_fadE,acyl-CoAdehydrogenase[EC:1.3.99.-];K06445_ko01212_Fattyacidmetabolism_Metabolism_Overview_fadE,acyl-CoAdehydrogenase[EC:1.3.99.-]	1,55589E-05	0	8,30537E-06
K02413_ko02040_Flagellarassembly_Organismalsystem_Cellmobility_fliJ,flagellarFliJprotein	3,11177E-05	2,54767E-05	2,49161E-05
K06674_ko04111_Cellcycle-yeast_CellularProcesses_Cellgrowthanddeath_SMC2,structuralmaintenanceofchromosome2	1,03726E-05	5,09533E-06	0
K14988_ko02020_Two-componentsystem_Environmentalinformationprocessing_Signaltrasduction_salK,two-componentsystem,NarLfamily,secretionsystemsensorhistidinekinaseSalK	4,66766E-05	5,09533E-05	0,000116275
K06928_ko00730_Thiaminemetabolism_Metabolism_Metabolismofcofactorsandvitamins_NTPCR,nucleoside-triphosphatase[EC:3.6.1.15];K06928_ko00230_Purinemetabolism_Metabolism_Nucleotidemetabolism_NTPCR,nucleoside-triphosphatase[EC:3.6.1.15]	3,6304E-05	1,01907E-05	3,32215E-05
K02704_ko00195_Photosynthesis_Metabolism_Energymetabolism_psbB,photosystemIICP47chlorophyllapoprotein	0	5,09533E-06	0
K05587_ko00190_Oxidativephosphorylation_Metabolism_Energymetabolism_hoxF,bidirectional[NiFe]hydrogenasediaphorasesubunit[EC:1.6.5.3]	0	5,09533E-06	0
K00334_ko00190_Oxidativephosphorylation_Metabolism_Energymetabolism_nuoE,NADH-quinoneoxidoreductasesubunitE[EC:1.6.5.3]	0,000207452	0,000193623	0,000207634
K09474_ko02020_Two-componentsystem_Environmentalinformationprocessing_Signaltrasduction_phoN,acidphosphatase(classA)[EC:3.1.3.2];K09474_ko00740_Riboflavinmetabolism_Metabolism_Metabolismofcofactorsandvitamins_phoN,acidphosphatase(class/	1,55589E-05	4,07627E-05	3,32215E-05
K02871_ko03010_Ribosome_GeneticinformationProcessing_Transcription_RP-L13,MRPL13,rplM,largesubunitribosomalproteinL13	0,000653473	0,000845825	0,000514933
K06726_ko02010_Ctransporters_Environmentalinformationprocessing_Membranetransport_rbsD,D-ribosepyranase[EC:5.-.-.-]	5,70492E-05	6,1144E-05	3,32215E-05
K00228_ko00830_Retinolmetabolism_Metabolism_Metabolismofcofactorsandvitamins_CPOX,hemF,coproporphyrinogenIIIoxidase[EC:1.3.3.3]	0	5,09533E-06	1,66107E-05
K09688_ko02010_Ctransporters_Environmentalinformationprocessing_Membranetransport_ABC-2.CPSE.P,capsularpolysaccharidetransportsystempermeaseprotein	2,59315E-05	3,0572E-05	2,49161E-05
K05658_ko02010_Ctransporters_Environmentalinformationprocessing_Membranetransport_ABCB1,ATP-bindingcassette,subfamilyB(MDR/TAP),member1[EC:3.6.3.44];K05658_ko05206_MicroRNAsincancer_HumanDiseases_Cancers_ABCB1,ATP-bindingcassette,su	5,18629E-06	0	1,66107E-05
K01512_ko00620_Pyruvatemetabolism_Metabolism_Carbohydratemetabolism_acyP,acylphosphatase[EC:3.6.1.7];K01512_ko00627_Aminobenzoatedegradation_Metabolism_Xenobioticsbiodegradationandmetabolism_acyP,acylphosphatase[EC:3.6.1.7]	9,33532E-05	7,643E-05	9,13591E-05
K03124_ko03022_Basaltranscriptionfactors_GeneticinformationProcessing_Transcription_TFIIB,GTF2B,SUA7,tfb,transcriptioninitiationfactorTFIIB;K03124_ko05203_Viralcarcinogenesis_HumanDiseases_Cancers_TFIIB,GTF2B,SUA7,tfb,transcriptioninitiationfactorTF	1,03726E-05	5,09533E-06	2,49161E-05
K02745_ko02010_Ctransporters_Environmentalinformationprocessing_Membranetransport_PTS-Aga-EIIB,agaV,PTSsystem,N-acetylgalactosamine-specificIIBcomponent[EC:2.7.1.69];K02745_ko00052_Galactosemetabolism_Metabolism_Carbohydratemetabolism_	3,6304E-05	4,5858E-05	3,32215E-05
K03037_ko03050_Proteasome_GeneticInformationProcessing_Folding,sortinganddegradation_PSMD6,RPN7,26Sproteasomeregulatorysubunit N7;K03037_ko05169_Epstein-Barrvirusinfection_HumanDiseases_Infectiousdiseases_PSMD6,RPN7,26Sproteasomeregul	5,18629E-06	0	0
K14005_ko04141_Proteinprocessinginendoplasmicreticulum_GeneticInformationProcessing_Folding,sortinganddegradation_SEC31,proteintransportproteinSEC31	5,18629E-06	0	0
K12304_ko00230_Purinemetabolism_Metabolism_Nucleotidemetabolism_CANT1,solublecalcium-activatednucleotidase1[EC:3.6.1.6];K12304_ko00240_Pyrimidinemetabolism_Metabolism_Nucleotidemetabolism_CANT1,solublecalcium-activatednucleotidase1[EC:	1,03726E-05	0	0
K07663_ko02020_Two-componentsystem_Environmentalinformationprocessing_Signaltrasduction_creB,two-componentsystem,OmpRfamily,catabolicregulationresponseregulatorCreB	1,03726E-05	2,03813E-05	8,30537E-06
K03518_ko01200_Carbonmetabolism_Metabolism_Overview_coxS,carbon-monoxidedehydrogenasesmallsubunit[EC:1.2.99.2];K03518_ko00633_Nitrotoluenedegradation_Metabolism_Xenobioticsbiodegradationandmetabolism_coxS,carbon-monoxidedehydroger	0,000114098	7,13347E-05	0,000132886
K02124_ko00190_Oxidativephosphorylation_Metabolism_Energymetabolism_ATPVK,ntpK,atpK,V/A-typeH+-transportingATPasesubunitK	0,000134844	0,000101907	0,000132886
K02422_ko02040_Flagellarassembly_Organismalsystem_Cellmobility_fliS,flagellarproteinFliS	6,22355E-05	5,60487E-05	8,30537E-05
K02878_ko03010_Ribosome_GeneticinformationProcessing_Transcription_RP-L16,MRPL16,rplP,largesubunitribosomalproteinL16	0,000757199	0,000698061	0,000506628
K01429_ko00791_Atrazinedegradation_Humandiseases_Xenobioticsbiodegradationandmetabolism_ureB,ureasesubunitbeta[EC:3.5.1.5];K01429_ko00330_Arginineandprolinemetabolism_Metabolism_Aminoacidmetabolism_ureB,ureasesubunitbeta[EC:3.5.1.5];K0	0,000114098	2,03813E-05	4,15269E-05
K01089_ko00340_Histidinemetabolism_Metabolism_Aminoacidmetabolism_hisB,imidazoleglycerol-phosphatedehydratase/histidinol-phosphatase[EC:4.2.1.193.1.3.15];K01089_ko01230_Biosynthesisofaminoacids_Metabolism_Overview_hisB,imidazoleglycerol-ph	0,000155589	0,000264957	0,00010797
K00294_ko00250_Alanine,aspartateandglutamatemetabolism_Metabolism_Aminoacidmetabolism_E1.2.1.88,1-pyrroline-5-carboxylatedehydrogenase[EC:1.2.1.88];K00294_ko00330_Arginineandprolinemetabolism_Metabolism_Aminoacidmetabolism_E1.2.1.88,1	5,18629E-05	2,03813E-05	5,81376E-05
K03252_ko03013_RNAtransport_GeneticinformationProcessing_Transcription_EIF3C,translationinitiationfactor3subunitC	5,18629E-06	0	0
K03338_ko00630_Glyoxylateanddicarboxylatemetabolism_Metabolism_Carbohydratemetabolism_iolC,5-dehydro-2-deoxygluconokinase[EC:2.7.1.92]	4,14903E-05	2,03813E-05	0,00010797
K01848_ko00280_Valine,leucineandisoleucinedegradation_Metabolism_Aminoacidmetabolism_E5.4.99.2A,mcmA1,methylmalonyl-CoAmutase,N-terminaldomain[EC:5.4.99.2];K01848_ko00630_Glyoxylateanddicarboxylatemetabolism_Metabolism_Carbohydraten	2,07452E-05	2,03813E-05	7,47483E-05
K02968_ko03010_Ribosome_GeneticinformationProcessing_Transcription_RP-S20,rpsT,smallsubunitribosomalproteinS20	0,000554933	0,000422913	0,000373742
K12869_ko03040_Spliceosome_GeneticinformationProcessing_Transcription_CRN,CRNKL1,CLF1,SYF3,crookedneck	0	5,09533E-06	0
K00196_ko01200_Carbonmetabolism_Metabolism_Overview_cooF,carbon-monoxidedehydrogenaseironsulfursubunit;K00196_ko00633_Nitrotoluenedegradation_Metabolism_Xenobioticsbiodegradationandmetabolism_cooF,carbon-monoxidedehydrogenaseiron	2,59315E-05	3,56673E-05	1,66107E-05
K00610_ko00250_Alanine,aspartateandglutamatemetabolism_Metabolism_Aminoacidmetabolism_pyrI,aspartatecarbamoyltransferaseregulatorysubunit;K00610_ko00240_Pyrimidinemetabolism_Metabolism_Nucleotidemetabolism_pyrI,aspartatecarbamoyltrans	0,000129657	0,000254767	6,6443E-05
K11181_ko00920_Sulfurmetabolism_Metabolism_Energymetabolism_dsrB,sulfitereductasebetasubunit[EC:1.8.99.31.8.99.1];K11181_ko00633_Nitrotoluenedegradation_Metabolism_Xenobioticsbiodegradationandmetabolism_dsrB,sulfitereductasebetasubunit[EC	6,74218E-05	5,09533E-06	3,32215E-05
K03117_ko02010_Ctransporters_Environmentalinformationprocessing_Membranetransport_tatB,sec-independentproteintranslocaseproteinTatB;K03117_ko04120_Ubiquitinmediatedproteolysis_GeneticInformationProcessing_Folding,sortinganddegradation_tatB	3,11177E-05	1,01907E-05	0
K02939_ko03010_Ribosome_GeneticinformationProcessing_Transcription_RP-L9,MRPL9,rplI,largesubunitribosomalproteinL9	0,000648286	0,000749014	0,000431879
K00156_ko00620_Pyruvatemetabolism_Metabolism_Carbohydratemetabolism_poxB,pyruvatedehydrogenase(quinone)[EC:1.2.5.1]	1,03726E-05	4,5858E-05	8,30537E-05
K03087_ko05111_Vibriocholeraepathogeniccycle_HumanDiseases_Infectiousdiseases_SIG2,rpoS,RNApolymerasenonessentialprimary-likesigmafactor	4,14903E-05	3,56673E-05	7,47483E-05
K09023_ko00240_Pyrimidinemetabolism_Metabolism_Nucleotidemetabolism_rutD,aminoacrylatehydrolase[EC:3.5.1.-]	1,03726E-05	1,01907E-05	0
K13479_ko00230_Purinemetabolism_Metabolism_Nucleotidemetabolism_ygeT,xdhB,xanthinedehydrogenaseFAD-bindingsubunit[EC:1.17.1.4]	6,22355E-05	2,54767E-05	4,15269E-05
K01608_ko00630_Glyoxylateanddicarboxylatemetabolism_Metabolism_Carbohydratemetabolism_gcl,tartronate-semialdehydesynthase[EC:4.1.1.47]	1,03726E-05	0	2,49161E-05
K02867_ko03010_Ribosome_GeneticinformationProcessing_Transcription_RP-L11,MRPL11,rplK,largesubunitribosomalproteinL11	0,001115053	0,000708251	0,000581376
K10914_ko02020_Two-componentsystem_Environmentalinformationprocessing_Signaltrasduction_crp,CRP/FNRfamilytranscriptionalregulator,cyclicAMPreceptorprotein;K10914_ko05111_Vibriocholeraepathogeniccycle_HumanDiseases_Infectiousdiseases_crp,Cl	5,70492E-05	2,03813E-05	2,49161E-05
K05850_ko04024_cAMPsignalingpathway_Environmentalinformationprocessing_Signaltrasduction_ATP2B,Ca2+transportingATPase,plasmamembrane[EC:3.6.3.8];K05850_ko04024_cAMPsignalingpathway_Environmentalinformationprocessing_Signaltrasduction_A	5,18629E-06	0	0
K02876_ko03010_Ribosome_GeneticinformationProcessing_Transcription_RP-L15,MRPL15,rplO,largesubunitribosomalproteinL15	0,000762385	0,000672584	0,00055646
K02821_ko02010_Ctransporters_Environmentalinformationprocessing_Membranetransport_PTS-Ula-EIIA,ulaC,sgaA,PTSsystem,ascorbate-specificIIAcomponent[EC:2.7.1.69];K02821_ko00052_Galactosemetabolism_Metabolism_Carbohydratemetabolism_PTS-Ula-	4,14903E-05	4,5858E-05	9,13591E-05
K02160_ko00630_Glyoxylateanddicarboxylatemetabolism_Metabolism_Carbohydratemetabolism_accB,bccP,acetyl-CoAcarboxylasebiotincarboxylcarrierprotein;K02160_ko00620_Pyruvatemetabolism_Metabolism_Carbohydratemetabolism_accB,bccP,acetyl-CoA	0,000202265	7,13347E-05	0,000332215
K10754_ko03030_DNAreplication_GeneticinformationProcessing_ReplicationandRepair_RFC1,replicationfactorCsubunit1;K10754_ko03430_Mismatchrepair_GeneticinformationProcessing_ReplicationandRepair_RFC1,replicationfactorCsubunit1;K10754_ko03420_	1,03726E-05	5,09533E-06	0
K02900_ko03010_Ribosome_GeneticinformationProcessing_Transcription_RP-L27Ae,RPL27A,largesubunitribosomalproteinL27Ae	0	1,01907E-05	2,49161E-05
K05916_ko05132_Salmonellainfection_HumanDiseases_Infectiousdiseases_hmp,YHB1,nitricoxidedioxygenase[EC:1.14.12.17]	5,18629E-06	0,000163051	2,49161E-05

K01444_ko04142_Lysosome_CellularProcesses_Transportandcatabolism_AGA,aspG,N4-(beta-N-acetylglucosaminyl)-L-asparaginase[EC:3.5.1.26];K01444_ko00511_Otherglycandegradation_Metabolism_Glycanbiosynthesisandmetabolism_AGA,aspG,N4-(beta-N-ac	1,55589E-05	0,000219099	7,47483E-05
K00368_ko00910_Nitrogenmetabolism_Metabolism_Energymetabolism_nirK,nitritereductase(NO-forming)[EC:1.7.2.1]	5,18629E-06	5,09533E-06	0
K07310_ko00450_Selenocompoundmetabolism_Metabolism_Metabolismofotheraminoacids_ynfF,Tat-targetedselenatereductasesubunitYnfF[EC:1.97.1.9]	0	1,01907E-05	1,66107E-05
K14941_ko00194_Photosynthesisproteins_Metabolism_Energymetabolism_cofC,2-phospho-L-lactateguanylyltransferase[EC:2.7.7.68]	1,03726E-05	0	3,32215E-05
K01718_ko00240_Pyrimidinemetabolism_Metabolism_Nucleotidemetabolism_E4.2.1.70,pseudouridylatesynthase[EC:4.2.1.70]	0	1,01907E-05	1,66107E-05
K02946_ko03010_Ribosome_GeneticinformationProcessing_Transcription_RP-S10,MRPS10,rpsJ,smallsubunitribosomalproteinS10	0,000663845	0,000560487	0,000431879
K02952_ko03010_Ribosome_GeneticinformationProcessing_Transcription_RP-S13,rpsM,smallsubunitribosomalproteinS13	0,00078313	0,000642012	0,000398658
K10795_ko00330_Arginineandprolinemetabolism_Metabolism_Aminoacidmetabolism_prdD,D-prolinereductase(dithiol)PrdD[EC:1.21.4.1]	4,14903E-05	0	0
K02773_ko02010_Ctransporters_Environmentalinformationprocessing_Membranetransport_PTS-Gat-EIIA,gatA,PTSsystem,galactitol-specificIIAcomponent[EC:2.7.1.69];K02773_ko00052_Galactosemetabolism_Metabolism_Carbohydratemetabolism_PTS-Gat-EIIA,(	0,000129657	9,1716E-05	0,000141191
K10126_ko02020_Two-componentsystem_Environmentalinformationprocessing_Signaltrasduction_dctD,two-componentsystem,NtrCfamily,C4-dicarboxylatetransportresponseregulatorDctD	2,59315E-05	7,13347E-05	4,15269E-05
K02618_ko00360_Phenylalaninemetabolism_Metabolism_Aminoacidmetabolism_paaZ,oxepin-CoAhydrolase/3-oxo-5,6-dehydrosuberyl-CoAsemialdehydedehydrogenase[EC:3.3.2.12 1.17.1.7]	0	2,03813E-05	8,30537E-06
K00940_ko00230_Purinemetabolism_Metabolism_Nucleotidemetabolism_ndk,NME,nucleoside-diphosphatekinase[EC:2.7.4.6];K00940_ko00240_Pyrimidinemetabolism_Metabolism_Nucleotidemetabolism_ndk,NME,nucleoside-diphosphatekinase[EC:2.7.4.6]	0,000160775	9,1716E-05	4,15269E-05
K03743_ko00760_Nicotinateandnicotinamidemetabolism_Metabolism_Metabolismofcofactorsandvitamins_pncC,nicotinamide-nucleotideamidase[EC:3.5.1.42]	6,22355E-05	1,01907E-05	6,6443E-05
K08730_ko00564_Glycerophospholipidmetabolism_Metabolism_Lipidmetabolism_PTDSS2,phosphatidylserinesynthase2[EC:2.7.8.29]	0	0	1,66107E-05
K02487_ko02020_Two-componentsystem_Environmentalinformationprocessing_Signaltrasduction_pilL,typeIVpilisensorhistidinekinaseandresponseregulator	5,18629E-06	1,01907E-05	8,30537E-06
K02194_ko02010_Ctransporters_Environmentalinformationprocessing_Membranetransport_ccmB,hemeexporterproteinB	1,03726E-05	0	0
K02456_ko02010_Ctransporters_Environmentalinformationprocessing_Membranetransport_gspG,generalsecretionpathwayproteinG	2,07452E-05	1,01907E-05	0
K07768_ko02020_Two-componentsystem_Environmentalinformationprocessing_Signaltrasduction_senX3,two-componentsystem,OmpRfamily,sensorhistidinekinaseSenX3[EC:2.7.13.3]	2,07452E-05	1,5286E-05	4,15269E-05
K01247_ko03410_Baseexcisionrepair_GeneticinformationProcessing_ReplicationandRepair_alkA,DNA-3-methyladeneineglycosylaseII[EC:3.2.2.21]	3,11177E-05	8,66207E-05	8,30537E-05
K00621_ko00520_Aminosugarandnucleotidesugarmetabolism_Metabolism_Carbohydratemetabolism_GNPNAT1,GNA1,glucosamine-phosphateN-acetyltransferase[EC:2.3.1.4]	1,55589E-05	1,01907E-05	0
K03075_ko02010_Ctransporters_Environmentalinformationprocessing_Membranetransport_secG,preproteintranslocasesubunitSecG;K03075_ko04120_Ubiquitinmediatedproteolysis_GeneticInformationProcessing_Folding,sortinganddegradation_secG,preproteir	0,000191893	0,000203813	0,00021594
K00324_ko00760_Nicotinateandnicotinamidemetabolism_Metabolism_Metabolismofcofactorsandvitamins_pntA,NAD(P)transhydrogenasesubunitalpha[EC:1.6.1.2]	6,74218E-05	5,09533E-06	8,30537E-06
K07785_ko02020_Two-componentsystem_Environmentalinformationprocessing_Signaltrasduction_nrsD,nreB,MFStransporter,NREfamily,putativenickelresistanceprotein	0	0	1,66107E-05
K02650_ko02020_Two-componentsystem_Environmentalinformationprocessing_Signaltrasduction_pilA,typeIVpilusassemblyproteinPilA	4,66766E-05	5,60487E-05	0,000132886
K12371_ko02010_Ctransporters_Environmentalinformationprocessing_Membranetransport_dppD,dipeptidetransportsystemATP-bindingprotein	5,18629E-06	0	1,66107E-05
K02204_ko00260_Glycine,serineandthreoninemetabolism_Metabolism_Aminoacidmetabolism_thrB2,homoserinekinasetypeII[EC:2.7.1.39];K02204_ko01230_Biosynthesisofaminoacids_Metabolism_Overview_thrB2,homoserinekinasetypeII[EC:2.7.1.39]	2,07452E-05	5,60487E-05	5,81376E-05
K02388_ko02040_Flagellarassembly_Organismalsystem_Cellmobility_flgC,flagellarbasal-bodyrodproteinFlgC	5,70492E-05	5,60487E-05	4,15269E-05
K01911_ko00130_Ubiquinoneandotherterpenoid-quinonebiosynthesis_Metabolism_Metabolismofcofactorsandvitamins_menE,O-succinylbenzoicacid--CoAligase[EC:6.2.1.26]	0,000108912	0,00015286	0,000116275
K06119_ko00561_Glycerolipidmetabolism_Metabolism_Lipidmetabolism_SQD2,sulfoquinovosyltransferase[EC:2.4.1.-]	1,03726E-05	2,54767E-05	3,32215E-05
K02614_ko00360_Phenylalaninemetabolism_Metabolism_Aminoacidmetabolism_paaI,acyl-CoAthioesterase[EC:3.1.2.-]	8,29807E-05	0,000127383	0,000141191
K07772_ko02020_Two-componentsystem_Environmentalinformationprocessing_Signaltrasduction_torR,two-componentsystem,OmpRfamily,torCADoperonresponseregulatorTorR	1,55589E-05	0	0
K03782_ko00360_Phenylalaninemetabolism_Metabolism_Aminoacidmetabolism_katG,catalase-peroxidase[EC:1.11.1.21];K03782_ko00380_Tryptophanmetabolism_Metabolism_Aminoacidmetabolism_katG,catalase-peroxidase[EC:1.11.1.21];K03782_ko00940_Ph	5,18629E-06	5,09533E-06	1,66107E-05
K11710_ko02010_Ctransporters_Environmentalinformationprocessing_Membranetransport_troB,mntB,znuC,manganese/zinc/irontransportsystemATP-bindingprotein	5,18629E-06	0	0
K02935_ko03010_Ribosome_GeneticinformationProcessing_Transcription_RP-L7,MRPL12,rplL,largesubunitribosomalproteinL7/L12	0,000834993	0,000606345	0,000506628
K13940_ko00785_Lipoicacidmetabolism_Metabolism_Metabolismofcofactorsandvitamins_sulD,dihydroneopterinaldolase/2-amino-4-hydroxy-6-hydroxymethyldihydropteridinediphosphokinase[EC:4.1.2.252.7.6.3]	0,000176334	7,643E-05	0,000124581
K02461_ko02010_Ctransporters_Environmentalinformationprocessing_Membranetransport_gspL,generalsecretionpathwayproteinL	5,18629E-06	0	1,66107E-05
K02887_ko03010_Ribosome_GeneticinformationProcessing_Transcription_RP-L20,MRPL20,rplT,largesubunitribosomalproteinL20	0,000710522	0,000601249	0,000631208
K02437_ko00260_Glycine,serineandthreoninemetabolism_Metabolism_Aminoacidmetabolism_gcvH,GCSH,glycinecleavagesystemHprotein;K02437_ko00630_Glyoxylateanddicarboxylatemetabolism_Metabolism_Carbohydratemetabolism_gcvH,GCSH,glycinecleav	0,000202265	0,000193623	0,000116275
K02850_ko00540_Lipopolysaccharidebiosynthesis_Metabolism_Glycanbiosynthesisandmetabolism_waaY,rfaY,heptose(II)phosphotransferase[EC:2.7.1.-]	4,14903E-05	4,07627E-05	2,49161E-05
K11618_ko02020_Two-componentsystem_Environmentalinformationprocessing_Signaltrasduction_liaR,two-componentsystem,NarLfamily,responseregulatorLiaR	7,77944E-05	3,56673E-05	3,32215E-05
K02560_ko00540_Lipopolysaccharidebiosynthesis_Metabolism_Glycanbiosynthesisandmetabolism_msbB,lipidAbiosynthesis(KDO)2-(lauroyl)-lipidivaacyltransferase[EC:2.3.1.-]	0	3,56673E-05	0
K13587_ko04112_Cellcycle-Caulobacter_CellularProcesses_Cellgrowthanddeath_cckA,two-componentsystem,cellcyclesensorhistidinekinaseandresponseregulatorCckA[EC:2.7.13.3];K13587_ko02020_Two-componentsystem_Environmentalinformationprocessing_S	2,59315E-05	0	0
K02890_ko03010_Ribosome_GeneticinformationProcessing_Transcription_RP-L22,MRPL22,rplV,largesubunitribosomalproteinL22	0,000788316	0,000606345	0,000440185
K01759_ko02020_Two-componentsystem_Environmentalinformationprocessing_Signaltrasduction_GLO1,gloA,lactoylglutathionelyase[EC:4.4.1.5];K01759_ko00620_Pyruvatemetabolism_Metabolism_Carbohydratemetabolism_GLO1,gloA,lactoylglutathionelyase[E	0,000311177	0,000280243	0,000307299
K00330_ko00190_Oxidativephosphorylation_Metabolism_Energymetabolism_nuoA,NADH-quinoneoxidoreductasesubunitA[EC:1.6.5.3]	0,000259315	0,000244576	0,000132886
K00758_ko05219_Bladdercancer_HumanDiseases_Cancers_deoA,TYMP,thymidinephosphorylase[EC:2.4.2.4];K00758_ko00240_Pyrimidinemetabolism_Metabolism_Nucleotidemetabolism_deoA,TYMP,thymidinephosphorylase[EC:2.4.2.4];K00758_ko00983_Drugm	1,03726E-05	3,0572E-05	0
K02114_ko00190_Oxidativephosphorylation_Metabolism_Energymetabolism_ATPF1E,atpC,F-typeH+-transportingATPasesubunitepsilon;K02114_ko00195_Photosynthesis_Metabolism_Energymetabolism_ATPF1E,atpC,F-typeH+-transportingATPasesubunitepsilon	0,000186706	0,000188527	0,000224245
K02911_ko03010_Ribosome_GeneticinformationProcessing_Transcription_RP-L32,MRPL32,rpmF,largesubunitribosomalproteinL32	0,000248942	0,000188527	0,000191024
K07711_ko02020_Two-componentsystem_Environmentalinformationprocessing_Signaltrasduction_glrK,qseE,two-componentsystem,NtrCfamily,sensorhistidinekinaseGlrK[EC:2.7.13.3]	1,55589E-05	2,54767E-05	8,30537E-06
K02955_ko03010_Ribosome_GeneticinformationProcessing_Transcription_RP-S14e,RPS14,smallsubunitribosomalproteinS14e	5,18629E-06	0	0
K03113_ko03013_RNAtransport_GeneticinformationProcessing_Transcription_EIF1,SUI1,translationinitiationfactor1	2,07452E-05	0,000127383	3,32215E-05
K10901_ko03460_Fanconianemiapathway_GeneticinformationProcessing_ReplicationandRepair_BLM,RECQL3,SGS1,bloomsyndromeprotein[EC:3.6.4.12];K10901_ko03440_Homologousrecombination_GeneticinformationProcessing_ReplicationandRepair_BLM,RE	0	1,01907E-05	4,15269E-05
K13522_ko00760_Nicotinateandnicotinamidemetabolism_Metabolism_Metabolismofcofactorsandvitamins_K13522,nadM,bifunctionalNMNadenylyltransferase/nudixhydrolase[EC:2.7.7.13.6.1.-]	0	1,01907E-05	1,66107E-05
K03006_ko03020_RNApolymerase_GeneticinformationProcessing_Transcription_RPB1,POLR2A,DNA-directedRNApolymeraseIIsubunitRPB1[EC:2.7.7.6];K03006_ko05016_Huntington'sdisease_HumanDiseases_Degenerativediseases_RPB1,POLR2A,DNA-directedRNA	0	0	1,66107E-05
K13920_ko00630_Glyoxylateanddicarboxylatemetabolism_Metabolism_Carbohydratemetabolism_pduE,propanedioldehydratasesmallsubunit[EC:4.2.1.28]	2,59315E-05	5,09533E-06	8,30537E-06
K10917_ko05111_Vibriocholeraepathogeniccycle_HumanDiseases_Infectiousdiseases_K10917,aphA,PadRfamilytranscriptionalregulator,regulatoryproteinAphA	2,59315E-05	2,03813E-05	3,32215E-05
K02783_ko02010_Ctransporters_Environmentalinformationprocessing_Membranetransport_PTS-Gut-EIIC,srlA,PTSsystem,glucitol/sorbitol-specificIICcomponent;K02783_ko00051_Fructoseandmannosemetabolism_Metabolism_Carbohydratemetabolism_PTS-Gut-	2,59315E-05	5,09533E-06	8,30537E-06
K00207_ko00770_PantothenateandCoAbiosynthesis_Metabolism_Metabolismofcofactorsandvitamins_DPYD,dihydropyrimidinedehydrogenase(NADP+)[EC:1.3.1.2];K00207_ko00410_beta-Alaninemetabolism_Metabolism_Metabolismofotheraminoacids_DPYD,dih	1,03726E-05	5,09533E-06	0
K09020_ko00240_Pyrimidinemetabolism_Metabolism_Nucleotidemetabolism_rutB,ureidoacrylateperacidhydrolase[EC:3.5.1.110]	3,11177E-05	2,03813E-05	0
K10094_ko02010_Ctransporters_Environmentalinformationprocessing_Membranetransport_cbiK,nickeltransportprotein	0	1,01907E-05	0
K00395_ko00920_Sulfurmetabolism_Metabolism_Energymetabolism_aprB,adenylylsulfatereductase,subunitB[EC:1.8.99.2]	2,07452E-05	1,5286E-05	0
K02183_ko04114_Oocytemeiosis_CellularProcesses_Cellgrowthanddeath_CALM,calmodulin;K02183_ko04721_Synapticvesiclecycle_Environmentalinformationprocessing_Signaltransduction_CALM,calmodulin;K02183_ko02020_twocomponentsistem_Environment	5,18629E-06	0	0
K01922_ko00770_PantothenateandCoAbiosynthesis_Metabolism_Metabolismofcofactorsandvitamins_PPCS,coaB,phosphopantothenate-cysteineligase[EC:6.3.2.5]	0	2,03813E-05	2,49161E-05
K02916_ko03010_Ribosome_GeneticinformationProcessing_Transcription_RP-L35,MRPL35,rpmI,largesubunitribosomalproteinL35	0,00036304	0,000219099	0,000249161
K04562_ko02040_Flagellarassembly_Organismalsystem_Cellmobility_flhG,fleN,flagellarbiosynthesisproteinFlhG	1,03726E-05	5,09533E-05	8,30537E-05
K05773_ko02010_Ctransporters_Environmentalinformationprocessing_Membranetransport_tupB,vupB,tungstatetransportsystempermeaseprotein	5,18629E-05	0	8,30537E-06
K02888_ko03010_Ribosome_GeneticinformationProcessing_Transcription_RP-L21,MRPL21,rplU,largesubunitribosomalproteinL21	0,000539374	0,000519724	0,000597987
K11384_ko02020_Two-componentsystem_Environmentalinformationprocessing_Signaltrasduction_algB,two-componentsystem,NtrCfamily,responseregulatorAlgB	0	2,03813E-05	0
K03060_ko03020_RNApolymerase_GeneticinformationProcessing_Transcription_rpoZ,DNA-directedRNApolymerasesubunitomega[EC:2.7.7.6];K03060_ko00230_Purinemetabolism_Metabolism_Nucleotidemetabolism_rpoZ,DNA-directedRNApolymerasesubuniton	0,000119285	0,000137574	9,96645E-05
K02970_ko03010_Ribosome_GeneticinformationProcessing_Transcription_RP-S21,MRPS21,rpsU,smallsubunitribosomalproteinS21	0,000300805	0,00030572	0,00021594

K02418_ko02040_Flagellarassembly_Organismalsystem_Cellmobility_fliOZ,fliO,flagellarproteinFliO/FliZ	2,07452E-05	3,56673E-05	3,32215E-05
K02996_ko03010_Ribosome_GeneticinformationProcessing_Transcription_RP-S9,MRPS9,rpsI,smallsubunitribosomalproteinS9	0,000736453	0,000606345	0,000506628
K01633_ko00785_Lipoicacidmetabolism_Metabolism_Metabolismofcofactorsandvitamins_folB,dihydroneopterinaldolase[EC:4.1.2.25]	0,000108912	0,000203813	0,000224245
K14297_ko03013_RNAtransport_GeneticinformationProcessing_Transcription_NUP98,ADAR2,NUP116,nuclearporecomplexproteinNup98-Nup96;K14297_ko05164_InfluenzaA_HumanDiseases_Infectiousdiseases_NUP98,ADAR2,NUP116,nuclearporecomplexprotei	5,18629E-06	1,01907E-05	1,66107E-05
K01523_ko00340_Histidinemetabolism_Metabolism_Aminoacidmetabolism_hisE,phosphoribosyl-ATPpyrophosphohydrolase[EC:3.6.1.31];K01523_ko01230_Biosynthesisofaminoacids_Metabolism_Overview_hisE,phosphoribosyl-ATPpyrophosphohydrolase[EC:3.6.	5,70492E-05	5,09533E-05	3,32215E-05
K11712_ko02020_Two-componentsystem_Environmentalinformationprocessing_Signaltrasduction_dctR,two-componentsystem,LuxRfamily,responseregulatorDctR	2,07452E-05	5,09533E-05	4,15269E-05
K01579_ko00770_PantothenateandCoAbiosynthesis_Metabolism_Metabolismofcofactorsandvitamins_panD,aspartate1-decarboxylase[EC:4.1.1.11];K01579_ko00410_beta-Alaninemetabolism_Metabolism_Metabolismofotheraminoacids_panD,aspartate1-decarbc	0,000134844	9,68113E-05	4,98322E-05
K07662_ko02020_Two-componentsystem_Environmentalinformationprocessing_Signaltrasduction_cpxR,two-componentsystem,OmpRfamily,responseregulatorCpxR	5,18629E-05	3,56673E-05	1,66107E-05
K14987_ko02020_Two-componentsystem_Environmentalinformationprocessing_Signaltrasduction_fixJ,two-componentsystem,LuxRfamily,responseregulatorFixJ	5,18629E-05	2,54767E-05	1,66107E-05
K00064_ko00051_Fructoseandmannosemetabolism_Metabolism_Carbohydratemetabolism_E1.1.1.122,D-threo-aldose1-dehydrogenase[EC:1.1.1.122];K00064_ko00052_Galactosemetabolism_Metabolism_Carbohydratemetabolism_E1.1.1.122,D-threo-aldose1-de	2,59315E-05	3,0572E-05	9,96645E-05
K02874_ko03010_Ribosome_GeneticinformationProcessing_Transcription_RP-L14,MRPL14,rplN,largesubunitribosomalproteinL14	0,00068459	0,000545201	0,000282383
K02881_ko03010_Ribosome_GeneticinformationProcessing_Transcription_RP-L18,MRPL18,rplR,largesubunitribosomalproteinL18	0,000565306	0,000621631	0,000614598
K02909_ko03010_Ribosome_GeneticinformationProcessing_Transcription_RP-L31,rpmE,largesubunitribosomalproteinL31	0,000539374	0,000387245	0,000531544
K02956_ko03010_Ribosome_GeneticinformationProcessing_Transcription_RP-S15,MRPS15,rpsO,smallsubunitribosomalproteinS15	0,000409717	0,000412722	0,00044849
K07771_ko02020_Two-componentsystem_Environmentalinformationprocessing_Signaltrasduction_basR,two-componentsystem,OmpRfamily,responseregulatorBasR	2,07452E-05	3,56673E-05	3,32215E-05
K03413_ko02020_Two-componentsystem_Environmentalinformationprocessing_Signaltrasduction_cheY,two-componentsystem,chemotaxisfamily,responseregulatorCheY;K03413_ko02030_Bacterialchemotaxis_Organismalsystem_Cellmobility_cheY,two-compone	0,00018152	0,000132479	7,47483E-05
K02464_ko02010_Ctransporters_Environmentalinformationprocessing_Membranetransport_gspO,generalsecretionpathwayproteinO[EC:3.4.23.432.1.1.-]	1,03726E-05	5,09533E-06	1,66107E-05
K10553_ko02010_Ctransporters_Environmentalinformationprocessing_Membranetransport_frcC,fructosetransportsystempermeaseprotein	0	1,01907E-05	0
K04412_ko04390_Hipposignalingpathway_Environmentalinformationprocessing_Signaltrasduction_STK3,MST2,serine/threoninekinase3;K04412_ko04390_Hipposignalingpathway_Environmentalinformationprocessing_Signaltrasduction_STK3,MST2,serine/threoni	2,07452E-05	2,03813E-05	0
K04354_ko04530_Tightjunction_Cellgrowthanddeath_Cellularcommunity_PPP2R2,serine/threonine-proteinphosphatase2AregulatorysubunitB;K04354_ko04111_Cellcycle-yeast_CellularProcesses_Cellgrowthanddeath_PPP2R2,serine/threonine-proteinphosphatas	0	5,09533E-06	1,66107E-05
K10562_ko02010_Ctransporters_Environmentalinformationprocessing_Membranetransport_rhaT,rhamnosetransportsystemATP-bindingprotein[EC:3.6.3.17]	1,55589E-05	0	1,66107E-05
K07719_ko02020_Two-componentsystem_Environmentalinformationprocessing_Signaltrasduction_ycbB,glnL,two-componentsystem,responseregulatorYcbB	1,55589E-05	1,01907E-05	1,66107E-05
K06193_ko00440_Phosphonateandphosphinatemetabolism_Metabolism_Metabolismofotheraminoacids_phnA,phosphonoacetatehydrolase[EC:3.11.1.2]	3,11177E-05	8,15253E-05	4,98322E-05
K05362_ko01005_Lipopolysaccharidebiosynthesisproteins_Metabolism_Glycanbiosynthesisandmetabolism_E6.3.2.7,murE,UDP-N-acetylmuramoyl-L-alanyl-D-glutamate-L-lysineligase[EC:6.3.2.7]	3,11177E-05	2,54767E-05	1,66107E-05
K02760_ko02010_Ctransporters_Environmentalinformationprocessing_Membranetransport_PTS-Cel-EIIB,celA,PTSsystem,cellobiose-specificIIBcomponent[EC:2.7.1.69]	7,77944E-05	0,000198718	0,000174413
K02320_ko03030_DNAreplication_GeneticinformationProcessing_ReplicationandRepair_POLA1,DNApolymerasealphasubunitA[EC:2.7.7.7];K02320_ko00230_Purinemetabolism_Metabolism_Nucleotidemetabolism_POLA1,DNApolymerasealphasubunitA[EC:2.7.7.7	0	0	8,30537E-06
K03602_ko03430_Mismatchrepair_GeneticinformationProcessing_ReplicationandRepair_xseB,exodeoxyribonucleaseVIIsmallsubunit[EC:3.1.11.6]	0,000202265	0,000692965	0,000705957
K10194_ko02010_Ctransporters_Environmentalinformationprocessing_Membranetransport_togN,oligogalacturonidetransportsystempermeaseprotein	4,14903E-05	1,5286E-05	2,49161E-05
K02892_ko03010_Ribosome_GeneticinformationProcessing_Transcription_RP-L23,MRPL23,rplW,largesubunitribosomalproteinL23	0,000414903	0,000422913	0,00055646
K03715_ko00561_Glycerolipidmetabolism_Metabolism_Lipidmetabolism_E2.4.1.46,1,2-diacylglycerol3-beta-galactosyltransferase[EC:2.4.1.46]	1,03726E-05	5,09533E-06	1,66107E-05
K02612_ko00360_Phenylalaninemetabolism_Metabolism_Aminoacidmetabolism_paaD,ring-1,2-phenylacetyl-CoAepoxidasesubunitPaaD	2,07452E-05	0	3,32215E-05
K01363_ko04142_Lysosome_CellularProcesses_Transportandcatabolism_CTSB,cathepsinB[EC:3.4.22.1];K01363_ko04612_Antigenprocessingandpresentation_Organismalsystem_Immunesystem_CTSB,cathepsinB[EC:3.4.22.1]	0	0	8,30537E-06
K07307_ko00920_Sulfurmetabolism_Metabolism_Energymetabolism_dmsB,anaerobicdimethylsulfoxidereductasesubunitB(DMSOreductaseiron-sulfursubunit)	5,70492E-05	6,1144E-05	0
K12486_ko04144_Endocytosis_CellularProcesses_Transportandcatabolism_SMAP,stromalmembrane-associatedprotein	0	5,09533E-06	0
K11294_ko05130_PathogenicEscherichiacoliinfection_HumanDiseases_Infectiousdiseases_NCL,NSR1,nucleolin	5,18629E-05	0,000132479	0,000116275
K00938_ko00900_Terpenoidbackbonebiosynthesis_Metabolism_Metabolismofterpenoidsandpolyketides_E2.7.4.2,mvaK2,phosphomevalonatekinase[EC:2.7.4.2]	2,59315E-05	5,09533E-06	3,32215E-05
K00242_ko00020_Citratecycle(TCAcycle)_Metabolism_Carbohydratemetabolism_sdhD,succinatedehydrogenasemembraneanchorsubunit;K00242_ko00630_Glyoxylateanddicarboxylatemetabolism_Metabolism_Carbohydratemetabolism_sdhD,succinatedehydroge	0	1,01907E-05	0
K00883_ko00052_Galactosemetabolism_Metabolism_Carbohydratemetabolism_dgoK,2-dehydro-3-deoxygalactonokinase[EC:2.7.1.58]	2,59315E-05	9,68113E-05	9,13591E-05
K13853_ko00400_Phenylalanine,tyrosineandtryptophanbiosynthesis_Metabolism_Aminoacidmetabolism_aroG,aroA,3-deoxy-7-phosphoheptulonatesynthase/chorismatemutase[EC:2.5.1.545.4.99.5];K13853_ko01230_Biosynthesisofaminoacids_Metabolism_Overv	0	5,09533E-06	0
K02439_ko00920_Sulfurmetabolism_Metabolism_Energymetabolism_glpE,thiosulfatesulfurtransferase[EC:2.8.1.1]	1,03726E-05	2,54767E-05	0
K12372_ko02010_Ctransporters_Environmentalinformationprocessing_Membranetransport_dppF,dipeptidetransportsystemATP-bindingprotein	5,18629E-06	1,01907E-05	0
K07640_ko02020_Two-componentsystem_Environmentalinformationprocessing_Signaltrasduction_cpxA,two-componentsystem,OmpRfamily,sensorhistidinekinaseCpxA[EC:2.7.13.3]	2,59315E-05	1,5286E-05	1,66107E-05
K01430_ko00791_Atrazinedegradation_Humandiseases_Xenobioticsbiodegradationandmetabolism_ureA,ureasesubunitgamma[EC:3.5.1.5];K01430_ko00330_Arginineandprolinemetabolism_Metabolism_Aminoacidmetabolism_ureA,ureasesubunitgamma[EC:3.5.1	9,33532E-05	3,0572E-05	3,32215E-05
K02954_ko03010_Ribosome_GeneticinformationProcessing_Transcription_RP-S14,MRPS14,rpsN,smallsubunitribosomalproteinS14	0,000539374	0,000438199	0,000406963
K05713_ko00360_Phenylalaninemetabolism_Metabolism_Aminoacidmetabolism_mhpB,2,3-dihydroxyphenylpropionate1,2-dioxygenase[EC:1.13.11.16];K05713_ko01220_Degradationofaromaticcompounds_Metabolism_Overview_mhpB,2,3-dihydroxyphenylprop	1,03726E-05	0	1,66107E-05
K02965_ko03010_Ribosome_GeneticinformationProcessing_Transcription_RP-S19,rpsS,smallsubunitribosomalproteinS19	0,000549747	0,000504438	0,000440185
K11521_ko02020_Two-componentsystem_Environmentalinformationprocessing_Signaltrasduction_K11521,manR,two-componentsystem,OmpRfamily,manganesesensingresponseregulator	3,6304E-05	5,09533E-06	2,49161E-05
K11179_ko04122_Sulfurrelaysystem_GeneticInformationProcessing_Folding,sortinganddegradation_tusE,dsrC,tRNA2-thiouridinesynthesizingproteinE[EC:2.8.1.-]	6,74218E-05	2,03813E-05	3,32215E-05
K01029_ko00280_Valine,leucineandisoleucinedegradation_Metabolism_Aminoacidmetabolism_E2.8.3.5B,scoB,3-oxoacidCoA-transferasesubunitB[EC:2.8.3.5];K01029_ko00630_Glyoxylateanddicarboxylatemetabolism_Metabolism_Carbohydratemetabolism_E2.8.	2,07452E-05	2,54767E-05	5,81376E-05
K02408_ko02040_Flagellarassembly_Organismalsystem_Cellmobility_fliE,flagellarhook-basalbodycomplexproteinFliE	2,07452E-05	2,03813E-05	1,66107E-05
K02122_ko00190_Oxidativephosphorylation_Metabolism_Energymetabolism_ATPVF,ntpF,atpF,V/A-typeH+-transportingATPasesubunitF	0,000129657	2,54767E-05	6,6443E-05
K03073_ko02010_Ctransporters_Environmentalinformationprocessing_Membranetransport_secE,preproteintranslocasesubunitSecE;K03073_ko04120_Ubiquitinmediatedproteolysis_GeneticInformationProcessing_Folding,sortinganddegradation_secE,preproteint	0,000269687	0,000264957	0,000257467
K03071_ko02010_Ctransporters_Environmentalinformationprocessing_Membranetransport_secB,preproteintranslocasesubunitSecB;K03071_ko04120_Ubiquitinmediatedproteolysis_GeneticInformationProcessing_Folding,sortinganddegradation_secB,preproteint	1,03726E-05	3,56673E-05	4,98322E-05
K12826_ko03040_Spliceosome_GeneticinformationProcessing_Transcription_SF3A2,SAP62,splicingfactor3Asubunit2	0	0	8,30537E-06
K00124_ko00630_Glyoxylateanddicarboxylatemetabolism_Metabolism_Carbohydratemetabolism_fdoH,formatedehydrogenaseiron-sulfursubunit;K00124_ko01200_Carbonmetabolism_Metabolism_Overview_fdoH,formatedehydrogenaseiron-sulfursubunit;K0012	2,07452E-05	2,54767E-05	1,66107E-05
K01857_ko01220_Degradationofaromaticcompounds_Metabolism_Overview_pcaB,3-carboxy-cis,cis-muconatecycloisomerase[EC:5.5.1.2];K01857_ko00362_Benzoatedegradation_Metabolism_Xenobioticsbiodegradationandmetabolism_pcaB,3-carboxy-cis,cis-mu	5,18629E-06	0	1,66107E-05
K11607_ko02010_Ctransporters_Environmentalinformationprocessing_Membranetransport_sitB,manganese/irontransportsystemATP-bindingprotein	5,18629E-06	1,5286E-05	0
K03048_ko03020_RNApolymerase_GeneticinformationProcessing_Transcription_rpoE,DNA-directedRNApolymerasesubunitdelta;K03048_ko00230_Purinemetabolism_Metabolism_Nucleotidemetabolism_rpoE,DNA-directedRNApolymerasesubunitdelta;K03048_k	3,6304E-05	3,0572E-05	3,32215E-05
K02902_ko03010_Ribosome_GeneticinformationProcessing_Transcription_RP-L28,MRPL28,rpmB,largesubunitribosomalproteinL28	0,000295619	0,000224195	0,000141191
K02774_ko02010_Ctransporters_Environmentalinformationprocessing_Membranetransport_PTS-Gat-EIIB,gatB,PTSsystem,galactitol-specificIIBcomponent[EC:2.7.1.69];K02774_ko00052_Galactosemetabolism_Metabolism_Carbohydratemetabolism_PTS-Gat-EIIB,g	4,66766E-05	7,643E-05	2,49161E-05
K00340_ko00190_Oxidativephosphorylation_Metabolism_Energymetabolism_nuoK,NADH-quinoneoxidoreductasesubunitK[EC:1.6.5.3]	0,000238569	0,000188527	0,000207634
K01631_ko00052_Galactosemetabolism_Metabolism_Carbohydratemetabolism_dgoA,2-dehydro-3-deoxyphosphogalactonatealdolase[EC:4.1.2.21]	0	1,5286E-05	0
K10107_ko02010_Ctransporters_Environmentalinformationprocessing_Membranetransport_ABC-2.CPSE.P1,capsularpolysaccharidetransportsystempermeaseprotein	2,07452E-05	0	2,49161E-05
K02899_ko03010_Ribosome_GeneticinformationProcessing_Transcription_RP-L27,MRPL27,rpmA,largesubunitribosomalproteinL27	0,000331923	0,000219099	0,000207634
K10794_ko00330_Arginineandprolinemetabolism_Metabolism_Aminoacidmetabolism_prdB,D-prolinereductase(dithiol)PrdB[EC:1.21.4.1]	8,29807E-05	4,07627E-05	1,66107E-05
K02110_ko00190_Oxidativephosphorylation_Metabolism_Energymetabolism_ATPF0C,atpE,F-typeH+-transportingATPasesubunitc;K02110_ko00195_Photosynthesis_Metabolism_Energymetabolism_ATPF0C,atpE,F-typeH+-transportingATPasesubunitc	0,000217824	0,000147765	0,000149497
K01646_ko02020_Two-componentsystem_Environmentalinformationprocessing_Signaltrasduction_citD,citratelyasesubunitgamma(acylcarrierprotein)	1,55589E-05	4,07627E-05	5,81376E-05
K05522_ko03410_Baseexcisionrepair_GeneticinformationProcessing_ReplicationandRepair_nei,endonucleaseVIII[EC:3.2.2.-4.2.99.18]	1,03726E-05	0	0
K02961_ko03010_Ribosome_GeneticinformationProcessing_Transcription_RP-S17,MRPS17,rpsQ,smallsubunitribosomalproteinS17	0,000560119	0,000545201	0,000240856
K02387_ko02040_Flagellarassembly_Organismalsystem_Cellmobility_flgB,flagellarbasal-bodyrodproteinFlgB	5,70492E-05	3,0572E-05	9,96645E-05

K03010_ko03020_RNApolymerase_GeneticinformationProcessing_Transcription_RPB2,POLR2B,DNA-directedRNApolymeraseIIsubunitRPB2[EC:2.7.7.6];K03010_ko05016_Huntington'sdisease_HumanDiseases_Degenerativediseases_RPB2,POLR2B,DNA-directedRN/	5,18629E-06	0	0
K02963_ko03010_Ribosome_GeneticinformationProcessing_Transcription_RP-S18,MRPS18,rpsR,smallsubunitribosomalproteinS18	0,000430462	0,000366864	0,000240856
K05394_ko00791_Atrazinedegradation_Humandiseases_Xenobioticsbiodegradationandmetabolism_atzA,atrazinechlorohydrolase[EC:3.8.1.8]	1,03726E-05	5,09533E-06	0
K11251_ko05322_Systemiclupuserythematosus_Humandiseases_Immunediseases_H2A,histoneH2A;K11251_ko05034_Alcoholism_HumanDiseases_SubstanceDependence_H2A,histoneH2A	8,8167E-05	0	4,15269E-05
K06045_ko00909_Sesquiterpenoidandtriterpenoidbiosynthesis_Metabolism_Metabolismofterpenoidsandpolyketides_shc,squalene-hopene/tetraprenyl-beta-curcumenecyclase[EC:5.4.99.174.2.1.129]	2,59315E-05	5,09533E-06	0
K02919_ko03010_Ribosome_GeneticinformationProcessing_Transcription_RP-L36,MRPL36,rpmJ,largesubunitribosomalproteinL36	0,000119285	0,000142669	8,30537E-05
K02995_ko03010_Ribosome_GeneticinformationProcessing_Transcription_RP-S8e,RPS8,smallsubunitribosomalproteinS8e	1,03726E-05	0	0
K02213_ko04111_Cellcycle-yeast_CellularProcesses_Cellgrowthanddeath_CDC6,celldivisioncontrolprotein6;K02213_ko04110_Cellcycle_CellularProcesses_Cellgrowthanddeath_CDC6,celldivisioncontrolprotein6;K02213_ko04113_Meiosis-yeast_CellularProcesses_C	0	0	8,30537E-06
K13829_ko00400_Phenylalanine,tyrosineandtryptophanbiosynthesis_Metabolism_Aminoacidmetabolism_aroKB,shikimatekinase/3-dehydroquinatesynthase[EC:2.7.1.714.2.3.4];K13829_ko01230_Biosynthesisofaminoacids_Metabolism_Overview_aroKB,shikimate	5,18629E-06	2,54767E-05	0
K02913_ko03010_Ribosome_GeneticinformationProcessing_Transcription_RP-L33,MRPL33,rpmG,largesubunitribosomalproteinL33	0,000243756	0,000285339	0,000166107
K01099_ko04066_HIF-1signalingpathway_EnvironmentalinformationprocessingSignaltrasduction_E3.1.3.36,phosphatidylinositol-bisphosphatase[EC:3.1.3.36];K01099_ko00630_Glyoxylateanddicarboxylatemetabolism_Metabolism_Carbohydratemetabolism_E3.1	0	1,01907E-05	8,30537E-06
K06677_ko04111_Cellcycle-yeast_CellularProcesses_Cellgrowthanddeath_YCS4,CNAP1,CAPD2,condensincomplexsubunit1	0	0	3,32215E-05
K14989_ko02020_Two-componentsystem_Environmentalinformationprocessing_SignaltrasductionsalR,two-componentsystem,NarLfamily,secretionsystemresponseregulatorSalR	2,07452E-05	2,03813E-05	2,49161E-05
K02782_ko02010_Ctransporters_Environmentalinformationprocessing_Membranetransport_PTS-Gut-EIIB,srlE,PTSsystem,glucitol/sorbitol-specificIIBcomponent[EC:2.7.1.69];K02782_ko00051_Fructoseandmannosemetabolism_Metabolism_Carbohydratemetaboli	1,55589E-05	0	1,66107E-05
K03366_ko00630_Glyoxylateanddicarboxylatemetabolism_Metabolism_Carbohydratemetabolism_butA,budC,meso-butanedioldehydrogenase/(S,S)-butanedioldehydrogenase/diacetylreductase[EC:1.1.1.-1.1.1.761.1.1.304]	1,03726E-05	1,01907E-05	4,15269E-05
K12973_ko05133_Pertussis_HumanDiseases_Infectiousdiseases_pagP,palmitoyltransferase[EC:2.3.1.-]	3,11177E-05	1,5286E-05	1,66107E-05
K14407_ko03015_mRNAsurveillancepathway_GeneticinformationProcessing_Transcription_CSTF2,RNA15,cleavagestimulationfactorsubunit2	2,59315E-05	0	0
K10219_ko00350_Tyrosinemetabolism_Metabolism_Aminoacidmetabolism_ligC,2-hydroxy-4-carboxymuconatesemialdehydehemiacetaldehydrogenase[EC:1.1.1.312];K10219_ko01220_Degradationofaromaticcompounds_Metabolism_Overview_ligC,2-hydroxy-4-c	0	0	8,30537E-06
K01573_ko00620_Pyruvatemetabolism_Metabolism_Carbohydratemetabolism_oadG,oxaloacetatedecarboxylase,gammasubunit[EC:4.1.1.3]	0	6,62393E-05	8,30537E-06
K02017_ko02010_Ctransporters_Environmentalinformationprocessing_Membranetransport_modC,molybdatetransportsystemATP-bindingprotein[EC:3.6.3.29]	2,59315E-05	1,5286E-05	4,15269E-05
K01821_ko01220_Degradationofaromaticcompounds_Metabolism_Overview_praC,xylH,4-oxalocrotonatetautomerase[EC:5.3.2.6];K01821_ko00362_Benzoatedegradation_Metabolism_Xenobioticsbiodegradationandmetabolism_praC,xylH,4-oxalocrotonatetautor	0,000399344	0,000249671	0,000199329
K02904_ko03010_Ribosome_GeneticinformationProcessing_Transcription_RP-L29,rpmC,largesubunitribosomalproteinL29	0,000223011	0,000259862	0,000290688
K10916_ko02020_Two-componentsystem_Environmentalinformationprocessing_SignaltrasductioncqsS,two-componentsystem,CAI-1autoinducersensorkinase/phosphataseCqsS[EC:2.7.13.33.1.3.-];K10916_ko05111_Vibriocholeraepathogeniccycle_HumanDisease	0	0	8,30537E-06
K03116_ko02010_Ctransporters_Environmentalinformationprocessing_Membranetransport_tatA,sec-independentproteintranslocaseproteinTatA;K03116_ko04120_Ubiquitinmediatedproteolysis_GeneticInformationProcessing_Folding,sortinganddegradation_tatA	0,000114098	8,66207E-05	0,000116275
K03154_ko04122_Sulfurrelaysystem_GeneticInformationProcessing_Folding,sortinganddegradation_thiS,sulfurcarrierprotein	3,11177E-05	8,66207E-05	8,30537E-06
K01598_ko00770_PantothenateandCoAbiosynthesis_Metabolism_Metabolismofcofactorsandvitamins_PPCDC,coaC,phosphopantothenoylcysteinedecarboxylase[EC:4.1.1.36]	2,07452E-05	5,09533E-06	1,66107E-05
K07213_ko04978_Mineralabsorption_Organismalsystem_Digestivesystem_ATOX1,ATX1,copZ,copperchaperone	1,03726E-05	2,03813E-05	3,32215E-05
K01641_ko00280_Valine,leucineandisoleucinedegradation_Metabolism_Aminoacidmetabolism_E2.3.3.10,hydroxymethylglutaryl-CoAsynthase[EC:2.3.3.10];K01641_ko00630_Glyoxylateanddicarboxylatemetabolism_Metabolism_Carbohydratemetabolism_E2.3.3.1	4,66766E-05	2,54767E-05	1,66107E-05
K02394_ko02040_Flagellarassembly_Organismalsystem_Cellmobility_flgI,flagellarP-ringproteinprecursorFlgI	2,07452E-05	0	8,30537E-06
K09251_ko00330_Arginineandprolinemetabolism_Metabolism_Aminoacidmetabolism_E2.6.1.82,putrescineaminotransferase[EC:2.6.1.82]	1,55589E-05	1,01907E-05	1,66107E-05
K02907_ko03010_Ribosome_GeneticinformationProcessing_Transcription_RP-L30,MRPL30,rpmD,largesubunitribosomalproteinL30	0,000254128	0,000203813	0,000124581
K11903_ko02010_Ctransporters_Environmentalinformationprocessing_Membranetransport_K11903,hcp,typeVIsecretionsystemsecretedproteinHcp	2,07452E-05	1,01907E-05	8,30537E-06
K11121_ko00760_Nicotinateandnicotinamidemetabolism_Metabolism_Metabolismofcofactorsandvitamins_SIR2,NAD-dependenthistonedeacetylaseSIR2[EC:3.5.1.-]	0	0	1,66107E-05
K12370_ko02010_Ctransporters_Environmentalinformationprocessing_Membranetransport_dppC,dipeptidetransportsystempermeaseprotein	0	1,5286E-05	0
K09553_ko05020_Priondiseases_HumanDiseases_Degenerativediseases_STIP1,stress-induced-phosphoprotein1	1,03726E-05	0	0
K02729_ko03050_Proteasome_GeneticInformationProcessing_Folding,sortinganddegradation_PSMA5,20Sproteasomesubunitalpha5[EC:3.4.25.1]	0	5,09533E-06	0
K11253_ko05230_Centralcarbonmetabolismincancer_HumanDiseases_Cancers_H3,histoneH3;K11253_ko05322_Systemiclupuserythematosus_Humandiseases_Immunediseases_H3,histoneH3;K11253_ko05034_Alcoholism_HumanDiseases_SubstanceDependence_	2,07452E-05	2,03813E-05	8,30537E-05
K02983_ko03010_Ribosome_GeneticinformationProcessing_Transcription_RP-S30e,RPS30,smallsubunitribosomalproteinS30e	1,03726E-05	0	0
K07535_ko01220_Degradationofaromaticcompounds_Metabolism_Overview_badH,2-hydroxycyclohexanecarboxyl-CoAdehydrogenase[EC:1.1.1.-];K07535_ko00362_Benzoatedegradation_Metabolism_Xenobioticsbiodegradationandmetabolism_badH,2-hydroxycy	1,55589E-05	1,5286E-05	1,66107E-05
K02726_ko03050_Proteasome_GeneticInformationProcessing_Folding,sortinganddegradation_PSMA2,20Sproteasomesubunitalpha2[EC:3.4.25.1]	1,55589E-05	0	0
K01819_ko00052_Galactosemetabolism_Metabolism_Carbohydratemetabolism_E5.3.1.26,lacA,lacB,galactose-6-phosphateisomerase[EC:5.3.1.26]	7,77944E-05	3,56673E-05	5,81376E-05
K03563_ko02020_Two-componentsystem_Environmentalinformationprocessing_Signaltrasduction_csrA,carbonstorageregulator	1,03726E-05	1,01907E-05	1,66107E-05
K04441_ko04550_Signalingpathwaysregulatingpluripotencyofstemcells_Cellgrowthanddeath_Cellularcommunity_P38,p38MAPkinase[EC:2.7.11.24];K04441_ko04723_Retrogradeendocannabinoidsignaling_Environmentalinformationprocessing_Signaltransduction_	1,03726E-05	0	0
K06019_ko00190_Oxidativephosphorylation_Metabolism_Energymetabolism_ppaX,pyrophosphatasePpaX[EC:3.6.1.1]	4,66766E-05	2,54767E-05	6,6443E-05
K05297_ko00071_Fattyaciddegradation_Metabolism_Lipidmetabolism_E1.18.1.1,rubredoxin-NAD+reductase[EC:1.18.1.1]	4,66766E-05	3,56673E-05	8,30537E-06
K03795_ko00830_Retinolmetabolism_Metabolism_Metabolismofcofactorsandvitamins_cbiX,sirohydrochlorincobaltochelatase[EC:4.99.1.3]	3,6304E-05	2,03813E-05	0
K07877_ko04151_PI3K-Aktsignalingpathway_Environmentalinformationprocessing_Signaltrasduction_RAB2A,Ras-relatedproteinRab-2A	1,03726E-05	0	0
K02759_ko02010_Ctransporters_Environmentalinformationprocessing_Membranetransport_PTS-Cel-EIIA,celC,PTSsystem,cellobiose-specificIIAcomponent[EC:2.7.1.69]	0,000150402	6,1144E-05	0,000174413
K02914_ko03010_Ribosome_GeneticinformationProcessing_Transcription_RP-L34,MRPL34,rpmH,largesubunitribosomalproteinL34	0,000103726	0,000127383	0,000141191
K10577_ko04064_NF-kappaBsignalingpathway_Environmentalinformationprocessing_SignaltrasductionUBE2I,UBC9,ubiquitin-conjugatingenzymeE2I[EC:6.3.2.19];K10577_ko04120_Ubiquitinmediatedproteolysis_GeneticInformationProcessing_Folding,sortingand	2,07452E-05	0	1,66107E-05
K12818_ko03040_Spliceosome_GeneticinformationProcessing_Transcription_DHX8,PRP22,ATP-dependentRNAhelicaseDHX8/PRP22[EC:3.6.4.13]	0	0	1,66107E-05
K10953_ko05110_Vibriocholeraeinfection_HumanDiseases_Infectiousdiseases_rtxA,RTXtoxinRtxA	5,18629E-06	2,54767E-05	3,32215E-05
K14195_ko05150_Staphylococcusaureusinfection_HumanDiseases_Infectiousdiseases_sasG,surfaceproteinG	5,18629E-06	1,5286E-05	0
K11533_ko00061_Fattyacidbiosynthesis_Metabolism_Lipidmetabolism_fas,fattyacidsynthase,bacteriatype[EC:2.3.1.-];K11533_ko01212_Fattyacidmetabolism_Metabolism_Overview_fas,fattyacidsynthase,bacteriatype[EC:2.3.1.-]	2,59315E-05	0	8,30537E-06
K13797_ko03020_RNApolymerase_GeneticinformationProcessing_Transcription_rpoBC,DNA-directedRNApolymerasesubunitbeta-beta'[EC:2.7.7.6];K13797_ko00230_Purinemetabolism_Metabolism_Nucleotidemetabolism_rpoBC,DNA-directedRNApolymerasesub	0	1,01907E-05	8,30537E-06
K07151_ko04141_Proteinprocessinginendoplasmicreticulum_GeneticInformationProcessing_Folding,sortinganddegradation_STT3,dolichyl-diphosphooligosaccharide--proteinglycosyltransferase[EC:2.4.99.18];K07151_ko00513_VariostypesofN-glycanbiosynthesis_	2,07452E-05	5,09533E-06	8,30537E-06
K01456_ko04141_Proteinprocessinginendoplasmicreticulum_GeneticInformationProcessing_Folding,sortinganddegradation_E3.5.1.52,NGLY1,PNG1,peptide-N4-(N-acetyl-beta-glucosaminyl)asparagineamidase[EC:3.5.1.52]	0	0	1,66107E-05
K04551_ko05012_Parkinson'sdisease_HumanDiseases_Degenerativediseases_UBB,ubiquitinB	0	0	3,32215E-05
K10939_ko05111_Vibriocholeraepathogenicycle_HumanDiseases_Infectiousdiseases_acfD,accessorycolonizationfactorAcfD	2,59315E-05	0	0
K01283_ko05410_Hypertrophiccardiomyopathy(HCM)_Humandiseases_Cardiovasculardiseases_E3.4.15.1,ACE,peptidyl-dipeptidaseA[EC:3.4.15.1];K01283_ko05142_Chagasdisease(Americantrypanosomiasis)_HumanDiseases_Infectiousdiseases_E3.4.15.1,ACE,pept	3,11177E-05	2,54767E-05	5,81376E-05
K11357_ko04112_Cellcycle-Caulobacter_CellularProcesses_Cellgrowthanddeath_divJ,two-componentsystem,cellcyclesensorhistidinekinaseDivJ[EC:2.7.13.3];K11357_ko02020_Two-componentsystem_Environmentalinformationprocessing_Signaltrasduction_divJ,tv	5,18629E-06	5,60487E-05	8,30537E-06
K00728_ko00514_OthertypesofO-glycanbiosynthesis_Metabolism_Glycanbiosynthesisandmetabolism_POMT,dolichyl-phosphate-mannose-proteinmannosyltransferase[EC:2.4.1.109]	4,14903E-05	5,09533E-05	9,96645E-05
K01365_ko04142_Lysosome_CellularProcesses_Transportandcatabolism_CTSL,cathepsinL[EC:3.4.22.15];K01365_ko04145_Phagosome_CellularProcesses_Transportandcatabolism_CTSL,cathepsinL[EC:3.4.22.15];K01365_ko05205_Proteoglycansincancer_HumanDis	0	5,09533E-06	3,32215E-05
K13798_ko03020_RNApolymerase_GeneticinformationProcessing_Transcription_K13798,rpoB,DNA-directedRNApolymerasesubunitB[EC:2.7.7.6];K13798_ko00230_Purinemetabolism_Metabolism_Nucleotidemetabolism_K13798,rpoB,DNA-directedRNApolymeras	2,07452E-05	0	1,66107E-05
K06665_ko04111_Cellcycle-yeast_CellularProcesses_Cellgrowthanddeath_SSN6,glucoserepressionmediatorprotein	1,55589E-05	1,5286E-05	0
K12679_ko05131_Shigellosis_HumanDiseases_Infectiousdiseases_icsA,virG,outermembraneproteinIcsA	1,03726E-05	0	0
K03403_ko00830_Retinolmetabolism_Metabolism_Metabolismofcofactorsandvitamins_chlH,bchH,magnesiumchelatasesubunitH[EC:6.6.1.1]	0	0	1,66107E-05
K02322_ko00230_Purinemetabolism_Metabolism_Nucleotidemetabolism_DPB1,DNApolymeraseIIlargesubunit[EC:2.7.7.7];K02322_ko00240_Pyrimidinemetabolism_Metabolism_Nucleotidemetabolism_DPB1,DNApolymeraseIIlargesubunit[EC:2.7.7.7]	0	0	2,49161E-05
K00692_ko02020_Two-componentsystem_Environmentalinformationprocessing_Signaltrasduction_sacB,levansucrase[EC:2.4.1.10];K00692_ko00500_Starchandsucrosemetabolism_Metabolism_Carbohydratemetabolism_sacB,levansucrase[EC:2.4.1.10]	1,55589E-05	1,5286E-05	0
K08357_ko02020_Two-componentsystem_Environmentalinformationprocessing_Signaltrasduction_ttrA,tetrathionatereductasesubunitA;K08357_ko00920_Sulfurmetabolism_Metabolism_Energymetabolism_ttrA,tetrathionatereductasesubunitA	2,07452E-05	2,03813E-05	1,66107E-05

K13482_ko00230_Purinemetabolism_Metabolism_Nucleotidemetabolism_xdhB,xanthinedehydrogenaselargesubunit[EC:1.17.1.4]	1,03726E-05	1,01907E-05	0
K10943_ko02020_Two-componentsystem_Environmentalinformationprocessing_Signaltrasduction_flrC,fleR,two-componentsystem,responseregulatorFlrC;K10943_ko05111_Vibriocholeraepathogeniccycle_HumanDiseases_Infectiousdiseases_flrC,fleR,two-compor	0,000108912	8,66207E-05	5,81376E-05
K13025_ko03015_mRNAsurveillancepathway_GeneticinformationProcessing_Transcription_EIF4A3,FAL1,ATP-dependentRNAhelicase[EC:3.6.4.13];K13025_ko03013_RNAtransport_GeneticinformationProcessing_Transcription_EIF4A3,FAL1,ATP-dependentRNAhelic	1,55589E-05	0	8,30537E-06
K07788_ko02020_Two-componentsystem_Environmentalinformationprocessing_Signaltrasduction_mdtB,RNDsuperfamily,multidrugtransportproteinMdtB	4,14903E-05	1,01907E-05	1,66107E-05
K15037_ko00280_Valine,leucineandisoleucinedegradation_Metabolism_Aminoacidmetabolism_K15037,biotincarboxylcarrierprotein;K15037_ko00630_Glyoxylateanddicarboxylatemetabolism_Metabolism_Carbohydratemetabolism_K15037,biotincarboxylcarrierp	4,14903E-05	3,0572E-05	1,66107E-05
K07647_ko02020_Two-componentsystem_Environmentalinformationprocessing_Signaltrasduction_torS,two-componentsystem,OmpRfamily,sensorhistidinekinaseTorS[EC:2.7.13.3]	3,6304E-05	3,56673E-05	0,000116275
K14980_ko02020_Two-componentsystem_Environmentalinformationprocessing_Signaltrasduction_chvG,two-componentsystem,OmpRfamily,sensorhistidinekinaseChvG[EC:2.7.13.3]	0	0	1,66107E-05
K08712_ko02010_Ctransporters_Environmentalinformationprocessing_Membranetransport_ABCG2.SNQ2,ATP-bindingcassette,subfamilyG(WHITE),member2,SNQ2	0	5,09533E-06	0
K12239_ko01053_Biosynthesisofsiderophoregroupnonribosomalpeptides_Metabolism_Metabolismofterpenoidsandpolyketides_pchE,dihydroaeruginoicacidsynthetase	1,03726E-05	0	0
K03693_ko00312_beta-Lactamresistance_HumanDiseases_Drugresistance_pbp,penicillin-bindingprotein;K03693_ko01005_Lipopolysaccharidebiosynthesisproteins_Metabolism_Glycanbiosynthesisandmetabolism_pbp,penicillin-bindingprotein	2,07452E-05	4,07627E-05	2,49161E-05
K12790_ko05130_PathogenicEscherichiacoliinfection_HumanDiseases_Infectiousdiseases_eae,intimin	1,03726E-05	5,09533E-06	0
K01228_ko04141_Proteinprocessinginendoplasmicreticulum_GeneticInformationProcessing_Folding,sortinganddegradation_GCS1,mannosyl-oligosaccharideglucosidase[EC:3.2.1.106];K01228_ko00513_VariaustypesofN-glycanbiosynthesis_Metabolism_Glycanbios	1,03726E-05	1,5286E-05	8,30537E-06
K12266_ko05132_Salmonellainfection_HumanDiseases_Infectiousdiseases_norR,anaerobicnitricoxidereductasetranscriptionregulator	1,03726E-05	1,01907E-05	0
K07676_ko02020_Two-componentsystem_Environmentalinformationprocessing_Signaltrasduction_rcsD,two-componentsystem,NarLfamily,sensorhistidinekinaseRcsD[EC:2.7.13.3]	2,07452E-05	0	8,30537E-06
K00163_ko00020_Citratecycle(TCAcycle)_Metabolism_Carbohydratemetabolism_aceE,pyruvatedehydrogenaseE1component[EC:1.2.4.1];K00163_ko00010_Glycolysis/Gluconeogenesis_Metabolism_Carbohydratemetabolism_aceE,pyruvatedehydrogenaseE1compo	0	1,01907E-05	4,15269E-05
K03042_ko03020_RNApolymerase_GeneticinformationProcessing_Transcription_rpoA2,DNA-directedRNApolymerasesubunitA[EC:2.7.7.6];K03042_ko00230_Purinemetabolism_Metabolism_Nucleotidemetabolism_rpoA2,DNA-directedRNApolymerasesubunitA[EC	1,03726E-05	0	0
K01909_ko00071_Fattyaciddegradation_Metabolism_Lipidmetabolism_mbtM,long-chain-fatty-acid--[acyl-carrier-protein]ligase[EC:6.2.1.20]	0	5,09533E-06	0
K01194_ko00500_Starchandsucrosemetabolism_Metabolism_Carbohydratemetabolism_E3.2.1.28,treA,treF,alpha,alpha-trehalase[EC:3.2.1.28]	3,11177E-05	4,07627E-05	4,15269E-05
K00376_ko00910_Nitrogenmetabolism_Metabolism_Energymetabolism_nosZ,nitrous-oxidereductase[EC:1.7.2.4]	0	1,01907E-05	8,30537E-06
K06044_ko00500_Starchandsucrosemetabolism_Metabolism_Carbohydratemetabolism_treY,glgY,(1->4)-alpha-D-glucan1-alpha-D-glucosylmutase[EC:5.4.99.15]	3,6304E-05	5,09533E-05	2,49161E-05
K02062_ko02010_Ctransporters_Environmentalinformationprocessing_Membranetransport_thiQ,thiaminetransportsystemATP-bindingprotein	1,03726E-05	1,5286E-05	2,49161E-05
K02840_ko00540_Lipopolysaccharidebiosynthesis_Metabolism_Glycanbiosynthesisandmetabolism_waaB,rfaB,UDP-D-galactose:(glucosyl)LPSalpha-1,6-D-galactosyltransferase[EC:2.4.1.-]	5,18629E-05	9,68113E-05	9,96645E-05
K01535_ko00190_Oxidativephosphorylation_Metabolism_Energymetabolism_E3.6.3.6,H+-transportingATPase[EC:3.6.3.6]	3,11177E-05	5,09533E-06	4,98322E-05
K01632_ko00194_Photosynthesisproteins_Metabolism_Energymetabolism_E4.1.2.22,fructose-6-phosphatephosphoketolase[EC:4.1.2.22]	1,55589E-05	0	0
K05668_ko02010_Ctransporters_Environmentalinformationprocessing_Membranetransport_ABCC5,ATP-bindingcassette,subfamilyC(CFTR/MRP),member5	1,03726E-05	0	0
K12525_ko00270_Cysteineandmethioninemetabolism_Metabolism_Aminoacidmetabolism_metL,bifunctionalaspartokinase/homoserinedehydrogenase2[EC:2.7.2.41.1.1.3];K12525_ko00260_Glycine,serineandthreoninemetabolism_Metabolism_Aminoacidmetabo	5,18629E-06	1,01907E-05	0
K07653_ko02020_Two-componentsystem_Environmentalinformationprocessing_Signaltrasduction_mprB,two-componentsystem,OmpRfamily,sensorhistidinekinaseMprB[EC:2.7.13.3]	0	0	1,66107E-05
K00117_ko00030_Pentosephosphatepathway_Metabolism_Carbohydratemetabolism_gcd,quinoproteinglucosedehydrogenase[EC:1.1.5.2]	5,18629E-06	1,5286E-05	1,66107E-05
K00260_ko00250_Alanine,aspartateandglutamatemetabolism_Metabolism_Aminoacidmetabolism_gudB,rocG,glutamatedehydrogenase[EC:1.4.1.2];K00260_ko00330_Arginineandprolinemetabolism_Metabolism_Aminoacidmetabolism_gudB,rocG,glutamatedehy	6,74218E-05	4,5858E-05	8,30537E-05
K07466_ko03030_DNAreplication_GeneticinformationProcessing_ReplicationandRepair_RFA1,RPA1,rpa,replicationfactorA1;K07466_ko03460_Fanconianemiapathway_GeneticinformationProcessing_ReplicationandRepair_RFA1,RPA1,rpa,replicationfactorA1;K074	0	1,5286E-05	3,32215E-05
K08351_ko00780_Biotinmetabolism_Metabolism_Metabolismofcofactorsandvitamins_bisC,biotin/methioninesulfoxidereductase[EC:1.-.-.-]	1,55589E-05	0	8,30537E-06
K12874_ko03040_Spliceosome_GeneticinformationProcessing_Transcription_AQR,intron-bindingproteinaquarius	0	0	8,30537E-06
K01434_ko00311_Penicillinandcephalosporinbiosynthesis_Metabolism_Biosynthesisofothersecondarymetabolites_E3.5.1.11,penicillinamidase[EC:3.5.1.11]	0	0	8,30537E-06
K06683_ko04111_Cellcycle-yeast_CellularProcesses_Cellgrowthanddeath_CDC15,celldivisioncontrolproteinCDC15[EC:2.7.11.1];K06683_ko04113_Meiosis-yeast_CellularProcesses_Cellgrowthanddeath_CDC15,celldivisioncontrolproteinCDC15[EC:2.7.11.1]	3,6304E-05	0	8,30537E-06
K11177_ko00230_Purinemetabolism_Metabolism_Nucleotidemetabolism_yagR,xanthinedehydrogenaseYagRmolybdenum-bindingsubunit[EC:1.17.1.4]	0	1,01907E-05	1,66107E-05
K09461_ko00627_Aminobenzoatedegradation_Metabolism_Xenobioticsbiodegradationandmetabolism_E1.14.13.40,anthraniloyl-CoAmonooxygenase[EC:1.14.13.40]	0	0	1,66107E-05
K08484_ko02010_Ctransporters_Environmentalinformationprocessing_Membranetransport_PTS-EI.PTSP,ptsP,phosphotransferasesystem,enzymeI,PtsP[EC:2.7.3.9]	2,07452E-05	1,01907E-05	3,32215E-05
K08653_ko04141_Proteinprocessinginendoplasmicreticulum_GeneticInformationProcessing_Folding,sortinganddegradation_MBTPS1,membrane-boundtranscriptionfactorsite-1protease[EC:3.4.21.112]	5,18629E-06	0	8,30537E-06
K02689_ko00195_Photosynthesis_Metabolism_Energymetabolism_psaA,photosystemIP700chlorophyllaapoproteinA1	0	0	1,66107E-05
K02660_ko02020_Two-componentsystem_Environmentalinformationprocessing_Signaltrasduction_pilJ,twitchingmotilityproteinPilJ	1,03726E-05	5,09533E-06	0
K06985_ko04112_Cellcycle-Caulobacter_CellularProcesses_Cellgrowthanddeath_K06985,aspartylproteasefamilyprotein	0,00018152	0,000321006	5,81376E-05
K03234_ko04151_PI3K-Aktsignalingpathway_Environmentalinformationprocessing_Signaltrasduction_EEF2,elongationfactor2;K03234_ko04917_Prolactinsignalingpathway_Organismalsystem_Endocrinsystem_EEF2,elongationfactor2	5,18629E-06	0	0
K07685_ko02020_Two-componentsystem_Environmentalinformationprocessing_Signaltrasduction_narP,two-componentsystem,NarLfamily,nitrate/nitriteresponseregulatorNarP	2,59315E-05	2,03813E-05	0
K13285_ko05100_Bacterialinvasionofepithelialcells_Humandiseases_Infectiousdiseases_sipB,ipaB,bipB,invasinB;K13285_ko05132_Salmonellainfection_HumanDiseases_Infectiousdiseases_sipB,ipaB,bipB,invasinB;K13285_ko05131_Shigellosis_HumanDiseases_Infe	5,18629E-06	0	1,66107E-05
K01115_ko04144_Endocytosis_CellularProcesses_Transportandcatabolism_PLD1_2,phospholipaseD1/2[EC:3.1.4.4];K01115_ko04024_cAMPsignalingpathway_Environmentalinformationprocessing_Signaltrasduction_PLD1_2,phospholipaseD1/2[EC:3.1.4.4];K01115_	1,55589E-05	1,5286E-05	3,32215E-05
K11632_ko02010_Ctransporters_Environmentalinformationprocessing_Membranetransport_bceB,bacitracintransportsystempermeaseprotein;K11632_ko02020_Two-componentsystem_Environmentalinformationprocessing_Signaltrasduction_bceB,bacitracintran	2,07452E-05	0	0
K03934_ko05010_Alzheimer'sdisease_HumanDiseases_Degenerativediseases_NDUFS1,NADHdehydrogenase(ubiquinone)Fe-Sprotein1[EC:1.6.5.31.6.99.3];K03934_ko05016_Huntington'sdisease_HumanDiseases_Degenerativediseases_NDUFS1,NADHdehydrogenas	5,18629E-06	0	0
K13950_ko00785_Lipoicacidmetabolism_Metabolism_Metabolismofcofactorsandvitamins_pabAB,para-aminobenzoatesynthetase[EC:2.6.1.85]	5,18629E-06	5,09533E-06	0
K01114_ko00630_Glyoxylateanddicarboxylatemetabolism_Metabolism_Carbohydratemetabolism_plcC,phospholipaseC[EC:3.1.4.3];K01114_ko00564_Glycerophospholipidmetabolism_Metabolism_Lipidmetabolism_plcC,phospholipaseC[EC:3.1.4.3];K01114_ko005	0	0,000117193	4,98322E-05
K01392_ko05143_Africantrypanosomiasis_HumanDiseases_Infectiousdiseases_THOP1,thimetoligopeptidase[EC:3.4.24.15];K01392_ko04919_Thyroidhormonesignalingpathway_Organismalsystem_Endocrinsystem_THOP1,thimetoligopeptidase[EC:3.4.24.15]	0	0	8,30537E-06
K07650_ko02020_Two-componentsystem_Environmentalinformationprocessing_Signaltrasduction_cssS,two-componentsystem,OmpRfamily,sensorhistidinekinaseCssS[EC:2.7.13.3]	6,74218E-05	0,000127383	0,00010797
K02802_ko02010_Ctransporters_Environmentalinformationprocessing_Membranetransport_PTS-Nag-EIIA,nagE,PTSsystem,N-acetylglucosamine-specificIIAcomponent[EC:2.7.1.69];K02802_ko00520_Aminosugarandnucleotidesugarmetabolism_Metabolism_Carbo	1,03726E-05	3,0572E-05	3,32215E-05
K02298_ko00190_Oxidativephosphorylation_Metabolism_Energymetabolism_cyoB,cytochromeoubiquinoloxidasesubunitI[EC:1.10.3.-]	1,55589E-05	0	3,32215E-05
K01184_ko00040_Pentoseandglucuronateinterconversions_Metabolism_Carbohydratemetabolism_E3.2.1.15,polygalacturonase[EC:3.2.1.15];K01184_ko00500_Starchandsucrosemetabolism_Metabolism_Carbohydratemetabolism_E3.2.1.15,polygalacturonase[EC:	1,55589E-05	1,01907E-05	1,66107E-05
K11328_ko02020_Two-componentsystem_Environmentalinformationprocessing_Signaltrasduction_nrsS,rppB,two-componentsystem,OmpRfamily,Ni(II)-sensorand/orredoxsensorkinaseNrsS[EC:2.7.13.3]	1,03726E-05	0	0
K04789_ko01053_Biosynthesisofsiderophoregroupnonribosomalpeptides_Metabolism_Metabolismofterpenoidsandpolyketides_mbtE,mycobactinpeptidesynthetaseMbtE	1,03726E-05	0	0
K06237_ko04510_Focaladhesion_Cellgrowthanddeath_Cellularcommunity_COL4A,collagen,typeIV,alpha;K06237_ko04151_PI3K-Aktsignalingpathway_Environmentalinformationprocessing_Signaltrasduction_COL4A,collagen,typeIV,alpha;K06237_ko04512_ECM-re	0	5,09533E-06	8,30537E-06
K05875_ko02020_Two-componentsystem_Environmentalinformationprocessing_Signaltrasduction_tar,methyl-acceptingchemotaxisproteinII,aspartatesensorreceptor;K05875_ko02030_Bacterialchemotaxis_Organismalsystem_Cellmobility_tar,methyl-acceptingch	2,59315E-05	1,01907E-05	0
K11198_ko02010_Ctransporters_Environmentalinformationprocessing_Membranetransport_PTS-Mng-EIIA,mngA,hrsA,PTSsystem,2-O-A-mannosyl-D-glycerate-specificIIAcomponent[EC:2.7.1.69]	1,03726E-05	0	0
K07709_ko02020_Two-componentsystem_Environmentalinformationprocessing_Signaltrasduction_zraS,hydH,two-componentsystem,NtrCfamily,sensorhistidinekinaseHydH[EC:2.7.13.3]	5,18629E-05	0	5,81376E-05
K13284_ko05100_Bacterialinvasionofepithelialcells_Humandiseases_Infectiousdiseases_sipA,ipaA,invasinA;K13284_ko05132_Salmonellainfection_HumanDiseases_Infectiousdiseases_sipA,ipaA,invasinA;K13284_ko05131_Shigellosis_HumanDiseases_Infectiousdise	0	5,09533E-06	0
K01460_ko00480_Glutathionemetabolism_Metabolism_Metabolismofotheraminoacids_gsp,glutathionylspermidineamidase/synthetase[EC:3.5.1.786.3.1.8]	1,03726E-05	5,09533E-06	0
K00316_ko00330_Arginineandprolinemetabolism_Metabolism_Aminoacidmetabolism_spdH,spermidinedehydrogenase[EC:1.5.99.6];K00316_ko00410_beta-Alaninemetabolism_Metabolism_Metabolismofotheraminoacids_spdH,spermidinedehydrogenase[EC:1.5.	5,18629E-06	0	0
K02001_ko02010_Ctransporters_Environmentalinformationprocessing_Membranetransport_proW,glycinebetaine/prolinetransportsystempermeaseprotein	1,55589E-05	4,07627E-05	6,6443E-05
K01690_ko00030_Pentosephosphatepathway_Metabolism_Carbohydratemetabolism_edd,phosphogluconatedehydratase[EC:4.2.1.12];K01690_ko01200_Carbonmetabolism_Metabolism_Overview_edd,phosphogluconatedehydratase[EC:4.2.1.12]	1,03726E-05	2,03813E-05	0
K01849_ko00280_Valine,leucineandisoleucinedegradation_Metabolism_Aminoacidmetabolism_E5.4.99.2B,mcmA2,methylmalonyl-CoAmutase,C-terminaldomain[EC:5.4.99.2];K01849_ko00630_Glyoxylateanddicarboxylatemetabolism_Metabolism_Carbohydratem	1,03726E-05	5,09533E-06	4,98322E-05
K03330_ko00970_Aminoacyl-tRNAbiosynthesis_Geneticinformationandprocessing_Transcription_gatE,glutamyl-tRNA(Gln)amidotransferasesubunitE[EC:6.3.5.7]	0	5,09533E-06	8,30537E-06
K13820_ko02040_Flagellarassembly_Organismalsystem_Cellmobility_fliR-flhB,flagellarbiosyntheticproteinFliR/FlhB	0	0	4,15269E-05
K00105_ko00564_Glycerophospholipidmetabolism_Metabolism_Lipidmetabolism_E1.1.3.21,alpha-glycerophosphateoxidase[EC:1.1.3.21]	5,18629E-06	0	1,66107E-05
K07683_ko02020_Two-componentsystem_Environmentalinformationprocessing_Signaltrasduction_nreB,two-componentsystem,NarLfamily,sensorhistidinekinaseNreB[EC:2.7.13.3]	1,55589E-05	1,01907E-05	8,30537E-06

K13791_ko05131_Shigellosis_HumanDiseases_Infectiousdiseases_ipaH9.8,invasionplasmidantigen	0	1,01907E-05	0
K07698_ko02020_Two-componentsystem_Environmentalinformationprocessing_Signaltrasduction_kinC,two-componentsystem,sporulationsensorkinaseC[EC:2.7.13.3]	1,03726E-05	0	1,66107E-05
K08269_ko04140_Regulationofautophagy_CellularProcesses_Transportandcatabolism_ULK1_2_3,ATG1,serine/threonine-proteinkinaseULK/ATG1[EC:2.7.11.1];K08269_ko04151_PI3K-Aktsignalingpathway_Environmentalinformationprocessing_Signaltrasduction_U	5,18629E-06	0	0
K11788_ko00230_Purinemetabolism_Metabolism_Nucleotidemetabolism_ADE5,phosphoribosylamine--glycineligase/phosphoribosylformylglycinamidinecyclo-ligase[EC:6.3.4.136.3.3.1]	1,03726E-05	0	0
K06132_ko00564_Glycerophospholipidmetabolism_Metabolism_Lipidmetabolism_ybhO,putativecardiolipinsynthase[EC:2.7.8.-]	1,03726E-05	1,5286E-05	0
K07769_ko02020_Two-componentsystem_Environmentalinformationprocessing_Signaltrasduction_nblS,two-componentsystem,OmpRfamily,sensorhistidinekinaseNblS[EC:2.7.13.3]	2,59315E-05	2,54767E-05	5,81376E-05
K08737_ko03430_Mismatchrepair_GeneticinformationProcessing_ReplicationandRepair_MSH6,DNAmismatchrepairproteinMSH6;K08737_ko05210_Colorectalcancer_HumanDiseases_Cancers_MSH6,DNAmismatchrepairproteinMSH6;K08737_ko05200_Pathwaysi	2,07452E-05	1,01907E-05	2,49161E-05
K06281_ko00633_Nitrotoluenedegradation_Metabolism_Xenobioticsbiodegradationandmetabolism_hyaB,hybC,hydrogenaselargesubunit[EC:1.12.99.6]	2,59315E-05	6,62393E-05	0,000149497
K12536_ko02010_Ctransporters_Environmentalinformationprocessing_Membranetransport_hasD,prtD,aprD,ATP-bindingcassette,subfamilyC,bacterialexporterforprotease/lipase	1,03726E-05	0	0
K10565_ko02040_Flagellarassembly_Organismalsystem_Cellmobility_motD,chemotaxisproteinMotD	0	0	8,30537E-06
K13892_ko02010_Ctransporters_Environmentalinformationprocessing_Membranetransport_gsiA,glutathionetransportsystemATP-bindingprotein	5,18629E-06	0	8,30537E-06
K03777_ko00620_Pyruvatemetabolism_Metabolism_Carbohydratemetabolism_dld,D-lactatedehydrogenase[EC:1.1.1.28]	2,07452E-05	1,5286E-05	0
K01474_ko00330_Arginineandprolinemetabolism_Metabolism_Aminoacidmetabolism_hyuB,N-methylhydantoinaseB[EC:3.5.2.14]	5,18629E-06	1,5286E-05	0
K02822_ko02010_Ctransporters_Environmentalinformationprocessing_Membranetransport_PTS-Ula-EIIB,ulaB,sgaB,PTSsystem,ascorbate-specificIIBcomponent[EC:2.7.1.69];K02822_ko00052_Galactosemetabolism_Metabolism_Carbohydratemetabolism_PTS-Ula-	4,14903E-05	2,03813E-05	3,32215E-05
K11212_ko00194_Photosynthesisproteins_Metabolism_Energymetabolism_cofD,LPPG:FO2-phospho-L-lactatetransferase[EC:2.7.8.28]	3,11177E-05	4,07627E-05	3,32215E-05
K03852_ko00430_Taurineandhypotaurinemetabolism_Metabolism_Metabolismofotheraminoacids_xsc,sulfoacetaldehydeacetyltransferase[EC:2.3.3.15]	1,55589E-05	0	0
K00274_ko02020_twocomponentsistem_Environmentalinformationprocessing_Signaltransduction_MAO,aofH,monoamineoxidase[EC:1.4.3.4];K00274_ko05034_Alcoholism_HumanDiseases_SubstanceDependence_MAO,aofH,monoamineoxidase[EC:1.4.3.4];K0027	2,07452E-05	1,01907E-05	8,30537E-06
K01638_ko00630_Glyoxylateanddicarboxylatemetabolism_Metabolism_Carbohydratemetabolism_E2.3.3.9,aceB,glcB,malatesynthase[EC:2.3.3.9];K01638_ko00620_Pyruvatemetabolism_Metabolism_Carbohydratemetabolism_E2.3.3.9,aceB,glcB,malatesynthase[E	0	0	2,49161E-05
K04771_ko02020_Two-componentsystem_Environmentalinformationprocessing_Signaltrasduction_degP,htrA,serineproteaseDo[EC:3.4.21.107]	3,11177E-05	5,09533E-06	0
K00400_ko00194_Photosynthesisproteins_Metabolism_Energymetabolism_K00400,methylcoenzymeMreductasesystem,componentA2	1,03726E-05	1,01907E-05	8,30537E-06
K11089_ko05322_Systemiclupuserythematosus_Humandiseases_Immunediseases_TROVE2,SSA2,60kDaSS-A/Roribonucleoprotein	3,6304E-05	0	2,49161E-05
K06210_ko00760_Nicotinateandnicotinamidemetabolism_Metabolism_Metabolismofcofactorsandvitamins_NMNAT,nicotinamidemononucleotideadenylyltransferase[EC:2.7.7.12.7.7.18]	0	0	1,66107E-05
K03821_ko00630_Glyoxylateanddicarboxylatemetabolism_Metabolism_Carbohydratemetabolism_phbC,phaC,polyhydroxyalkanoatesynthase[EC:2.3.1.-]	0	0	3,32215E-05
K00108_ko00260_Glycine,serineandthreoninemetabolism_Metabolism_Aminoacidmetabolism_E1.1.99.1,betA,CHDH,cholinedehydrogenase[EC:1.1.99.1]	1,03726E-05	5,09533E-06	0
K05874_ko02020_Two-componentsystem_Environmentalinformationprocessing_Signaltrasduction_tsr,methyl-acceptingchemotaxisproteinI,serinesensorreceptor;K05874_ko02030_Bacterialchemotaxis_Organismalsystem_Cellmobility_tsr,methyl-acceptingchemo	2,07452E-05	0	1,66107E-05
K01594_ko00430_Taurineandhypotaurinemetabolism_Metabolism_Metabolismofotheraminoacids_CSAD,sulfinoalaninedecarboxylase[EC:4.1.1.29]	0	0	8,30537E-06
K00710_ko00512_MucintypeO-glycanbiosynthesis_Metabolism_Glycanbiosynthesisandmetabolism_GALNT,polypeptideN-acetylgalactosaminyltransferase[EC:2.4.1.41]	1,03726E-05	0	0
K06120_ko00561_Glycerolipidmetabolism_Metabolism_Lipidmetabolism_dhaB,glyceroldehydrataselargesubunit[EC:4.2.1.30]	0	1,01907E-05	1,66107E-05
K07700_ko02020_Two-componentsystem_Environmentalinformationprocessing_Signaltrasduction_dpiB,citA,two-componentsystem,CitBfamily,citoperonsensorhistidinekinaseCitA[EC:2.7.13.3]	3,11177E-05	2,54767E-05	0,000116275
K06159_ko02010_Ctransporters_Environmentalinformationprocessing_Membranetransport_yojI,putativeATP-bindingcassettetransporter	0	5,09533E-06	8,30537E-06
K00875_ko00040_Pentoseandglucuronateinterconversions_Metabolism_Carbohydratemetabolism_E2.7.1.47,D-ribulokinase[EC:2.7.1.47]	1,03726E-05	0	0
K01568_ko00010_Glycolysis/Gluconeogenesis_Metabolism_Carbohydratemetabolism_E4.1.1.1,pdc,pyruvatedecarboxylase[EC:4.1.1.1]	0	0	1,66107E-05
K06151_ko00030_Pentosephosphatepathway_Metabolism_Carbohydratemetabolism_E1.1.99.3A,gluconate2-dehydrogenasealphachain[EC:1.1.99.3]	5,18629E-06	0	0
K05310_ko00563_Glycosylphosphatidylinositol(GPI)-anchorbiosynthesis_Metabolism_Glycanbiosynthesisandmetabolism_GPI7,ethanolaminephosphotransferase[EC:2.7.-.-]	4,14903E-05	9,1716E-05	2,49161E-05
K02515_ko04111_Cellcycle-yeast_CellularProcesses_Cellgrowthanddeath_HSL1,serine/threonine-proteinkinaseHSL1,negativeregulatorofSwe1kinase[EC:2.7.11.-]	5,18629E-06	0	0
K12784_ko05130_PathogenicEscherichiacoliinfection_HumanDiseases_Infectiousdiseases_tir,translocatedintiminreceptor	5,18629E-06	0	0
K13527_ko03050_Proteasome_GeneticInformationProcessing_Folding,sortinganddegradation_mpa,proteasome-associatedATPase	0	5,09533E-06	0
K02363_ko01053_Biosynthesisofsiderophoregroupnonribosomalpeptides_Metabolism_Metabolismofterpenoidsandpolyketides_entE,dhbE,vibE,mxcE,2,3-dihydroxybenzoate-AMPligase[EC:2.7.7.58]	5,18629E-06	0	8,30537E-06
K01312_ko04080_Neuroactiveligand-receptorinteraction_EnvironmentalInformationProcessing_Signalingmoleculesandinteraction_PRSS,trypsin[EC:3.4.21.4];K01312_ko05164_InfluenzaA_HumanDiseases_Infectiousdiseases_PRSS,trypsin[EC:3.4.21.4];K01312_ko0	0	0	8,30537E-06
K12368_ko02010_Ctransporters_Environmentalinformationprocessing_Membranetransport_dppA,dipeptidetransportersystemsubstrate-bindingprotein;K12368_ko02030_Bacterialchemotaxis_Organismalsystem_Cellmobility_dppA,dipeptidetransportersystemsubstra	1,55589E-05	2,03813E-05	1,66107E-05
K14519_ko01220_Degradationofaromaticcompounds_Metabolism_Overview_aldH,NADP-dependentaldehydedehydrogenase[EC:1.2.1.4];K14519_ko00930_Caprolactamdegradation_Metabolism_Xenobioticsbiodegradationandmetabolism_aldH,NADP-dependenta	1,03726E-05	0	0
K03776_ko02020_Two-componentsystem_Environmentalinformationprocessing_Signaltrasduction_aer,aerotaxisreceptor;K03776_ko02030_Bacterialchemotaxis_Organismalsystem_Cellmobility_aer,aerotaxisreceptor	5,18629E-06	5,09533E-06	0
K14156_ko00564_Glycerophospholipidmetabolism_Metabolism_Lipidmetabolism_CHK,choline/ethanolaminekinase[EC:2.7.1.32.2.7.1.82]	0	5,09533E-06	1,66107E-05
K00138_ko00010_Glycolysis/Gluconeogenesis_Metabolism_Carbohydratemetabolism_aldB,aldehydedehydrogenase[EC:1.2.1.-];K00138_ko00620_Pyruvatemetabolism_Metabolism_Carbohydratemetabolism_aldB,aldehydedehydrogenase[EC:1.2.1.-]	0	1,01907E-05	0
K05876_ko02020_Two-componentsystem_Environmentalinformationprocessing_Signaltrasduction_trg,methyl-acceptingchemotaxisproteinIII,ribosedangalactosesensorreceptor;K05876_ko02030_Bacterialchemotaxis_Organismalsystem_Cellmobility_trg,methyl-a	2,07452E-05	0	0
K07784_ko02020_Two-componentsystem_Environmentalinformationprocessing_Signaltrasduction_uhpT,MFStransporter,OPAfamily,hexosephosphatetransportproteinUhpT	5,18629E-06	1,01907E-05	0
K01713_ko00400_Phenylalanine,tyrosineandtryptophanbiosynthesis_Metabolism_Aminoacidmetabolism_pheC,cyclohexadienyldehydratase[EC:4.2.1.514.2.1.91];K01713_ko01230_Biosynthesisofaminoacids_Metabolism_Overview_pheC,cyclohexadienyldehydrata	5,18629E-06	1,01907E-05	8,30537E-06
K03045_ko03020_RNApolymerase_GeneticinformationProcessing_Transcription_rpoB2,DNA-directedRNApolymerasesubunitB[EC:2.7.7.6];K03045_ko00230_Purinemetabolism_Metabolism_Nucleotidemetabolism_rpoB2,DNA-directedRNApolymerasesubunitB[EC:	0	1,01907E-05	0
K01908_ko00630_Glyoxylateanddicarboxylatemetabolism_Metabolism_Carbohydratemetabolism_E6.2.1.17,prpE,propionyl-CoAsynthetase[EC:6.2.1.17]	0	0	8,30537E-06
K07964_ko05205_Proteoglycansincancer_HumanDiseases_Cancers_HPSE,heparanase1[EC:3.2.1.166];K07964_ko00531_Glycosaminoglycandegradation_Metabolism_Glycanbiosynthesisandmetabolism_HPSE,heparanase1[EC:3.2.1.166]	1,03726E-05	1,01907E-05	0
K01513_ko00500_Starchandsucrosemetabolism_Metabolism_Carbohydratemetabolism_ENPP1_3,ectonucleotidepyrophosphatase/phosphodiesterasefamilymember1/3[EC:3.1.4.13.6.1.9];K01513_ko00760_Nicotinateandnicotinamidemetabolism_Metabolism_Me	0	0	8,30537E-06
K11617_ko02020_Two-componentsystem_Environmentalinformationprocessing_Signaltrasduction_liaS,two-componentsystem,NarLfamily,sensorhistidinekinaseLiaS[EC:2.7.13.3]	0	1,01907E-05	3,32215E-05
K10539_ko02010_Ctransporters_Environmentalinformationprocessing_Membranetransport_araG,L-arabinosetransportsystemATP-bindingprotein[EC:3.6.3.17]	0	0	1,66107E-05
K11017_ko02010_Ctransporters_Environmentalinformationprocessing_Membranetransport_shlB,hhdB,hpmB,hemolysinactivation/secretionprotein	0	0	1,66107E-05
K06125_ko00130_Ubiquinoneandotherterpenoid-quinonebiosynthesis_Metabolism_Metabolismofcofactorsandvitamins_COQ2,4-hydroxybenzoatehexaprenyltransferase[EC:2.5.1.-]	0	1,01907E-05	3,32215E-05
K00187_ko00280_Valine,leucineandisoleucinedegradation_Metabolism_Aminoacidmetabolism_vorB,2-oxoisovalerateferredoxinoxidoreductase,betasubunit[EC:1.2.7.7]	0	0	8,30537E-06
K13832_ko00400_Phenylalanine,tyrosineandtryptophanbiosynthesis_Metabolism_Aminoacidmetabolism_aroDE,DHQ-SDH,3-dehydroquinatedehydratase/shikimatedehydrogenase[EC:4.2.1.101.1.1.25];K13832_ko01230_Biosynthesisofaminoacids_Metabolism_Ov	0	5,09533E-06	0
K09472_ko00330_Arginineandprolinemetabolism_Metabolism_Aminoacidmetabolism_puuC,aldH,gamma-glutamyl-gamma-aminobutyraldehydedehydrogenase[EC:1.2.1.-]	2,07452E-05	0	1,66107E-05
K07190_ko04066_HIF-1signalingpathway_Environmentalinformationprocessing_Signaltrasduction_PHKA_B,phosphorylasekinasealpha/betasubunit;K07190_ko04910_Insulinsignalingpathway_Organismalsystem_Endocrinsystem_PHKA_B,phosphorylasekinasealpha	1,03726E-05	0	0
K02575_ko00910_Nitrogenmetabolism_Metabolism_Energymetabolism_NRT,narK,nrtP,nasA,MFStransporter,NNPfamily,nitrate/nitritetransporter	2,59315E-05	2,54767E-05	8,30537E-06
K03391_ko00361_Chlorocyclohexaneandchlorobenzenedegradation_Metabolism_Xenobioticsbiodegradationandmetabolism_E1.14.13.50,pentachlorophenolmonooxygenase[EC:1.14.13.50];K03391_ko00364_Fluorobenzoatedegradation_Metabolism_Xenobioticsb	0	5,09533E-06	0
K13790_ko05131_Shigellosis_HumanDiseases_Infectiousdiseases_icsB,bopA,virulenceproteinIcsB	0	1,01907E-05	0
K08139_ko04113_Meiosis-yeast_CellularProcesses_Cellgrowthanddeath_HXT,MFStransporter,SPfamily,sugar:H+symporter	4,14903E-05	2,03813E-05	6,6443E-05
K04110_ko00627_Aminobenzoatedegradation_Metabolism_Xenobioticsbiodegradationandmetabolism_badA,benzoate-CoAligase[EC:6.2.1.25];K04110_ko00362_Benzoatedegradation_Metabolism_Xenobioticsbiodegradationandmetabolism_badA,benzoate-CoAli	5,18629E-06	0	1,66107E-05
K01565_ko04142_Lysosome_CellularProcesses_Transportandcatabolism_SGSH,N-sulfoglucosaminesulfohydrolase[EC:3.10.1.1];K01565_ko00531_Glycosaminoglycandegradation_Metabolism_Glycanbiosynthesisandmetabolism_SGSH,N-sulfoglucosaminesulfohydr	1,03726E-05	1,01907E-05	2,49161E-05
K00808_ko00960_Tropane,piperidineandpyridinealkaloidbiosynthesis_Metabolism_Biosynthesisofothersecondarymetabolites_hss,homospermidinesynthase[EC:2.5.1.44]	1,03726E-05	0	0
K07637_ko02020_Two-componentsystem_Environmentalinformationprocessing_Signaltrasduction_phoQ,two-componentsystem,OmpRfamily,sensorhistidinekinasePhoQ[EC:2.7.13.3]	1,03726E-05	0	1,66107E-05
K09477_ko02020_Two-componentsystem_Environmentalinformationprocessing_Signaltrasduction_citT,citrate:succinateantiporter	0	5,09533E-06	0
K02323_ko00230_Purinemetabolism_Metabolism_Nucleotidemetabolism_DPB2,DNApolymeraseIIsmallsubunit[EC:2.7.7.7];K02323_ko00240_Pyrimidinemetabolism_Metabolism_Nucleotidemetabolism_DPB2,DNApolymeraseIIsmallsubunit[EC:2.7.7.7]	1,03726E-05	0	0
K05577_ko00190_Oxidativephosphorylation_Metabolism_Energymetabolism_ndhF,NAD(P)H-quinoneoxidoreductasesubunit5[EC:1.6.5.3]	0	0	1,66107E-05

K11191_ko02010_Ctransporters_Environmentalinformationprocessing_Membranetransport_PTS-Mur-EIIB,murP,PTSsystem,N-acetylmuramicacid-specificIIBcomponent[EC:2.7.1.69];K11191_ko00520_Aminosugarandnucleotidesugarmetabolism_Metabolism_Carb	5,18629E-06	0	0
K13481_ko00230_Purinemetabolism_Metabolism_Nucleotidemetabolism_xdhA,xanthinedehydrogenasesmallsubunit[EC:1.17.1.4]	0	0	1,66107E-05
K11626_ko02020_Two-componentsystem_Environmentalinformationprocessing_Signaltrasduction_glnT,putativesodium/glutaminesymporter	0	0	8,30537E-06
K01593_ko05034_Alcoholism_HumanDiseases_SubstanceDependence_DDC,aromatic-L-amino-aciddecarboxylase[EC:4.1.1.28];K01593_ko05031_Amphetamineaddiction_HumanDiseases_SubstanceDependence_DDC,aromatic-L-amino-aciddecarboxylase[EC:4.1.1.:	0	0	8,30537E-06
K09693_ko02010_Ctransporters_Environmentalinformationprocessing_Membranetransport_tagH,teichoicacidtransportsystemATP-bindingprotein[EC:3.6.3.40]	3,11177E-05	1,5286E-05	4,15269E-05
K02496_ko00830_RetinolMetabolism_Metabolism_Metabolismofcofactorsandvitamins_hemX,uroporphyrin-IIIC-methyltransferase[EC:2.1.1.107]	2,07452E-05	0	8,30537E-06
K11003_ko02010_Ctransporters_Environmentalinformationprocessing_Membranetransport_hlyD,cyaD,hemolysinD;K11003_ko05133_Pertussis_HumanDiseases_Infectiousdiseases_hlyD,cyaD,hemolysinD	2,07452E-05	1,5286E-05	0
K00918_ko00010_Glycolysis/Gluconeogenesis_Metabolism_Carbohydratemetabolism_pfkC,ADP-dependentphosphofructokinase/glucokinase[EC:2.7.1.1462.7.1.147];K00918_ko00030_Pentosephosphatepathway_Metabolism_Carbohydratemetabolism_pfkC,ADP-d	1,55589E-05	1,01907E-05	1,66107E-05
K07649_ko02020_Two-componentsystem_Environmentalinformationprocessing_Signaltrasduction_tctE,two-componentsystem,OmpRfamily,sensorhistidinekinaseTctE[EC:2.7.13.3]	1,03726E-05	1,5286E-05	0
K14275_ko00040_Pentoseandglucuronateinterconversions_Metabolism_Carbohydratemetabolism_xad,D-xylonatedehydratase	5,18629E-06	0	1,66107E-05
K01093_ko00630_Glyoxylateanddicarboxylatemetabolism_Metabolism_Carbohydratemetabolism_appA,4-phytase/acidphosphatase[EC:3.1.3.263.1.3.2];K01093_ko00740_Riboflavinmetabolism_Metabolism_Metabolismofcofactorsandvitamins_appA,4-phytase/ac	1,03726E-05	0	0
K12293_ko02020_Two-componentsystem_Environmentalinformationprocessing_Signaltrasduction_comB,competencefactortransportaccessoryproteinComB	1,03726E-05	1,01907E-05	1,66107E-05
K08710_ko00791_Atrazinedegradation_Humandiseases_Xenobioticsbiodegradationandmetabolism_atzC,N-isopropylammelideisopropylaminohydrolase[EC:3.5.99.4]	0	2,54767E-05	0
K01659_ko00630_Glyoxylateanddicarboxylatemetabolism_Metabolism_Carbohydratemetabolism_prpC,2-methylcitratesynthase[EC:2.3.3.5]	1,55589E-05	1,01907E-05	8,30537E-06
K04480_ko01200_Carbonmetabolism_Metabolism_Overview_mtaB,methanol---5-hydroxybenzimidazolylcobamideCo-methyltransferase[EC:2.1.1.90];K04480_ko00194_Photosynthesisproteins_Metabolism_Energymetabolism_mtaB,methanol---5-hydroxybenzimi	0	5,09533E-06	0
K14681_ko00250_Alanine,aspartateandglutamatemetabolism_Metabolism_Aminoacidmetabolism_argHA,argininosuccinatelyase/amino-acidN-acetyltransferase[EC:4.3.2.12.3.1.1];K14681_ko00330_Arginineandprolinemetabolism_Metabolism_Aminoacidmetabol	5,18629E-06	0	0
K00231_ko00830_RetinolMetabolism_Metabolism_Metabolismofcofactorsandvitamins_PPOX,hemY,oxygen-dependentprotoporphyrinogenoxidase[EC:1.3.3.4]	2,07452E-05	4,07627E-05	0,000116275
K01706_ko00052_Galactosemetabolism_Metabolism_Carbohydratemetabolism_gudD,glucaratedehydratase[EC:4.2.1.40]	6,22355E-05	1,5286E-05	4,98322E-05
K01132_ko04142_Lysosome_CellularProcesses_Transportandcatabolism_GALNS,N-acetylgalactosamine-6-sulfatase[EC:3.1.6.4];K01132_ko00531_Glycosaminoglycandegradation_Metabolism_Glycanbiosynthesisandmetabolism_GALNS,N-acetylgalactosamine-6-sul	0	5,09533E-06	0
K01230_ko04141_Proteinprocessinginendoplasmicreticulum_GeneticInformationProcessing_Folding,sortinganddegradation_MAN1,mannosyl-oligosaccharidealpha-1,2-mannosidase[EC:3.2.1.113];K01230_ko00513_VarioustypesofN-glycanbiosynthesis_Metabolism	0	5,09533E-06	0
K13507_ko00561_Glycerolipidmetabolism_Metabolism_Lipidmetabolism_GAT,glycerol-3-phosphateO-acyltransferase/dihydroxyacetonephosphateacyltransferase[EC:2.3.1.152.3.1.42];K13507_ko00564_Glycerophospholipidmetabolism_Metabolism_Lipidmetabol	0	5,09533E-06	0
K06269_ko04510_Focaladhesion_Cellgrowthanddeath_Cellularcommunity_PPP1C,serine/threonine-proteinphosphatasePP1catalyticsubunit[EC:3.1.3.16];K06269_ko04113_Meiosis-yeast_CellularProcesses_Cellgrowthanddeath_PPP1C,serine/threonine-proteinpho	1,03726E-05	0	0
K05831_ko00300_Lysinebiosynthesis_Metabolism_Aminoacidmetabolism_argE1,lysK,LysW-gamma-L-lysinecarboxypeptidase;K05831_ko01210_Oxocarboxylicacidmetabolism_Metabolism_Overview_argE1,lysK,LysW-gamma-L-lysinecarboxypeptidase;K05831_ko0	1,03726E-05	0	1,66107E-05
K14682_ko00330_Arginineandprolinemetabolism_Metabolism_Aminoacidmetabolism_argAB,amino-acidN-acetyltransferase[EC:2.3.1.1];K14682_ko01210_Oxocarboxylicacidmetabolism_Metabolism_Overview_argAB,amino-acidN-acetyltransferase[EC:2.3.1.1];K1	1,55589E-05	1,5286E-05	1,66107E-05
K04781_ko01053_Biosynthesisofsiderophoregroupnonribosomalpeptides_Metabolism_Metabolismofterpenoidsandpolyketides_mbtI,irp9,ybtS,salicylatesynthetase[EC:5.4.4.24.2.99.21]	0	5,09533E-06	8,30537E-06
K05236_ko04080_Neuroactiveligand-receptorinteraction_EnvironmentalInformationProcessing_Signalingmoleculesandinteraction_COPA,coatomerproteincomplex,subunitalpha(xenin)	0	1,01907E-05	0
K00383_ko00480_Glutathionemetabolism_Metabolism_Metabolismofotheraminoacids_GSR,gor,glutathionereductase(NADPH)[EC:1.8.1.7];K00383_ko04918_Thyroidhormonesynthesis_Organismalsystem_Endocrinsystem_GSR,gor,glutathionereductase(NADPH)[E	5,18629E-06	2,54767E-05	4,98322E-05
K11382_ko02020_Two-componentsystem_Environmentalinformationprocessing_Signaltrasduction_pgtP,MFStransporter,OPAfamily,phosphoglyceratetransporterprotein	0	0	1,66107E-05
K00032_ko00030_Pentosephosphatepathway_Metabolism_Carbohydratemetabolism_E1.1.1.43,phosphogluconate2-dehydrogenase[EC:1.1.1.43];K00032_ko00480_Glutathionemetabolism_Metabolism_Metabolismofotheraminoacids_E1.1.1.43,phosphogluconate	0	1,01907E-05	0
K14596_ko00906_Carotenoidbiosynthesis_Metabolism_Metabolismofterpenoidsandpolyketides_crtX,zeaxanthinglucosyltransferase[EC:2.4.1.276]	1,03726E-05	1,01907E-05	1,66107E-05
K01904_ko00360_Phenylalaninemetabolism_Metabolism_Aminoacidmetabolism_4CL,4-coumarate--CoAligase[EC:6.2.1.12];K01904_ko00940_Phenylpropanoidbiosynthesis_Metabolism_Biosynthesisofothersecondarymetabolites_4CL,4-coumarate--CoAligase[EC:6	0	5,09533E-06	0
K05549_ko01220_Degradationofaromaticcompounds_Metabolism_Overview_benA-xylX,benzoate/toluate1,2-dioxygenasealphasubunit[EC:1.14.12.101.14.12.-];K05549_ko00362_Benzoatedegradation_Metabolism_Xenobioticsbiodegradationandmetabolism_benA	5,18629E-06	0	0
K06634_ko04110_Cellcycle_CellularProcesses_Cellgrowthanddeath_CCNH,cyclinH;K06634_ko03420_Nucleotideexcisionrepair_GeneticinformationProcessing_ReplicationandRepair_CCNH,cyclinH;K06634_ko03022_Basaltranscriptionfactors_GeneticinformationPro	0	5,09533E-06	8,30537E-06
K07359_ko04151_PI3K-Aktsignalingpathway_Environmentalinformationprocessing_Signaltrasduction_CAMKK,calcium/calmodulin-dependentproteinkinasekinase[EC:2.7.11.17];K07359_ko05034_Alcoholism_HumanDiseases_SubstanceDependence_CAMKK,calciun	1,03726E-05	0	0
K03103_ko00010_Glycolysis/Gluconeogenesis_Metabolism_Carbohydratemetabolism_MINPP1,multipleinositol-polyphosphatephosphatase/2,3-bisphosphoglycerate3-phosphatase[EC:3.1.3.623.1.3.80];K03103_ko00630_Glyoxylateanddicarboxylatemetabolism_M	6,22355E-05	0	0
K05281_ko00943_Isoflavonoidbiosynthesis_Metabolism_Biosynthesisofothersecondarymetabolites_E1.3.1.45,2'-hydroxyisoflavonereductase[EC:1.3.1.45]	0	1,01907E-05	4,15269E-05
K03062_ko03050_Proteasome_GeneticInformationProcessing_Folding,sortinganddegradation_PSMC1,RPT2,26Sproteasomeregulatorysubunit T2;K03062_ko05203_Viralcarcinogenesis_HumanDiseases_Cancers_PSMC1,RPT2,26Sproteasomeregulatorysubunit T2;K03	5,18629E-06	1,01907E-05	0
K00401_ko01200_Carbonmetabolism_Metabolism_Overview_mcrB,methyl-coenzymeMreductasebetasubunit[EC:2.8.4.1];K00401_ko00194_Photosynthesisproteins_Metabolism_Energymetabolism_mcrB,methyl-coenzymeMreductasebetasubunit[EC:2.8.4.1]	2,07452E-05	1,5286E-05	0
K03277_ko00540_Lipopolysaccharidebiosynthesis_Metabolism_Glycanbiosynthesisandmetabolism_waaU,rfaK,heptosyltransferaseIV[EC:2.4.-.-]	1,55589E-05	1,01907E-05	0
K00835_ko00290_Valine,leucineandisoleucinebiosynthesis_Metabolism_Aminoacidmetabolism_avtA,valine--pyruvateaminotransferase[EC:2.6.1.66]	1,03726E-05	2,03813E-05	8,30537E-06
K01637_ko00630_Glyoxylateanddicarboxylatemetabolism_Metabolism_Carbohydratemetabolism_E4.1.3.1,aceA,isocitratelyase[EC:4.1.3.1];K01637_ko01200_Carbonmetabolism_Metabolism_Overview_E4.1.3.1,aceA,isocitratelyase[EC:4.1.3.1]	1,03726E-05	5,09533E-06	8,30537E-06
K03224_ko02010_Ctransporters_Environmentalinformationprocessing_Membranetransport_yscN,sctN,hrcN,ATPsynthaseintypeIIIsecretionproteinN[EC:3.6.3.14]	5,18629E-06	0	0
K10380_ko05205_Proteoglycansincancer_HumanDiseases_Cancers_ANK,ankyrin	0	0	8,30537E-06
K09482_ko00970_Aminoacyl-tRNAbiosynthesis_Geneticinformationandprocessing_Transcription_gatD,glutamyl-tRNA(Gln)amidotransferasesubunitD[EC:6.3.5.7]	1,03726E-05	1,01907E-05	2,49161E-05
K00993_ko00564_Glycerophospholipidmetabolism_Metabolism_Lipidmetabolism_EPT1,ethanolaminephosphotransferase[EC:2.7.8.1];K00993_ko00564_Glycerophospholipidmetabolism_Metabolism_Lipidmetabolism_EPT1,ethanolaminephosphotransferase[EC:2.	5,18629E-06	0	0
K11695_ko01005_Lipopolysaccharidebiosynthesisproteins_Metabolism_Glycanbiosynthesisandmetabolism_femB,peptidoglycanpentaglycineglycinetransferase(thefourthandfifthglycine)[EC:2.3.2.18]	5,18629E-06	2,54767E-05	8,30537E-06
K07516_ko00071_Fattyaciddegradation_Metabolism_Lipidmetabolism_fadN,3-hydroxyacyl-CoAdehydrogenase[EC:1.1.1.35];K07516_ko01212_Fattyacidmetabolism_Metabolism_Overview_fadN,3-hydroxyacyl-CoAdehydrogenase[EC:1.1.1.35];K07516_ko01200_Ca	2,59315E-05	0	4,15269E-05
K00285_ko00360_Phenylalaninemetabolism_Metabolism_Aminoacidmetabolism_dadA,D-amino-aciddehydrogenase[EC:1.4.99.1]	1,55589E-05	5,09533E-06	8,30537E-06
K02000_ko02010_Ctransporters_Environmentalinformationprocessing_Membranetransport_proV,glycinebetaine/prolinetransportsystemATP-bindingprotein[EC:3.6.3.32]	5,18629E-05	9,1716E-05	0,00010797
K01344_ko04610_Complementandcoagulationcascades_OrganismalSystems_Immunesystem_PROC,proteinC(activated)[EC:3.4.21.69]	5,18629E-06	5,09533E-06	0
K01455_ko00630_Glyoxylateanddicarboxylatemetabolism_Metabolism_Carbohydratemetabolism_E3.5.1.49,formamidase[EC:3.5.1.49];K01455_ko00910_Nitrogenmetabolism_Metabolism_Energymetabolism_E3.5.1.49,formamidase[EC:3.5.1.49];K01455_ko00460	2,59315E-05	7,643E-05	4,15269E-05
K00819_ko00330_Arginineandprolinemetabolism_Metabolism_Aminoacidmetabolism_E2.6.1.13,rocD,ornithine--oxo-acidtransaminase[EC:2.6.1.13]	2,07452E-05	6,62393E-05	0,000132886
K14265_ko00380_Tryptophanmetabolism_Metabolism_Aminoacidmetabolism_Tam1,tryptophanaminotransferase[EC:2.6.1.27]	1,55589E-05	0	0
K00825_ko00300_Lysinebiosynthesis_Metabolism_Aminoacidmetabolism_AADAT,KAT2,kynurenine/2-aminoadipateaminotransferase[EC:2.6.1.72.6.1.39];K00825_ko00310_Lysinedegradation_Metabolism_Aminoacidmetabolism_AADAT,KAT2,kynurenine/2-aminoa	0	1,01907E-05	0
K09471_ko00330_Arginineandprolinemetabolism_Metabolism_Aminoacidmetabolism_puuB,ordL,gamma-glutamylputrescineoxidase[EC:1.4.3.-]	5,18629E-06	0	0
K00252_ko00310_Lysinedegradation_Metabolism_Aminoacidmetabolism_GCDH,gcdH,glutaryl-CoAdehydrogenase[EC:1.3.8.6];K00252_ko00380_Tryptophanmetabolism_Metabolism_Aminoacidmetabolism_GCDH,gcdH,glutaryl-CoAdehydrogenase[EC:1.3.8.6];K00	0	1,01907E-05	0
K07708_ko02020_Two-componentsystem_Environmentalinformationprocessing_Signaltrasduction_glnL,ntrB,two-componentsystem,NtrCfamily,nitrogenregulationsensorhistidinekinaseGlnL[EC:2.7.13.3]	0	3,0572E-05	4,15269E-05
K13245_ko04112_Cellcycle-Caulobacter_CellularProcesses_Cellgrowthanddeath_pdeA,c-di-GMP-specificphosphodiesterase[EC:3.1.4.52]	5,18629E-06	0	0
K07697_ko02020_Two-componentsystem_Environmentalinformationprocessing_Signaltrasduction_kinB,two-componentsystem,sporulationsensorkinaseB[EC:2.7.13.3]	4,66766E-05	3,0572E-05	9,13591E-05
K13713_ko00230_Purinemetabolism_Metabolism_Nucleotidemetabolism_purCD,fusionproteinPurCD[EC:6.3.2.66.3.4.13]	2,07452E-05	0	2,49161E-05
K02847_ko00540_Lipopolysaccharidebiosynthesis_Metabolism_Glycanbiosynthesisandmetabolism_waaL,rfaL,O-antigenligase[EC:6.-.-.-]	0	2,03813E-05	8,30537E-06
K10815_ko00460_Cyanoaminoacidmetabolism_Metabolism_Metabolismofotheraminoacids_hcnB,hydrogencyanidesynthaseHcnB[EC:1.4.99.5]	1,03726E-05	0	0
K00517_ko00945_Stilbenoid,diarylheptanoidandgingerolbiosynthesis_Metabolism_Biosynthesisofothersecondarymetabolites_E1.14.-.-,[EC:1.14.-.-];K00517_ko00903_Limoneneandpinenedegradation_Metabolism_Metabolismofterpenoidsandpolyketides_E1.14.-.-	5,18629E-06	3,56673E-05	0
K03231_ko03013_RNAtransport_GeneticinformationProcessing_Transcription_EEF1A,elongationfactor1-alpha;K03231_ko05134_Legionellosis_HumanDiseases_Infectiousdiseases_EEF1A,elongationfactor1-alpha	5,18629E-06	0	0
K08476_ko02020_Two-componentsystem_Environmentalinformationprocessing_Signaltrasduction_pgtA,two-componentsystem,NtrCfamily,phosphoglyceratetransportsystemresponseregulatorPgtA	2,07452E-05	0	1,66107E-05
K00333_ko00190_Oxidativephosphorylation_Metabolism_Energymetabolism_nuoD,NADH-quinoneoxidoreductasesubunitD[EC:1.6.5.3]	1,03726E-05	5,09533E-06	8,30537E-06
K00414_ko05010_Alzheimer'sdisease_HumanDiseases_Degenerativediseases_QCR1,UQCRC1,ubiquinol-cytochromecreductasecoresubunit1;K00414_ko05016_Huntington'sdisease_HumanDiseases_Degenerativediseases_QCR1,UQCRC1,ubiquinol-cytochromecredu	0	0	1,66107E-05
K12342_ko02010_Ctransporters_Environmentalinformationprocessing_Membranetransport_yadB_C,adhesinYadB/C	3,6304E-05	5,09533E-06	2,49161E-05
K07542_ko00563_Glycosylphosphatidylinositol(GPI)-anchorbiosynthesis_Metabolism_Glycanbiosynthesisandmetabolism_PIGV,phosphatidylinositolglycan,classV[EC:2.4.1.-]	5,18629E-06	1,5286E-05	1,66107E-05
K03265_ko03015_mRNAsurveillancepathway_GeneticinformationProcessing_Transcription_ETF1,ERF1,peptidechainreleasefactorsubunit1	1,03726E-05	0	1,66107E-05

K11076_ko02010_Ctransporters_Environmentalinformationprocessing_Membranetransport_potG,putrescinetransportsystemATP-bindingprotein	0	1,01907E-05	0
K08260_ko00830_Retinolmetabolism_Metabolism_Metabolismofcofactorsandvitamins_cbiZ,adenosylcobinamidehydrolase[EC:3.5.1.90]	2,59315E-05	1,5286E-05	1,66107E-05
K01601_ko00630_Glyoxylateanddicarboxylatemetabolism_Metabolism_Carbohydratemetabolism_rbcL,ribulose-bisphosphatecarboxylaselargechain[EC:4.1.1.39];K01601_ko01200_Carbonmetabolism_Metabolism_Overview_rbcL,ribulose-bisphosphatecarboxylase	1,55589E-05	5,09533E-06	0
K00121_ko05204_Chemicalcarcinogenesis_HumanDiseases_Cancers_frmA,ADH5,adhC,S-(hydroxymethyl)glutathionedehydrogenase/alcoholdehydrogenase[EC:1.1.1.2841.1.1.1];K00121_ko00350_Tyrosinemetabolism_Metabolism_Aminoacidmetabolism_frmA,AD	1,55589E-05	1,01907E-05	1,66107E-05
K03242_ko03013_RNAtransport_GeneticinformationProcessing_Transcription_EIF2S3,translationinitiationfactor2subunit3	2,07452E-05	5,09533E-06	8,30537E-06
K14656_ko00740_RiboflavinmetabolismMetabolism_Metabolismofcofactorsandvitamins_ribL,FADsynthetase	0	2,03813E-05	0
K14565_ko03008_Ribosomebiogenesisineukaryotes_GeneticinformationProcessing_Transcription_NOP58,nucleolarprotein58	0	1,01907E-05	0
K12773_ko04113_Meiosis-yeast_CellularProcesses_Cellgrowthanddeath_SPR3,sporulation-regulatedprotein3	0	1,01907E-05	0
K10977_ko00300_Lysinebiosynthesis_Metabolism_Aminoacidmetabolism_aksA,methanogenhomocitratesynthase[EC:2.3.3.142.3.3.-];K10977_ko00620_Pyruvatemetabolism_Metabolism_Carbohydratemetabolism_aksA,methanogenhomocitratesynthase[EC:2.3.3.	1,03726E-05	5,09533E-06	0
K14446_ko00630_Glyoxylateanddicarboxylatemetabolism_Metabolism_Carbohydratemetabolism_ccr,crotonyl-CoAcarboxylase/reductase[EC:1.3.1.85]	0	5,09533E-06	0
K10846_ko03420_Nucleotideexcisionrepair_GeneticinformationProcessing_ReplicationandRepair_ERCC5,XPG,RAD2,DNAexcisionrepairproteinERCC-5	0	5,09533E-06	1,66107E-05
K11637_ko02020_Two-componentsystem_Environmentalinformationprocessing_Signaltrasduction_citS,two-componentsystem,CitBfamily,sensorhistidinekinaseCitS[EC:2.7.13.3]	1,03726E-05	0	0
K00932_ko00630_Glyoxylateanddicarboxylatemetabolism_Metabolism_Carbohydratemetabolism_E2.7.2.15,tdcD,pduW,propionatekinase[EC:2.7.2.15]	0	5,09533E-06	0
K10960_ko00830_RetinolmetabolismMetabolism_Metabolismofcofactorsandvitamins_chlP,bchP,geranylgeranylreductase[EC:1.3.1.83];K10960_ko00900_Terpenoidbackbonebiosynthesis_Metabolism_Metabolismofterpenoidsandpolyketides_chlP,bchP,geranylge	1,03726E-05	0,000147765	3,32215E-05
K10555_ko02010_Ctransporters_Environmentalinformationprocessing_Membranetransport_lsrB,AI-2transportsystemsubstrate-bindingprotein	5,18629E-05	1,01907E-05	2,49161E-05
K13057_ko00500_Starchandsucrosemetabolism_Metabolism_Carbohydratemetabolism_treT,trehalosesynthase[EC:2.4.1.245]	1,03726E-05	0	0
K13849_ko05144_Malaria_HumanDiseases_Infectiousdiseases_RBP,reticulocyte-bindingprotein	0	5,09533E-06	0
K01730_ko00040_Pentoseandglucuronateinterconversions_Metabolism_Carbohydratemetabolism_ogl,oligogalacturonidelyase[EC:4.2.2.6]	1,55589E-05	5,09533E-06	0
K12785_ko05100_Bacterialinvasionofepithelialcells_Humandiseases_Infectiousdiseases_espG,virA,LEE-encodedeffectorEspG;K12785_ko05130_PathogenicEscherichiacoliinfection_HumanDiseases_Infectiousdiseases_espG,virA,LEE-encodedeffectorEspG;K12785_k	0	0	8,30537E-06
K03225_ko02010_Ctransporters_Environmentalinformationprocessing_Membranetransport_yscQ,sctQ,hrcQ,typeIIIsecretionproteinQ	1,55589E-05	5,09533E-06	1,66107E-05
K00481_ko01220_Degradationofaromaticcompounds_Metabolism_Overview_pobA,p-hydroxybenzoate3-monooxygenase[EC:1.14.13.2];K00481_ko00362_Benzoatedegradation_Metabolism_Xenobioticsbiodegradationandmetabolism_pobA,p-hydroxybenzoate3-m	0	5,09533E-06	8,30537E-06
K15045_ko05164_InfluenzaA_HumanDiseases_Infectiousdiseases_RSAD2,radicalS-adenosylmethioninedomain-containingprotein2	2,59315E-05	3,0572E-05	4,98322E-05
K12196_ko04144_Endocytosis_CellularProcesses_Transportandcatabolism_VPS4,vacuolarprotein-sorting-associatedprotein4	1,03726E-05	1,01907E-05	1,66107E-05
K14273_ko00040_Pentoseandglucuronateinterconversions_Metabolism_Carbohydratemetabolism_xdh,xylosedehydrogenase(NAD/NADP)	5,18629E-06	0	0
K14403_ko03015_mRNAsurveillancepathway_GeneticinformationProcessing_Transcription_CPSF3,YSH1,cleavageandpolyadenylationspecificityfactorsubunit3[EC:3.1.27.-]	5,18629E-06	0	8,30537E-06
K00028_ko00620_Pyruvatemetabolism_Metabolism_Carbohydratemetabolism_E1.1.1.39,malatedehydrogenase(decarboxylating)[EC:1.1.1.39];K00028_ko01200_Carbonmetabolism_Metabolism_Overview_E1.1.1.39,malatedehydrogenase(decarboxylating)[EC:1.1	0	1,01907E-05	0
K08687_ko00330_Arginineandprolinemetabolism_Metabolism_Aminoacidmetabolism_E3.5.1.59,N-carbamoylsarcosineamidase[EC:3.5.1.59]	1,03726E-05	5,09533E-06	8,30537E-06
K00318_ko00330_Arginineandprolinemetabolism_Metabolism_Aminoacidmetabolism_PRODH,prolinedehydrogenase[EC:1.5.-.-]	5,18629E-06	5,09533E-05	6,6443E-05
K03184_ko00130_Ubiquinoneandotherterpenoid-quinonebiosynthesis_Metabolism_Metabolismofcofactorsandvitamins_ubiF,2-octaprenyl-3-methyl-6-methoxy-1,4-benzoquinolhydroxylase[EC:1.14.13.-]	5,18629E-06	0	0
K03063_ko03050_Proteasome_GeneticInformationProcessing_Folding,sortinganddegradation_PSMC4,RPT3,26Sproteasomeregulatorysubunit3;K03063_ko05169_Epstein-Barrvirusinfection_HumanDiseases_Infectiousdiseases_PSMC4,RPT3,26Sproteasomeregulat	5,18629E-06	0	0
K06228_ko04340_Hedgehogsignalingpathway_Environmentalinformationprocessing_Signaltrasduction_FU,fused[EC:2.7.11.1];K06228_ko05217_Basalcellcarcinoma_HumanDiseases_Cancers_FU,fused[EC:2.7.11.1];K06228_ko05200_Pathwaysincancer_HumanDise	1,03726E-05	0	0
K11440_ko00260_Glycine,serineandthreonineMetabolism_Metabolism_Aminoacidmetabolism_gbsB,cholinedehydrogenase[EC:1.1.1.1]	0	0	8,30537E-06
K02079_ko00052_Galactosemetabolism_Metabolism_Carbohydratemetabolism_agaA,N-acetylgalactosamine-6-phosphatedeacetylase[EC:3.5.1.25]	0	1,01907E-05	0
K01592_ko00350_Tyrosinemetabolism_Metabolism_Aminoacidmetabolism_E4.1.1.25,tyrosinedecarboxylase[EC:4.1.1.25];K01592_ko00950_Isoquinolinealkaloidbiosynthesis_Metabolism_Biosynthesisofothersecondarymetabolites_E4.1.1.25,tyrosinedecarboxylase	5,18629E-06	0	0
K07797_ko02020_Two-componentsystem_Environmentalinformationprocessing_Signaltrasduction_emrK,multidrugresistanceproteinK	0	5,09533E-06	0
K15038_ko01200_Carbonmetabolism_Metabolism_Overview_K15038,succinyl-CoAreductase[EC:1.2.1.76];K15038_ko00194_Photosynthesisproteins_Metabolism_Energymetabolism_K15038,succinyl-CoAreductase[EC:1.2.1.76]	0	0	1,66107E-05
K10544_ko02010_Ctransporters_Environmentalinformationprocessing_Membranetransport_xylH,D-xylosetransportsystempermeaseprotein	0	5,09533E-06	8,30537E-06
K04112_ko01220_Degradationofaromaticcompounds_Metabolism_Overview_bcrC,badD,benzoyl-CoAreductasesubunitC[EC:1.3.7.8];K04112_ko00362_Benzoatedegradation_Metabolism_Xenobioticsbiodegradationandmetabolism_bcrC,badD,benzoyl-CoAreductas	0	5,09533E-06	8,30537E-06
K00314_ko00260_Glycine,serineandthreonineMetabolism_Metabolism_Aminoacidmetabolism_SARDH,sarcosinedehydrogenase[EC:1.5.8.3]	1,03726E-05	0	0
K10747_ko03410_BaseexcisionrepairGeneticinformationProcessing_ReplicationandRepair_LIG1,DNAligase1[EC:6.5.1.1];K10747_ko03030_DNAreplication_GeneticinformationProcessing_ReplicationandRepair_LIG1,DNAligase1[EC:6.5.1.1];K10747_ko03430_Mism	0	5,09533E-06	0
K07375_ko04540_Gapjunction_Cellgrowthanddeath_Cellularcommunity_TUBB,tubulinbeta;K07375_ko04145_Phagosome_CellularProcesses_Transportandcatabolism_TUBB,tubulinbeta;K07375_ko05130_PathogenicEscherichiacoliinfection_HumanDiseases_Infect	1,03726E-05	0	0
K00830_ko04146_Peroxisome_CellularProcesses_Transportandcatabolism_AGXT,alanine-glyoxylatetransaminase/serine-glyoxylatetransaminase/serine-pyruvatetransaminase[EC:2.6.1.442.6.1.452.6.1.51];K00830_ko00250_Alanine,aspartateandglutamatemetaboli	1,03726E-05	0	0
K00613_ko00330_Arginineandprolinemetabolism_Metabolism_Aminoacidmetabolism_GATM,glycineamidinotransferase[EC:2.1.4.1];K00613_ko00260_Glycine,serineandthreonineMetabolism_Metabolism_Aminoacidmetabolism_GATM,glycineamidinotransferase	3,11177E-05	0	0
K01622_ko00051_Fructoseandmannosemetabolism_Metabolism_Carbohydratemetabolism_K01622,fructose1,6-bisphosphatealdolase/phosphatase[EC:4.1.2.133.1.3.11];K01622_ko00010_Glycolysis/Gluconeogenesis_Metabolism_Carbohydratemetabolism_K0162	0	1,01907E-05	0
K12265_ko05132_Salmonellainfection_HumanDiseases_Infectiousdiseases_norW,nitricoxidereductaseFlRd-NAD(+)reductase[EC:1.18.1.-]	0	1,01907E-05	0
K13921_ko00630_Glyoxylateanddicarboxylatemetabolism_Metabolism_Carbohydratemetabolism_pduQ,1-propanoldehydrogenase	2,59315E-05	2,03813E-05	2,49161E-05
K03532_ko02020_Two-componentsystem_Environmentalinformationprocessing_Signaltrasduction_torC,trimethylamine-N-oxidereductase(cytochromec),cytochromec-typesubunitTorC	0	1,01907E-05	8,30537E-06
K14187_ko00400_Phenylalanine,tyrosineandtryptophanbiosynthesis_Metabolism_Aminoacidmetabolism_tyrA,chorismatemutase/prephenatedehydrogenase[EC:5.4.99.51.3.1.12];K14187_ko00401_Novobiocinbiosynthesis_Metabolism_Biosynthesisofthesecond	2,59315E-05	0	8,30537E-06
K03229_ko02010_Ctransporters_Environmentalinformationprocessing_Membranetransport_yscU,sctU,hrcU,typeIIIsecretionproteinU	3,6304E-05	4,5858E-05	4,98322E-05
K09475_ko02020_Two-componentsystem_Environmentalinformationprocessing_Signaltrasduction_ompC,outermembraneporeproteinC;K09475_ko00312_beta-Lactamresistance_HumanDiseases_Drugresistance_ompC,outermembraneporeproteinC	1,03726E-05	5,09533E-06	1,66107E-05
K11784_ko00130_Ubiquinoneandotherterpenoid-quinonebiosynthesis_Metabolism_Metabolismofcofactorsandvitamins_mqnC,cyclicdehypoxanthinylfutalosinesynthase[EC:1.21.99.2]	0	5,09533E-06	1,66107E-05
K10111_ko02010_Ctransporters_Environmentalinformationprocessing_Membranetransport_malK,mtlK,thuK,multiplesugartransportsystemATP-bindingprotein[EC:3.6.3.-]	5,18629E-06	0	0
K00855_ko01200_Carbonmetabolism_Metabolism_Overview_PRK,prkB,phosphoribulokinase[EC:2.7.1.19];K00855_ko00194_Photosynthesisproteins_Metabolism_Energymetabolism_PRK,prkB,phosphoribulokinase[EC:2.7.1.19]	1,03726E-05	1,5286E-05	0
K13016_ko00520_Aminosugarandnucleotidesugarmetabolism_Metabolism_Carbohydratemetabolism_wbpB,UDP-N-acetyl-2-amino-2-deoxyglucuronatedehydrogenase[EC:1.1.1.335]	5,18629E-06	1,01907E-05	1,66107E-05
K09476_ko02020_Two-componentsystem_Environmentalinformationprocessing_Signaltrasduction_ompF,outermembraneporeproteinF;K09476_ko00312_beta-Lactamresistance_HumanDiseases_Drugresistance_ompF,outermembraneporeproteinF	0	5,09533E-06	8,30537E-06
K11709_ko02010_Ctransporters_Environmentalinformationprocessing_Membranetransport_troD,mntD,znuB,manganese/zinc/irontransportsystempermeaseprotein	2,07452E-05	5,09533E-06	0
K01141_ko03430_Mismatchrepair_GeneticinformationProcessing_ReplicationandRepair_E3.1.11.1,sbcB,exodeoxyribonucleaseI[EC:3.1.11.1]	0	1,01907E-05	0
K03472_ko00750_VitaminB6metabolism_Metabolism_Metabolismofcofactorsandvitamins_epd,D-erythrose4-phosphatedehydrogenase[EC:1.2.1.72]	1,03726E-05	0	0
K10680_ko00633_Nitrotoluenedegradation_Metabolism_Xenobioticsbiodegradationandmetabolism_nemA,N-ethylmaleimidereductase[EC:1.-.-.-]	0	0	1,66107E-05
K07643_ko02020_Two-componentsystem_Environmentalinformationprocessing_Signaltrasduction_basS,two-componentsystem,OmpRfamily,sensorhistidinekinaseBasS[EC:2.7.13.3]	0	1,01907E-05	8,30537E-06
K00094_ko00052_Galactosemetabolism_Metabolism_Carbohydratemetabolism_E1.1.1.251,gatD,galactitol-1-phosphate5-dehydrogenase[EC:1.1.1.251]	5,18629E-06	1,01907E-05	0
K12241_ko01053_Biosynthesisofsiderophoregroupnonribosomalpeptides_Metabolism_Metabolismofterpenoidsandpolyketides_pchG,pyochelinbiosyntheticproteinPchG	0	5,09533E-06	1,66107E-05
K13019_ko00520_Aminosugarandnucleotidesugarmetabolism_Metabolism_Carbohydratemetabolism_wbpI,wlbD,UDP-GlcNAc3NAcAepimerase[EC:5.1.3.23]	1,55589E-05	5,09533E-06	0,000141191
K09971_ko02010_Ctransporters_Environmentalinformationprocessing_Membranetransport_aapM,bztC,generalL-aminoacidtransportsystempermeaseprotein	0	5,09533E-06	0
K11780_ko00194_Photosynthesisproteins_Metabolism_Energymetabolism_cofG,FOsynthasesubunit1[EC:2.5.1.77]	5,18629E-06	0	0
K14082_ko01200_Carbonmetabolism_Metabolism_Overview_mtbA,[methyl-Co(III)methylamine-specificcorrinoidprotein]:coenzymeMmethyltransferase[EC:2.1.1.247];K14082_ko00194_Photosynthesisproteins_Metabolism_Energymetabolism_mtbA,[methyl-Co(I	1,03726E-05	1,01907E-05	1,66107E-05
K09969_ko02010_Ctransporters_Environmentalinformationprocessing_Membranetransport_aapJ,bztA,generalL-aminoacidtransportsystemsubstrate-bindingprotein	1,03726E-05	0	1,66107E-05
K09523_ko04141_Proteinprocessinginendoplasmicreticulum_GeneticInformationProcessing_Folding,sortinganddegradation_DNAJC3,DnaJhomologsubfamilyCmember3;K09523_ko05164_InfluenzaA_HumanDiseases_Infectiousdiseases_DNAJC3,DnaJhomologsubfa	1,03726E-05	0	0
K02064_ko02010_Ctransporters_Environmentalinformationprocessing_Membranetransport_thiB,tbpA,thiaminetransportsystemsubstrate-bindingprotein	2,07452E-05	3,0572E-05	0
K02703_ko00195_Photosynthesis_Metabolism_Energymetabolism_psbA,photosystemIIP680reactioncenterD1protein	0	5,09533E-06	0

K06965_ko03015_mRNAsurveillancepathway_GeneticinformationProcessing_Transcription_PELO,DOM34,pelA,proteinpelota	0	5,09533E-06	0
K13339_ko04146_Peroxisome_CellularProcesses_Transportandcatabolism_PEX6,PXAAA1,peroxin-6	0	1,01907E-05	2,49161E-05
K00004_ko00630_Glyoxylateanddicarboxylatemetabolism_Metabolism_Carbohydratemetabolism_BDH,butB,(R,R)-butanedioldehydrogenase/meso-butanedioldehydrogenase/diacetylreductase[EC:1.1.1.41.1.1.-1.1.1.303]	1,03726E-05	2,03813E-05	8,30537E-06
K00186_ko00280_Valine,leucineandisoleucinedegradation_Metabolism_Aminoacidmetabolism_vorA,2-oxoisovaleratеferredoxinoxidoreductase,alphasubunit[EC:1.2.7.7]	0	5,09533E-06	0
K01777_ko00330_Arginineandprolinemetabolism_Metabolism_Aminoacidmetabolism_E5.1.1.4,prolineracemase[EC:5.1.1.4]	4,66766E-05	3,56673E-05	3,32215E-05
K03201_ko02010_Ctransporters_Environmentalinformationprocessing_Membranetransport_virB6,lvhB6,typeIVsecretionsystemproteinVirB6	0	5,09533E-06	3,32215E-05
K03408_ko02020_Two-componentsystem_Environmentalinformationprocessing_Signaltrasduction_cheW,purine-bindingchemotaxisproteinCheW;K03408_ko02030_Bacterialchemotaxis_Organismalsystem_Cellmobility_cheW,purine-bindingchemotaxisproteinChe	4,66766E-05	5,09533E-06	1,66107E-05
K03417_ko00630_Glyoxylateanddicarboxylatemetabolism_Metabolism_Carbohydratemetabolism_prpB,methylisocitratelyase[EC:4.1.3.30]	2,59315E-05	1,5286E-05	8,30537E-06
K04568_ko00970_Aminoacyl-tRNAbiosynthesis_Geneticinformationandprocessing_Transcription_poxA,lysyl-tRNAsynthetase,classII[EC:6.1.1.6]	0	0	8,30537E-06
K00413_ko02020_Two-componentsystem_Environmentalinformationprocessing_Signaltrasduction_CYC1,CYT1,petC,ubiquinol-cytochromecreductasecytochromec1subunit;K00413_ko05010_Alzheimer'sdisease_HumanDiseases_Degenerativediseases_CYC1,CYT1,p	0	5,09533E-06	0
K00374_ko02020_Two-componentsystem_Environmentalinformationprocessing_Signaltrasduction_narI,nitratereductasegammasubunit[EC:1.7.99.4];K00374_ko00910_Nitrogenmetabolism_Metabolism_Energymetabolism_narI,nitratereductasegammasubunit[EC	5,18629E-06	1,5286E-05	0
K00673_ko00330_Arginineandprolinemetabolism_Metabolism_Aminoacidmetabolism_astA,argininеN-succinyltransferase[EC:2.3.1.109]	1,55589E-05	1,01907E-05	0
K10681_ko02020_Two-componentsystem_Environmentalinformationprocessing_Signaltrasduction_saeS,two-componentsystem,OmpRfamily,sensorhistidinekinaseSaeS[EC:2.7.13.3]	5,18629E-06	1,01907E-05	0
K00263_ko00290_Valine,leucineandisoleucinebiosynthesis_Metabolism_Aminoacidmetabolism_E1.4.1.9,leucinedehydrogenase[EC:1.4.1.9];K00263_ko00280_Valine,leucineandisoleucinedegradation_Metabolism_Aminoacidmetabolism_E1.4.1.9,leucinedehydroge	1,03726E-05	0	0
K12339_ko00270_Cysteineandmethioninemetabolism_Metabolism_Aminoacidmetabolism_cysM,cysteinesynthaseB[EC:2.5.1.47];K12339_ko00920_Sulfurmetabolism_Metabolism_Energymetabolism_cysM,cysteinesynthaseB[EC:2.5.1.47];K12339_ko01230_Biosyn	4,14903E-05	2,03813E-05	3,32215E-05
K12454_ko00520_Aminosugarandnucleotidesugarmetabolism_Metabolism_Carbohydratemetabolism_rfbE,CDP-paratose2-epimerase[EC:5.1.3.10]	0	5,09533E-06	0
K11629_ko02020_Two-componentsystem_Environmentalinformationprocessing_Signaltrasduction_bceS,two-componentsystem,OmpRfamily,bacitracinresistancesensorhistidinekinaseBceS[EC:2.7.13.3]	4,14903E-05	4,5858E-05	0,000132886
K11517_ko04146_Peroxisome_CellularProcesses_Transportandcatabolism_HAO,(S)-2-hydroxy-acidoxidase[EC:1.1.3.15];K11517_ko00630_Glyoxylateanddicarboxylatemetabolism_Metabolism_Carbohydratemetabolism_HAO,(S)-2-hydroxy-acidoxidase[EC:1.1.3.15]	1,03726E-05	0	8,30537E-06
K05921_ko00350_Tyrosinemetabolism_Metabolism_Aminoacidmetabolism_hpaG,5-oxopent-3-ene-1,2,5-tricarboxylatedecarboxylase/2-hydroxyhepta-2,4-diene-1,7-dioateisomerase[EC:4.1.1.685.3.3.-];K05921_ko01220_Degradationofaromaticcompounds_Metab	2,07452E-05	5,09533E-06	8,30537E-06
K14080_ko01200_Carbonmetabolism_Metabolism_Overview_mtaA,[methyl-Co(III)methanol-specificcorrinoidprotein]:coenzymeMmethyltransferase[EC:2.1.1.246];K14080_ko00194_Photosynthesisproteins_Metabolism_Energymetabolism_mtaA,[methyl-Co(III)m	1,03726E-05	5,09533E-06	0
K03278_ko00540_Lipopolysaccharidebiosynthesis_Metabolism_Glycanbiosynthesisandmetabolism_waaI,rfaI,UDP-D-galactose:(glucosyl)LPSalpha-1,3-D-galactosyltransferase[EC:2.4.1.44]	2,07452E-05	2,03813E-05	0
K04109_ko01220_Degradationofaromaticcompounds_Metabolism_Overview_hcrB,hbaD,4-hydroxybenzoyl-CoAreductasesubunitbeta[EC:1.3.7.9];K04109_ko00627_Aminobenzoatedegradation_Metabolism_Xenobioticsbiodegradationandmetabolism_hcrB,hbaD,4	0	0	1,66107E-05
K01502_ko00643_Styrenedegradation_Metabolism_Xenobioticsbiodegradationandmetabolism_E3.5.5.7,aliphaticnitrilase[EC:3.5.5.7]	5,18629E-06	0	0
K12675_ko00331_Clavulanicacidbiosynthesis_Metabolism_Biosynthesisofthersecondarymetabolites_cs,clavaminatesynthase[EC:1.14.11.21]	5,18629E-06	0	0
K14333_ko00627_Aminobenzoatedegradation_Metabolism_Xenobioticsbiodegradationandmetabolism_DHBD,2,3-dihydroxybenzoatedecarboxylase[EC:4.1.1.46];K14333_ko00362_Benzoatedegradation_Metabolism_Xenobioticsbiodegradationandmetabolism_DH	0	1,01907E-05	0
K01920_ko00480_Glutathionemetabolism_Metabolism_Metabolismofotheraminoacids_gshB,GSS,glutathionesynthase[EC:6.3.2.3]	0	5,09533E-06	8,30537E-06
K10550_ko02010_Ctransporters_Environmentalinformationprocessing_Membranetransport_alsC,D-allosetransportsystempermeaseprotein	5,18629E-06	0	1,66107E-05
K04020_ko00620_Pyruvatemetabolism_Metabolism_Carbohydratemetabolism_eutD,phosphotransacetylase	1,03726E-05	0	0
K00166_ko00280_Valine,leucineandisoleucinedegradation_Metabolism_Aminoacidmetabolism_BCKDHA,bkdA1,2-oxoisovaleratedehydrogenaseE1componentalphasubunit[EC:1.2.4.4]	0	1,01907E-05	0
K13890_ko02010_Ctransporters_Environmentalinformationprocessing_Membranetransport_gsiC,glutathionetransportsystempermeaseprotein	5,18629E-06	5,09533E-06	1,66107E-05
K01640_ko04146_Peroxisome_CellularProcesses_Transportandcatabolism_E4.1.3.4,HMGCL,hmgL,hydroxymethylglutaryl-CoAlyase[EC:4.1.3.4];K01640_ko00280_Valine,leucineandisoleucinedegradation_Metabolism_Aminoacidmetabolism_E4.1.3.4,HMGCL,hmgL,I	6,22355E-05	5,09533E-06	4,15269E-05
K03680_ko03013_RNAtransport_GeneticinformationProcessing_Transcription_EIF2B4,translationinitiationfactorIF-2Bsubunitdelta	0	2,54767E-05	0
K06073_ko02010_Ctransporters_Environmentalinformationprocessing_Membranetransport_ABC.VB12.P,btuC,vitaminB12transportsystempermeaseprotein	0	5,09533E-06	0
K01499_ko01200_Carbonmetabolism_Metabolism_Overview_mch,methenyltetrahydromethanopterincyclohydrolase[EC:3.5.4.27];K01499_ko00194_Photosynthesisproteins_Metabolism_Energymetabolism_mch,methenyltetrahydromethanopterincyclohydrolase|	1,55589E-05	0	0
K02317_ko03440_Homologousrecombination_GeneticinformationProcessing_ReplicationandRepair_dnaT,DNAreplicationproteinDnaT	2,07452E-05	1,01907E-05	0
K04799_ko03410_Baseexcisionrepair_GeneticinformationProcessing_ReplicationandRepair_FEN1,RAD2,flapendonuclease-1[EC:3.-.-.-];K04799_ko03030_DNAreplication_GeneticinformationProcessing_ReplicationandRepair_FEN1,RAD2,flapendonuclease-1[EC:3.-.-	0	0	1,66107E-05
K00885_ko00520_Aminosugarandnucleotidesugarmetabolism_Metabolism_Carbohydratemetabolism_nanK,N-acylmannosaminekinase[EC:2.7.1.60]	5,18629E-06	0	0
K02452_ko02010_Ctransporters_Environmentalinformationprocessing_Membranetransport_gspC,generalsecretionpathwayproteinC	1,03726E-05	1,5286E-05	0
K04102_ko00624_Polycyclicaromatichydrocarbondegradation_Metabolism_Xenobioticsbiodegradationandmetabolism_pht5,4,5-dihydroxyphthalatedecarboxylase[EC:4.1.1.55]	0	5,09533E-06	0
K01597_ko00900_Terpenoidbackbonebiosynthesis_Metabolism_Metabolismofterpenoidsandpolyketides_MVD,mvaD,diphosphomevalonatedecarboxylase[EC:4.1.1.33]	3,11177E-05	1,01907E-05	8,30537E-06
K05714_ko00360_Phenylalaninemetabolism_Metabolism_Aminoacidmetabolism_mhpC,2-hydroxy-6-oxonona-2,4-dienedioatehydrolase[EC:3.7.1.14];K05714_ko01220_Degradationofaromaticcompounds_Metabolism_Overview_mhpC,2-hydroxy-6-oxonona-2,4-di	2,07452E-05	4,07627E-05	4,15269E-05
K00090_ko00030_Pentosephosphatepathway_Metabolism_Carbohydratemetabolism_E1.1.1.215,gluconate2-dehydrogenase[EC:1.1.1.215]	5,18629E-06	1,5286E-05	0
K11131_ko03008_Ribosomebiogenesisineukaryotes_GeneticinformationProcessing_Transcription_DKC1,NOLA4,CBF5,H/ACAribonucleoproteincomplexsubunit4[EC:5.4.99.-]	5,18629E-06	0	0
K01233_ko00520_Aminosugarandnucleotidesugarmetabolism_Metabolism_Carbohydratemetabolism_csn,chitosanase[EC:3.2.1.132]	1,03726E-05	0	0
K15039_ko01200_Carbonmetabolism_Metabolism_Overview_K15039,3-hydroxypropionatedehydrogenase(NADP+)[EC:1.1.1.298];K15039_ko00194_Photosynthesisproteins_Metabolism_Energymetabolism_K15039,3-hydroxypropionatedehydrogenase(NADP+)[EC	0	2,03813E-05	0
K11708_ko02010_Ctransporters_Environmentalinformationprocessing_Membranetransport_troC,mntC,znuB,manganese/zinc/irontransportsystempermeaseprotein	5,18629E-06	5,09533E-06	8,30537E-06
K05526_ko00330_Arginineandprolinemetabolism_Metabolism_Aminoacidmetabolism_astE,succinylglutamatedesuccinylase[EC:3.5.1.96]	0	5,09533E-06	0
K11124_ko03015_mRNAsurveillancepathway_GeneticinformationProcessing_Transcription_SMG6,EST1A,proteinSMG6[EC:3.1.-.-]	5,18629E-06	0	0
K00869_ko04146_Peroxisome_CellularProcesses_Transportandcatabolism_E2.7.1.36,MVK,mvaK1,mevalonatekinase[EC:2.7.1.36];K00869_ko00900_Terpenoidbackbonebiosynthesis_Metabolism_Metabolismofterpenoidsandpolyketides_E2.7.1.36,MVK,mvaK1,mev	5,18629E-06	1,5286E-05	8,30537E-06
K02634_ko00195_Photosynthesis_Metabolism_Energymetabolism_petA,apocytochromef	0	0	1,66107E-05
K05356_ko00900_Terpenoidbackbonebiosynthesis_Metabolism_Metabolismofterpenoidsandpolyketides_SPS,sds,all-trans-nonaprenyl-diphosphatesynthase[EC:2.5.1.842.5.1.85]	3,11177E-05	3,56673E-05	2,49161E-05
K01590_ko00340_Histidinemetabolism_Metabolism_Aminoacidmetabolism_hdc,HDC,histidinedecarboxylase[EC:4.1.1.22]	0	1,01907E-05	8,30537E-06
K05288_ko00563_Glycosylphosphatidylinositol(GPI)-anchorbiosynthesis_Metabolism_Glycanbiosynthesisandmetabolism_PIGO,phosphatidylinositolglycan,classO	5,18629E-06	6,1144E-05	0
K11075_ko02010_Ctransporters_Environmentalinformationprocessing_Membranetransport_potH,putrescinetransportsystempermeaseprotein	0	0	1,66107E-05
K10755_ko03030_DNAreplication_GeneticinformationProcessing_ReplicationandRepair_RFC2_4,replicationfactorCsubunit2/4;K10755_ko03430_Mismatchrepair_GeneticinformationProcessing_ReplicationandRepair_RFC2_4,replicationfactorCsubunit2/4;K10755_	1,03726E-05	0	1,66107E-05
K07790_ko02020_Two-componentsystem_Environmentalinformationprocessing_Signaltrasduction_pagO,putativemembraneproteinPagO	0	2,03813E-05	0
K00194_ko01200_Carbonmetabolism_Metabolism_Overview_cdhD,acsD,acetyl-CoAdecarbonylase/synthasecomplexsubunitdelta[EC:2.1.1.245];K00194_ko00194_Photosynthesisproteins_Metabolism_Energymetabolism_cdhD,acsD,acetyl-CoAdecarbonylase/synth	1,55589E-05	0,000147765	9,13591E-05
K01458_ko00340_Histidinemetabolism_Metabolism_Aminoacidmetabolism_E3.5.1.68,N-formylglutamatedeformylase[EC:3.5.1.68];K01458_ko00630_Glyoxylateanddicarboxylatemetabolism_Metabolism_Carbohydratemetabolism_E3.5.1.68,N-formylglutamatede	0	5,09533E-06	2,49161E-05
K02301_ko00190_Oxidativephosphorylation_Metabolism_Energymetabolism_cyoE,protohemeIXfarnesyltransferase[EC:2.5.1.-];K02301_ko00830_Retinolmetabolism_Metabolism_Metabolismofcofactorsandvitamins_cyoE,protohemeIXfarnesyltransferase[EC:2.5.1	0	1,01907E-05	1,66107E-05
K13874_ko00052_Galactosemetabolism_Metabolism_Carbohydratemetabolism_K13874,araB,L-arabinonolactonase[EC:3.1.1.15]	1,03726E-05	0	4,98322E-05
K01068_ko01040_Biosynthesisofunsaturatedfattyacids_Metabolism_Lipidmetabolism_ACOT1_2_4,acyl-coenzymeAthioesterase1/2/4[EC:3.1.2.2];K01068_ko00062_fattyacidelongation_Metabolism_Lipidmetabolism_ACOT1_2_4,acyl-coenzymeAthioesterase1/2/4[	1,03726E-05	0	0
K00220_ko00400_Phenylalanine,tyrosineandtryptophanbiosynthesis_Metabolism_Aminoacidmetabolism_tyrC,cyclohexadieny/prephenatedehydrogenase[EC:1.3.1.431.3.1.12];K00220_ko00401_Novobiocinbiosynthesis_Metabolism_Biosynthesisofthersecondaryı	1,03726E-05	1,01907E-05	1,66107E-05
K01561_ko00625_Chloroalkaneandchloroalkenedegradation_Metabolism_Xenobioticsbiodegradationandmetabolism_dehH,haloacetatedehalogenase[EC:3.8.1.3];K01561_ko00361_Chlorocyclohexaneandchlorobenzenedegradation_Metabolism_Xenobioticsbiodeg	0	0	8,30537E-06
K12605_ko03018_RNAdegradation_GeneticInformationProcessing_Folding,sortinganddegradation_CNOT2,NOT2,CCR4-NOTtranscriptioncomplexsubunit2	1,03726E-05	0	0
K00446_ko01220_Degradationofaromaticcompounds_Metabolism_Overview_dmpB,xylE,catechol2,3-dioxygenase[EC:1.13.11.2];K00446_ko00362_Benzoatedegradation_Metabolism_Xenobioticsbiodegradationandmetabolism_dmpB,xylE,catechol2,3-dioxygenase	5,18629E-06	0	0
K07252_ko00513_VarioustypesofN-glycanbiosynthesis_Metabolism_Glycanbiosynthesisandmetabolism_E3.6.1.43,dolichyldiphosphatase[EC:3.6.1.43]	0	0	8,30537E-06
K01061_ko00361_Chlorocyclohexaneandchlorobenzenedegradation_Metabolism_Xenobioticsbiodegradationandmetabolism_E3.1.1.45,carboxymethylenebutenolidase[EC:3.1.1.45];K01061_ko00364_Fluorobenzoatedegradation_Metabolism_Xenobioticsbiodegrac	3,6304E-05	0	0
K06606_ko00630_Glyoxylateanddicarboxylatemetabolism_Metabolism_Carbohydratemetabolism_iolI,2-keto-myo-inositolisomerase[EC:5.3.99.11]	2,59315E-05	1,01907E-05	0
K01440_ko00760_Nicotinateandnicotinamidemetabolism_Metabolism_Metabolismofcofactorsandvitamins_PNC1,nicotinamidase[EC:3.5.1.19]	0	0	8,30537E-06
K00543_ko00380_Tryptophanmetabolism_Metabolism_Aminoacidmetabolism_ASMT,acetylserotoninN-methyltransferase[EC:2.1.1.4]	0	1,01907E-05	0

K12405_ko04146_Peroxisome_CellularProcesses_Transportandcatabolism_HSD17B4,3-hydroxyacyl-CoAdehydrogenase/3a,7a,12a-trihydroxy-5b-cholest-24-enoyl-CoAhydratase[EC:1.1.1.354.2.1.107];K12405_ko00120_Primarybileacidbiosynthesis_Metabolism_Lipi	0	5,09533E-06	0
K14168_ko04122_Sulfurrelaysystem_GeneticInformationProcessing_Folding,sortinganddegradation_CTU1,NCS6,cytoplasmictRNA2-thiolationprotein1[EC:2.7.7.-]	1,55589E-05	0	2,49161E-05
K10001_ko02010_Ctransporters_Environmentalinformationprocessing_Membranetransport_gltI,aatJ,glutamate/aspartatetransportsystemsubstrate-bindingprotein;K10001_ko02020_Two-componentsystem_Environmentalinformationprocessing_Signaltrasductior	0	0	1,66107E-05
K14629_ko01057_BiosynthesisoftypeIIpolyketideproducts_Metabolism_Metabolismofterpenoidsandpolyketides_actVI4,enoylreductase	0	5,09533E-06	1,66107E-05
K01517_ko00564_Glycerophospholipidmetabolism_Metabolism_Lipidmetabolism_ADPRM,manganese-dependentADP-ribose/CDP-alcoholdiphosphatase[EC:3.6.1.133.6.1.163.6.1.53];K01517_ko00230_Purinemetabolism_Metabolism_Nucleotidemetabolism_ADPI	5,18629E-06	0	1,66107E-05
K00423_ko00052_Galactosemetabolism_Metabolism_Carbohydratemetabolism_E1.10.3.3,L-ascorbateoxidase[EC:1.10.3.3]	1,03726E-05	0	0
K14274_ko00040_Pentoseandglucuronateinterconversions_Metabolism_Carbohydratemetabolism_K14274,D-xylonolactonase	0	0	1,66107E-05
K03066_ko03050_Proteasome_GeneticInformationProcessing_Folding,sortinganddegradation_PSMC5,RPT6,26Sproteasomeregulatorysubunit6;K03066_ko05169_Epstein-Barrvirusinfection_HumanDiseases_Infectiousdiseases_PSMC5,RPT6,26Sproteasomeregulat	0	1,01907E-05	0
K04073_ko00360_Phenylalaninemetabolism_Metabolism_Aminoacidmetabolism_mhpF,acetaldehydedehydrogenase[EC:1.2.1.10];K04073_ko00630_Glyoxylateanddicarboxylatemetabolism_Metabolism_Carbohydratemetabolism_mhpF,acetaldehydedehydrogena	0	0	8,30537E-06
K03064_ko03050_Proteasome_GeneticInformationProcessing_Folding,sortinganddegradation_PSMC6,RPT4,26Sproteasomeregulatorysubunit4;K03064_ko05169_Epstein-Barrvirusinfection_HumanDiseases_Infectiousdiseases_PSMC6,RPT4,26Sproteasomeregulat	0	0	1,66107E-05
K00412_ko02020_Two-componentsystem_Environmentalinformationprocessing_Signaltrasduction_CYTB,petB,ubiquinol-cytochromecreductasecytochromebsubunit;K00412_ko05010_Alzheimer'sdisease_HumanDiseases_Degenerativediseases_CYTB,petB,ubiquin	5,18629E-06	0	0
K13519_ko00561_Glycerolipidmetabolism_Metabolism_Lipidmetabolism_LPT1,ALE1,lysophospholipidacyltransferase[EC:2.3.1.512.3.1.232.3.1.-];K13519_ko00564_Glycerophospholipidmetabolism_Metabolism_Lipidmetabolism_LPT1,ALE1,lysophospholipidacyltra	1,03726E-05	0	0
K00672_ko01200_Carbonmetabolism_Metabolism_Overview_ftr,formylmethanofuran--tetrahydromethanopterinN-formyltransferase[EC:2.3.1.101];K00672_ko00194_Photosynthesisproteins_Metabolism_Energymetabolism_ftr,formylmethanofuran--tetrahydrom	5,18629E-06	0	0
K08318_ko00630_Glyoxylateanddicarboxylatemetabolism_Metabolism_Carbohydratemetabolism_yihU,4-hydroxybutyratedehydrogenase/sulfolactaldehyde3-reductase[EC:1.1.1.611.1.1.373];K08318_ko01200_Carbonmetabolism_Metabolism_Overview_yihU,4-hy	0	0	1,66107E-05
K13799_ko00770_PantothenateandCoAbiosynthesis_Metabolism_MetabolismofcofactorsandvitaminspanC-cmk,pantoateligase/cytidylatekinase[EC:6.3.2.12.7.4.14];K13799_ko00410_beta-Alaninemetabolism_Metabolism_MetabolismofotheraminoacidspanC-cr	0	5,09533E-06	0
K01431_ko00770_PantothenateandCoAbiosynthesis_Metabolism_MetabolismofcofactorsandvitaminsUPB1,beta-ureidopropionase[EC:3.5.1.6];K01431_ko00410_beta-Alaninemetabolism_Metabolism_MetabolismofotheraminoacidsUPB1,beta-ureidopropionase	5,18629E-06	0	0
K02046_ko02010_Ctransporters_Environmentalinformationprocessing_Membranetransport_cysU,sulfatetransportsystempermeaseprotein;K02046_ko00920_Sulfurmetabolism_Metabolism_Energymetabolism_cysU,sulfatetransportsystempermeaseprotein	3,6304E-05	5,09533E-06	1,66107E-05
K10805_ko01040_BiosynthesisofunsaturatedfattyacidsMetabolism_Lipidmetabolism_tesB,acyl-CoAthioesteraseII[EC:3.1.2.-]	1,03726E-05	1,01907E-05	0
K06685_ko04111_Cellcycle-yeast_CellularProcesses_Cellgrowthanddeath_MOB1,Mats,MOBkinaseactivator1;K06685_ko04390_Hipposignalingpathway_Environmentalinformationprocessing_Signaltrasduction_MOB1,Mats,MOBkinaseactivator1;K06685_ko04390_I	0	0	1,66107E-05
K04071_ko00785_Lipoicacidmetabolism_Metabolism_Metabolismofcofactorsandvitamins_E1.1.1.220,6-pyruvoyltetrahydropterin2'-reductase[EC:1.1.1.220]	0	5,09533E-06	0
K05523_ko00620_Pyruvatemetabolism_Metabolism_Carbohydratemetabolism_hchA,molecularchaperoneHsp31andglyoxalase3[EC:4.2.1.130]	5,18629E-06	0	0
K10202_ko02010_Ctransporters_Environmentalinformationprocessing_Membranetransport_ABC.NGC.P1,N-acetylglucosaminetransportsystempermeaseprotein	2,07452E-05	0,000183432	0,00249161
K11605_ko02010_Ctransporters_Environmentalinformationprocessing_Membranetransport_sitC,manganese/irontransportsystempermeaseprotein	0	0	8,30537E-06
K00218_ko00830_RetinolmetabolismMetabolismofcofactorsandvitamins_E1.3.1.33,por,protochlorophyllidereductase[EC:1.3.1.33]	1,55589E-05	0	6,6443E-05
K02289_ko00195_Photosynthesis_Metabolism_Energymetabolism_cpcF,phycocyanobilinlyasebetasubunit	0	5,09533E-06	8,30537E-06
K00205_ko01200_Carbonmetabolism_Metabolism_Overview_fwdF,fmdF,4Fe-4Sferredoxin;K00205_ko00194_Photosynthesisproteins_Metabolism_Energymetabolism_fwdF,fmdF,4Fe-4Sferredoxin	1,03726E-05	0	1,66107E-05
K00551_ko00564_Glycerophospholipidmetabolism_Metabolism_Lipidmetabolism_PEMT,phosphatidylethanolamineN-methyltransferase[EC:2.1.1.17]	0	1,01907E-05	1,66107E-05
K01252_ko01053_BiosynthesisofsiderophoregroupnonribosomalpeptidesMetabolism_Metabolismofterpenoidsandpolyketides_entB,dhbB,vibB,mxcF,bifunctionalisochorismatelyase/arylcarrierprotein[EC:3.3.2.1]	1,03726E-05	0	0
K03119_ko00920_Sulfurmetabolism_Metabolism_Energymetabolism_tauD,taurinedioxygenase[EC:1.14.11.17];K03119_ko00430_Taurineandhypotaurinemetabolism_Metabolism_Metabolismofotheraminoacids_tauD,taurinedioxygenase[EC:1.14.11.17]	5,18629E-06	0	8,30537E-06
K06163_ko00440_PhosphonateandphosphinatemetabolismMetabolism_Metabolismofotheraminoacids_phnJ,alpha-D-ribose1-methylphosphonate5-phosphateC-Plyase[EC:4.7.1.1]	1,03726E-05	0	8,30537E-06
K07688_ko02020_Two-componentsystem_Environmentalinformationprocessing_Signaltrasduction_fimZ,two-componentsystem,NarLfamily,responseregulator,fimbrialZprotein,FimZ	0	5,09533E-06	0
K03047_ko03020_RNApolymerase_GeneticinformationProcessing_Transcription_rpoD,DNA-directedRNApolymerasesubunitD[EC:2.7.7.6];K03047_ko00230_Purinemetabolism_Metabolism_Nucleotidemetabolism_rpoD,DNA-directedRNApolymerasesubunitD[EC:2.	1,55589E-05	0	0
K13509_ko00561_Glycerolipidmetabolism_Metabolism_Lipidmetabolism_LPAAT,AGPAT1,AGPAT2,lysophosphatidateacyltransferase[EC:2.3.1.51];K13509_ko00564_Glycerophospholipidmetabolism_Metabolism_Lipidmetabolism_LPAAT,AGPAT1,AGPAT2,lysophosp	0	5,09533E-06	0
K02815_ko02010_Ctransporters_Environmentalinformationprocessing_Membranetransport_PTS-Sor-EIID,sorM,PTSsystem,sorbose-specificIIDcomponent;K02815_ko00051_Fructoseandmannosemetabolism_Metabolism_Carbohydratemetabolism_PTS-Sor-EIID,so	0	5,09533E-06	0
K07026_ko00051_Fructoseandmannosemetabolism_Metabolism_Carbohydratemetabolism_E3.1.3.70,mannosyl-3-phosphoglyceratephosphatase[EC:3.1.3.70]	2,07452E-05	0	0
K00319_ko01200_Carbonmetabolism_Metabolism_Overview_mtd,methylenetetrahydromethanopterindehydrogenase[EC:1.5.98.1];K00319_ko00194_Photosynthesisproteins_Metabolism_Energymetabolism_mtd,methylenetetrahydromethanopterindehydrogena	0	0	1,66107E-05
K14727_ko01220_Degradationofaromaticcompounds_Metabolism_Overview_pcaL,3-oxoadipateenol-lactonase/4-carboxymuconolactonedecarboxylase[EC:3.1.1.244.1.1.44];K14727_ko00362_Benzoatedegradation_Metabolism_Xenobioticsbiodegradationandmet	1,03726E-05	1,01907E-05	0
K14598_ko00906_Carotenoidbiosynthesis_Metabolism_Metabolismofterpenoidsandpolyketides_cruD,chlorobactenelauroyltransferase	5,18629E-06	5,09533E-06	0
K14538_ko03008_Ribosomebiogenesisineukaryotes_GeneticinformationProcessing_Transcription_NUG1,GNL3,nuclearGTP-bindingprotein	1,03726E-05	0	0
K10702_ko01220_Degradationofaromaticcompounds_Metabolism_Overview_todF,2-hydroxy-6-oxohepta-2,4-dienoatehydroxylase[EC:3.7.1.-];K10702_ko00622_Xylenedegradation_Metabolism_Xenobioticsbiodegradationandmetabolism_todF,2-hydroxy-6-oxohep	1,03726E-05	5,09533E-06	8,30537E-06
K00019_ko00630_Glyoxylateanddicarboxylatemetabolism_Metabolism_Carbohydratemetabolism_E1.1.1.30,bdh,3-hydroxybutyratedehydrogenase[EC:1.1.1.30];K00019_ko00071_Fattyaciddegradation_Metabolism_Lipidmetabolism_E1.1.1.30,bdh,3-hydroxybutyra	2,07452E-05	3,0572E-05	2,49161E-05
K00591_ko00130_Ubiquinoneandotherterpenoid-quinonebiosynthesis_Metabolism_MetabolismofcofactorsandvitaminsCOQ3,hexaprenyldihydroxybenzoatemethyltransferase[EC:2.1.1.114]	0	0	1,66107E-05
K11641_ko02020_Two-componentsystem_Environmentalinformationprocessing_Signaltrasduction_natR,two-componentsystem,LytTfamily,responseregulatorNatR	1,03726E-05	5,09533E-06	3,32215E-05
K02509_ko00350_Tyrosinemetabolism_Metabolism_Aminoacidmetabolism_hpaH,2-oxo-hept-3-ene-1,7-dioatehydratase[EC:4.2.1.-]	1,03726E-05	5,09533E-06	0
K06858_ko02010_Ctransporters_Environmentalinformationprocessing_Membranetransport_ABC.VB12.S1,btuF,vitaminB12transportsystemsubstrate-bindingprotein	1,03726E-05	5,09533E-06	0
K07695_ko02020_Two-componentsystem_Environmentalinformationprocessing_Signaltrasduction_devR,two-componentsystem,NarLfamily,responseregulatorDevR	0	0	8,30537E-06
K12660_ko00051_Fructoseandmannosemetabolism_Metabolism_Carbohydratemetabolism_rhmA,2-dehydro-3-deoxy-L-rhamnonatealdolase[EC:4.1.2.53]	0	0	2,49161E-05
K01366_ko04142_Lysosome_CellularProcesses_Transportandcatabolism_CTSH,cathepsinH[EC:3.4.22.16]	0	0	8,30537E-06
K07782_ko02020_Two-componentsystem_Environmentalinformationprocessing_Signaltrasduction_sdiA,LuxRfamilytranscriptionalregulator	1,03726E-05	1,01907E-05	0
K08059_ko04612_Antigenprocessingandpresentation_Organismalsystem_Immunesystem_IFI30,GILT,interferon,gamma-inducibleprotein30	1,03726E-05	0	8,30537E-06
K02386_ko02040_Flagellarassembly_Organismalsystem_Cellmobility_flgA,flagellabasalbodyP-ringformationproteinFlgA	3,11177E-05	0	8,30537E-06
K05573_ko00190_Oxidativephosphorylation_Metabolism_Energymetabolism_ndhB,NAD(P)H-quinoneoxidoreductasesubunit2[EC:1.6.5.3]	1,03726E-05	0	8,30537E-06
K10921_ko05111_Vibriocholeraepathogeniccycle_HumanDiseases_Infectiousdiseases_toxR,choleratoxintranscriptionalactivator	0	0	1,66107E-05
K00332_ko00190_Oxidativephosphorylation_Metabolism_Energymetabolism_nuoC,NADH-quinoneoxidoreductasesubunitC[EC:1.6.5.3]	1,55589E-05	1,01907E-05	0
K14555_ko03008_Ribosomebiogenesisineukaryotes_GeneticinformationProcessing_Transcription_UTP13,TBL3,U3smallnucleolarRNA-associatedprotein13	0	2,03813E-05	0
K11264_ko00630_Glyoxylateanddicarboxylatemetabolism_Metabolism_Carbohydratemetabolism_mmcD,methylmalonyl-CoAdecarboxylase[EC:4.1.1.41]	0	0	1,66107E-05
K03237_ko04141_Proteinprocessinginendoplasmicreticulum_GeneticInformationProcessing_Folding,sortinganddegradation_EIF2S1,translationinitiationfactor2subunit1;K03237_ko03013_RNAtransport_GeneticinformationProcessing_Transcription_EIF2S1,translat	5,18629E-06	0	0
K02391_ko02040_Flagellarassembly_Organismalsystem_Cellmobility_flgF,flagellarbasal-bodyrodproteinFlgF	5,18629E-06	0	0
K08723_ko00760_Nicotinateandnicotinamidemetabolism_Metabolism_MetabolismofcofactorsandvitaminsyjjG,5'-nucleotidase[EC:3.1.3.5];K08723_ko00230_Purinemetabolism_Metabolism_Nucleotidemetabolism_yjjG,5'-nucleotidase[EC:3.1.3.5];K08723_ko002	1,03726E-05	1,5286E-05	0
K10780_ko00061_Fattyacidbiosynthesis_Metabolism_Lipidmetabolism_fabL,enoyl-[acyl-carrierprotein]reductaseII[EC:1.3.1.104];K10780_ko01212_Fattyacidmetabolism_Metabolism_Overview_fabL,enoyl-[acyl-carrierprotein]reductaseII[EC:1.3.1.104]	0	5,09533E-06	0
K00886_ko00520_Aminosugarandnucleotidesugarmetabolism_Metabolism_Carbohydratemetabolism_ppgK,polyphosphateglucokinase[EC:2.7.1.63];K00886_ko00010_Glycolysis/Gluconeogenesis_Metabolism_Carbohydratemetabolism_ppgK,polyphosphateglucok	0	5,09533E-06	1,66107E-05
K03228_ko02010_Ctransporters_Environmentalinformationprocessing_Membranetransport_yscT,sctT,hrcT,typeIIIsecretionproteinT	0	5,09533E-06	0
K10017_ko02010_Ctransporters_Environmentalinformationprocessing_Membranetransport_hisP,histidinetransportsystemATP-bindingprotein[EC:3.6.3.21]	1,03726E-05	0	0
K12234_ko00194_Photosynthesisproteins_Metabolism_Energymetabolism_cofE,fbiB,coenzymeF420-0:L-glutamateligase/coenzymeF420-1:gamma-L-glutamateligase[EC:6.3.2.316.3.2.34]	2,07452E-05	0	8,30537E-06
K08096_ko00740_RiboflavinmetabolismMetabolism_Metabolismofcofactorsandvitamins_gch3,GTPcyclohydrolaseIIa[EC:3.5.4.29]	0	1,01907E-05	8,30537E-06
K00729_ko00513_VariousstypesofN-glycanbiosynthesis_Metabolism_Glycanbiosynthesisandmetabolism_ALG5,dolichyl-phosphatebeta-glucosyltransferase[EC:2.4.1.117]	0	1,5286E-05	3,32215E-05
K15226_ko00400_Phenylalanine,tyrosineandtryptophanbiosynthesis_Metabolism_Aminoacidmetabolism_tyrAa,arogenatedehydrogenase(NADP+)[EC:1.3.1.78];K15226_ko01230_Biosynthesisofaminoacids_Metabolism_Overview_tyrAa,arogenatedehydrogenase(N	0	5,09533E-06	0
K10938_ko05111_Vibriocholeraepathogeniccycle_HumanDiseases_Infectiousdiseases_acfC,accessorycolonizationfactorAcfC	0	5,09533E-06	0
K15053_ko04144_Endocytosis_CellularProcesses_Transportandcatabolism_CHMP7,chargedmultivesicularbodyprotein7	0	1,5286E-05	1,66107E-05
K01674_ko00910_Nitrogenmetabolism_Metabolism_Energymetabolism_cah,carbonicanhydrase[EC:4.2.1.1]	5,18629E-06	0	1,66107E-05

K11631_ko02010_Ctransporters_Environmentalinformationprocessing_Membranetransport_bceA,bacitracintransportsystemATP-bindingprotein;K11631_ko02020_Two-componentsystem_Environmentalinformationprocessing_Signaltrasduction_bceA,bacitracintr	1,03726E-05	5,09533E-06	0
K11211_ko00540_Lipopolysaccharidebiosynthesis_Metabolism_Glycanbiosynthesisandmetabolism_kdkA,3-deoxy-D-manno-octulosonicacidkinase[EC:2.7.1.166]	5,18629E-06	1,01907E-05	0
K01906_ko00780_Biotinmetabolism_Metabolism_Metabolismofcofactorsandvitamins_bioW,6-carboxyhexanoate--CoAligase[EC:6.2.1.14]	0	5,09533E-06	8,30537E-06
K12852_ko03040_Spliceosome_GeneticinformationProcessing_Transcription_EFTUD2,116kDaU5smallnuclearribonucleoproteincomponent	5,18629E-06	0	8,30537E-06
K08081_ko00960_Tropane,piperidineandpyridinealkaloidbiosynthesis_Metabolism_Biosynthesisofothersecondarymetabolites_TR1,Tropinonereductase1[EC:1.1.1.206]	0	0	8,30537E-06
K05979_ko00194_Photosynthesisproteins_Metabolism_Energymetabolism_E3.1.3.71,comB,2-phosphosulfolactatephosphatase[EC:3.1.3.71]	1,55589E-05	3,0572E-05	6,6443E-05
K06596_ko02020_Two-componentsystem_Environmentalinformationprocessing_Signaltrasduction_chpA,chemosensorypilisystemproteinChpA(sensorhistidinekinase/responseregulator)	0	0	1,66107E-05
K00023_ko00630_Glyoxylateanddicarboxylatemetabolism_Metabolism_Carbohydratemetabolism_E1.1.1.36,phbB,acetoacetyl-CoAreductase[EC:1.1.1.36];K00023_ko00630_Glyoxylateanddicarboxylatemetabolism_Metabolism_Carbohydratemetabolism_E1.1.1.36	0	1,5286E-05	3,32215E-05
K09722_ko00770_PantothenateandCoABiosynthesis_Metabolism_Metabolismofcofactorsandvitamins_K09722,pps,4-phosphopantoate--beta-alanineligase[EC:6.3.2.36]	1,55589E-05	1,01907E-05	0
K11783_ko00130_Ubiquinoneandotherterpenoid-quinonebiosynthesis_Metabolism_Metabolismofcofactorsandvitamins_mqnB,futalosinehydrolase[EC:3.2.2.26]	5,18629E-06	0	0
K00904_ko00230_Purinemetabolism_Metabolism_Nucleotidemetabolism_DGUOK,deoxyguanosinekinase[EC:2.7.1.113]	2,59315E-05	0,000157955	6,6443E-05
K10000_ko02010_Ctransporters_Environmentalinformationprocessing_Membranetransport_artP,argininetransportsystemATP-bindingprotein[EC:3.6.3.-]	2,07452E-05	0	0
K00216_ko01053_Biosynthesisofsiderophoregroupnonribosomalpeptides_Metabolism_Metabolismofterpenoidsandpolyketides_entA,2,3-dihydro-2,3-dihydroxybenzoatedehydrogenase[EC:1.3.1.28]	0	5,09533E-06	0
K04802_ko04110_Cellcycle_CellularProcesses_Cellgrowthanddeath_PCNA,proliferatingcellnuclearantigen;K04802_ko03410_Baseexcisionrepair_GeneticinformationProcessing_ReplicationandRepair_PCNA,proliferatingcellnuclearantigen;K04802_ko03030_DNArep	5,18629E-06	0	0
K11023_ko05133_Pertussis_HumanDiseases_Infectiousdiseases_ptxA,pertussistoxinsubunit1[EC:2.4.2.-]	1,03726E-05	0	0
K08093_ko00030_Pentosephosphatepathway_Metabolism_Carbohydratemetabolism_hxlA,3-hexulose-6-phosphatesynthase[EC:4.1.2.43];K08093_ko01230_Biosynthesisofaminoacids_Metabolism_Overview_hxlA,3-hexulose-6-phosphatesynthase[EC:4.1.2.43];K080	3,6304E-05	1,5286E-05	2,49161E-05
K03203_ko02010_Ctransporters_Environmentalinformationprocessing_Membranetransport_virB8,lvhB8,typeIVsecretionsystemproteinVirB8	1,03726E-05	2,03813E-05	2,49161E-05
K13938_ko00785_Lipoicacidmetabolism_Metabolism_Metabolismofcofactorsandvitamins_folM,dihydromonapterinreductase/dihydrofolatereductase[EC:1.5.1.-1.5.1.3];K13938_ko00670_Onecarbonpoolbyfolate_Metabolism_Metabolismofcofactorsandvitamins_f	0	0	1,66107E-05
K09997_ko02010_Ctransporters_Environmentalinformationprocessing_Membranetransport_artI,argininetransportsystemsubstrate-bindingprotein	5,18629E-06	0	0
K07773_ko02020_Two-componentsystem_Environmentalinformationprocessing_Signaltrasduction_arcA,two-componentsystem,OmpRfamily,aerobicrespirationcontrolproteinArcA	1,03726E-05	1,01907E-05	1,66107E-05
K10015_ko02010_Ctransporters_Environmentalinformationprocessing_Membranetransport_hisM,histidinetransportsystempermeaseprotein	0	5,09533E-06	0
K05780_ko00440_Phosphonateandphosphinatemetabolism_Metabolism_Metabolismofotheraminoacids_phnL,alpha-D-ribose1-methylphosphonate5-triphosphatesynthasesubunitPhnL[EC:2.7.8.37]	1,03726E-05	5,09533E-06	8,30537E-06
K09999_ko02010_Ctransporters_Environmentalinformationprocessing_Membranetransport_artQ,argininetransportsystempermeaseprotein	0	1,01907E-05	0
K07672_ko02020_Two-componentsystem_Environmentalinformationprocessing_Signaltrasduction_trcR,two-componentsystem,OmpRfamily,responseregulatorTrcR	3,6304E-05	2,54767E-05	2,49161E-05
K01557_ko00350_Tyrosinemetabolism_Metabolism_Aminoacidmetabolism_FAHD1,acylpyruvatehydrolase[EC:3.7.1.5]	0	5,09533E-06	0
K03788_ko00740_Riboflavinmetabolism_Metabolism_Metabolismofcofactorsandvitamins_aphA,acidphosphatase(classB)[EC:3.1.3.2];K03788_ko00627_Aminobenzoatedegradation_Metabolism_Xenobioticsbiodegradationandmetabolism_aphA,acidphosphatase(cl	5,18629E-06	0	1,66107E-05
K13584_ko04112_Cellcycle-Caulobacter_CellularProcesses_Cellgrowthanddeath_ctrA,two-componentsystem,cellcycleresponseregulatorCtrA;K13584_ko02020_Two-componentsystem_Environmentalinformationprocessing_Signaltrasduction_ctrA,two-component	1,03726E-05	0	0
K07687_ko02020_Two-componentsystem_Environmentalinformationprocessing_Signaltrasduction_rcsB,two-componentsystem,NarLfamily,captularsynthesisresponseregulatorRcsB	0	1,01907E-05	0
K02080_ko00052_Galactosemetabolism_Metabolism_Carbohydratemetabolism_agal,galactosamine-6-phosphateisomerase[EC:5.3.1.-]	1,03726E-05	0	0
K05368_ko00830_Retinolmetabolism_Metabolism_Metabolismofcofactorsandvitamins_fre,ubiB,aquacobalaminreductase/NAD(P)H-flavinreductase[EC:1.16.1.31.5.1.41];K05368_ko00740_Riboflavinmetabolism_Metabolism_Metabolismofcofactorsandvitamins_fn	0	0	8,30537E-06
K13919_ko00630_Glyoxylateanddicarboxylatemetabolism_Metabolism_Carbohydratemetabolism_pduD,propanedioldehydratasemediumsubunit[EC:4.2.1.28]	3,6304E-05	0	1,66107E-05
K11622_ko02020_Two-componentsystem_Environmentalinformationprocessing_Signaltrasduction_liaF,liaoperonproteinLiaF	5,18629E-06	1,01907E-05	8,30537E-06
K03080_ko00040_Pentoseandglucuronateinterconversions_Metabolism_Carbohydratemetabolism_sgbE,L-ribulose-5-phosphate4-epimerase[EC:5.1.3.4]	0	1,01907E-05	0
K02865_ko03010_Ribosome_GeneticinformationProcessing_Transcription_RP-L10Ae,RPL10A,largesubunitribosomalproteinL10Ae	1,03726E-05	1,5286E-05	0
K07702_ko02020_Two-componentsystem_Environmentalinformationprocessing_Signaltrasduction_dpiA,citB,two-componentsystem,CitBfamily,responseregulatorCitB	0	5,09533E-06	0
K08966_ko00270_Cysteineandmethioninemetabolism_Metabolism_Aminoacidmetabolism_mtnX,2-hydroxy-3-keto-5-methylthiopentenyl-1-phosphatephosphatase[EC:3.1.3.87]	1,03726E-05	0	0
K02193_ko02010_Ctransporters_Environmentalinformationprocessing_Membranetransport_ccmA,hemeexporterproteinA[EC:3.6.3.41]	0	5,09533E-06	0
K14048_ko05120_EpithelialcellsignalinginHelicobacterpyloriinfection_HumanDiseases_Infectiousdiseases_ureAB,ureasesubunitgamma/beta[EC:3.5.1.5];K14048_ko00791_Atrazinedegradation_Humandiseases_Xenobioticsbiodegradationandmetabolism_ureAB,ure	0	4,5858E-05	8,30537E-06
K09880_ko00270_Cysteineandmethioninemetabolism_Metabolism_Aminoacidmetabolism_mtnC,ENOPH1,enolase-phosphataseE1[EC:3.1.3.77]	0	0	1,66107E-05
K03414_ko02030_Bacterialchemotaxis_Organismalsystem_Cellmobility_cheZ,chemotaxisproteinCheZ	1,03726E-05	0	1,66107E-05
K10002_ko02010_Ctransporters_Environmentalinformationprocessing_Membranetransport_gltK,aatM,glutamate/aspartatetransportsystempermeaseprotein;K10002_ko02020_Two-componentsystem_Environmentalinformationprocessing_Signaltrasduction_gltK	0	1,01907E-05	3,32215E-05
K08964_ko00270_Cysteineandmethioninemetabolism_Metabolism_Aminoacidmetabolism_mtnB,methylthioribulose-1-phosphatedehydratase[EC:4.2.1.109]	0	0	8,30537E-06
K00246_ko02020_Two-componentsystem_Environmentalinformationprocessing_Signaltrasduction_frdC,fumaratereductasesubunitC;K00246_ko00020_Citratecycle(TCAcycle)_Metabolism_Carbohydratemetabolism_frdC,fumaratereductasesubunitC;K00246_ko00(	1,55589E-05	0	0
K07780_ko02020_Two-componentsystem_Environmentalinformationprocessing_Signaltrasduction_appY,AraCfamilytranscriptionalregulator,transcriptionalregulatorrequiredforanaerobicandstationaryphaseinductionofgenes	1,03726E-05	0	0
K06857_ko02010_Ctransporters_Environmentalinformationprocessing_Membranetransport_tupC,vupC,tungstatetransportsystemATP-bindingprotein[EC:3.6.3.55]	1,55589E-05	1,01907E-05	0
K09689_ko02010_Ctransporters_Environmentalinformationprocessing_Membranetransport_ABC-2.CPSE.A,capsularpolysaccharidetransportsystemATP-bindingprotein	1,03726E-05	1,5286E-05	4,15269E-05
K09998_ko02010_Ctransporters_Environmentalinformationprocessing_Membranetransport_artM,arginineransportsystempermeaseprotein	0	0	1,66107E-05
K03226_ko02010_Ctransporters_Environmentalinformationprocessing_Membranetransport_yscR,sctR,hrcR,typeIIsecretionproteinR	0	1,01907E-05	1,66107E-05
K10009_ko02010_Ctransporters_Environmentalinformationprocessing_Membranetransport_ABC.CYST.P,cystinetransportsystempermeaseprotein	5,18629E-06	0	0
K14979_ko02020_Two-componentsystem_Environmentalinformationprocessing_Signaltrasduction_ssrB,two-componentsystem,LuxRfamily,secretionsystemresponseregulatorSsrB	0	0	1,66107E-05
K14981_ko02020_Two-componentsystem_Environmentalinformationprocessing_Signaltrasduction_chvI,two-componentsystem,OmpRfamily,responseregulatorChvI	0	1,01907E-05	8,30537E-06
K03081_ko00040_Pentoseandglucuronateinterconversions_Metabolism_Carbohydratemetabolism_sgbH,3-dehydro-L-gulonate-6-phosphatedecarboxylase[EC:4.1.1.85]	0	0	1,66107E-05
K00484_ko00350_Tyrosinemetabolism_Metabolism_Aminoacidmetabolism_hpaC,flavinreductase(NADH)[EC:1.5.1.36];K00484_ko01220_Degradationofaromaticcompounds_Metabolism_Overview_hpaC,flavinreductase(NADH)[EC:1.5.1.36]	1,03726E-05	0	0
K07732_ko00740_Riboflavinmetabolism_Metabolism_Metabolismofcofactorsandvitamins_rfk,riboflavinkinase,archaeatype[EC:2.7.1.161]	5,18629E-06	0	0
K03078_ko00052_Galactosemetabolism_Metabolism_Carbohydratemetabolism_ulaD,sgaH,3-dehydro-L-gulonate-6-phosphatedecarboxylase[EC:4.1.1.85]	0	5,09533E-06	0
K10006_ko02010_Ctransporters_Environmentalinformationprocessing_Membranetransport_gluC,glutamatetransportsystempermeaseprotein	1,03726E-05	0	0
K08350_ko02020_Two-componentsystem_Environmentalinformationprocessing_Signaltrasduction_fdnI,formatedehydrogenase-N,gammasubunit	1,03726E-05	0	1,66107E-05
K01035_ko02020_Two-componentsystem_Environmentalinformationprocessing_Signaltrasduction_atoA,acetateCoA/acetoacetateCoA-transferasebetasubunit[EC:2.8.3.82.8.3.9];K01035_ko00310_Lysinedegradation_Metabolism_Aminoacidmetabolism_atoA,aceta	3,11177E-05	0	1,66107E-05
K00007_ko00051_Fructoseandmannosemetabolism_Metabolism_Carbohydratemetabolism_dalD,D-arabinitol4-dehydrogenase[EC:1.1.1.11];K00007_ko00040_Pentoseandglucuronateinterconversions_Metabolism_Carbohydratemetabolism_dalD,D-arabinitol4-del	1,03726E-05	0	0
K04719_ko00740_Riboflavinmetabolism_Metabolism_Metabolismofcofactorsandvitamins_bluB,5,6-dimethylbenzimidazolesynthase[EC:1.13.11.79]	3,6304E-05	3,56673E-05	5,81376E-05
K10353_ko00230_Purinemetabolism_Metabolism_Nucleotidemetabolism_E2.7.1.76,dak,deoxyadenosinekinase[EC:2.7.1.76]	0	0,000107002	3,32215E-05
K14570_ko03008_Ribosomebiogenesisineukaryotes_GeneticinformationProcessing_Transcription_REX1,REXO1,RNH70,RNAexonuclease1[EC:3.1.-.-]	0	0	8,30537E-06
K03410_ko02030_Bacterialchemotaxis_Organismalsystem_Cellmobility_cheC,chemotaxisproteinCheC	2,59315E-05	2,54767E-05	4,15269E-05
K03194_ko02010_Ctransporters_Environmentalinformationprocessing_Membranetransport_virB1,typeIVsecretionsystemproteinVirB1	0	1,5286E-05	4,15269E-05
K02877_ko03010_Ribosome_GeneticinformationProcessing_Transcription_RP-L15e,RPL15,largesubunitribosomalproteinL15e	0	0	8,30537E-06
K07690_ko02020_Two-componentsystem_Environmentalinformationprocessing_Signaltrasduction_evgA,bvgA,two-componentsystem,NarLfamily,responseregulatorEvgA;K07690_ko05133_Pertussis_HumanDiseases_Infectiousdiseases_evgA,bvgA,two-components	5,18629E-06	0	0
K07323_ko02010_Ctransporters_Environmentalinformationprocessing_Membranetransport_mlaC,phospholipidtransportsystemsubstrate-bindingprotein	0	5,09533E-06	1,66107E-05
K03238_ko03013_RNAtransport_GeneticinformationProcessing_Transcription_EIF2S2,translationinitiationfactor2subunit2	1,03726E-05	0	0
K13923_ko00630_Glyoxylateanddicarboxylatemetabolism_Metabolism_Carbohydratemetabolism_pduL,phosphatepropanoyltransferase[EC:2.3.1.222]	1,03726E-05	1,01907E-05	0
K13317_ko00523_Polyketidesugarunitbiosynthesis_Metabolism_Metabolismofterpenoidsandpolyketides_eryBIII,NDP-4-keto-2,6-dideoxyhexose3-C-methyltransferase	5,18629E-06	0	0

K08054_ko04145_Phagosome_CellularProcesses_Transportandcatabolism_CANX,calnexin;K08054_ko04141_Proteinprocessinginendoplasmicreticulum_GeneticInformationProcessing_Folding,sortinganddegradation_CANX,calnexin;K08054_ko05166_HTLV-Iinfectic	5,18629E-06	0	0
K09024_ko00240_Pyrimidinemetabolism_Metabolism_Nucleotidemetabolism_rutF,flavinreductase[EC:1.5.1.-]	0	1,5286E-05	2,49161E-05
K07781_ko02020_Two-componentsystem_Environmentalinformationprocessing_Signaltrasduction_rcsA,LuxRfamilytranscriptionalregulator,capsularbiosynthesispositivetranscriptionfactor	0	5,09533E-06	0
K07804_ko02020_Two-componentsystem_Environmentalinformationprocessing_Signaltrasduction_pagC,putativevirulencerelatedproteinPagC	1,03726E-05	0	1,66107E-05
K02299_ko00190_Oxidativephosphorylation_Metabolism_Energymetabolism_cyoC,cytochromeoubiquinoloxidasesubunitIII[EC:1.10.3.-]	5,18629E-06	1,01907E-05	8,30537E-06
K03635_ko04122_Sulfurrelaysystem_GeneticInformationProcessing_Folding,sortinganddegradation_MOCS2,moaE,molybdopterinsynthasecatalyticsubunit[EC:2.8.1.12];K03635_ko00785_Lipoicacidmetabolism_Metabolism_Metabolismofcofactorsandvitamins_MC	2,07452E-05	2,03813E-05	2,49161E-05
K13583_ko04112_Cellcycle-Caulobacter_CellularProcesses_Cellgrowthanddeath_gcrA,GcrAcellcycleregulator	1,03726E-05	1,01907E-05	8,30537E-06
K12827_ko03040_Spliceosome_GeneticinformationProcessing_Transcription_SF3A3,SAP61,PRP9,splicingfactor3Asubunit3	2,07452E-05	2,03813E-05	0
K12813_ko03040_Spliceosome_GeneticinformationProcessing_Transcription_DHX16,pre-mRNA-splicingfactorATP-dependentRNAhelicaseDHX16[EC:3.6.4.13]	5,18629E-06	5,09533E-06	8,30537E-06
K06697_ko03050_Proteasome_GeneticInformationProcessing_Folding,sortinganddegradation_PSME2,proteasomeactivatorsubunit2(PA28beta);K06697_ko04612_Antigenprocessingandpresentation_Organismalsystem_Immunesystem_PSME2,proteasomeactivato	1,03726E-05	0	0
K02541_ko04111_Cellcycle-yeast_CellularProcesses_Cellgrowthanddeath_MCM3,DNAreplicationlicensingfactorMCM3[EC:3.6.4.12];K02541_ko04110_Cellcycle_CellularProcesses_Cellgrowthanddeath_MCM3,DNAreplicationlicensingfactorMCM3[EC:3.6.4.12];K025	3,11177E-05	5,09533E-06	8,30537E-06
K02191_ko00830_Retinolmetabolism_Metabolism_Metabolismofcofactorsandvitamins_cbiT,cobalt-precorrin-6B(C15)-methyltransferase[EC:2.1.1.196]	1,55589E-05	1,01907E-05	1,66107E-05
K06165_ko00440_Phosphonateandphosphinatemetabolism_Metabolism_Metabolismofotheraminoacids_phnH,alpha-D-ribose1-methylphosphonate5-triphosphatesynthasesubunitPhnH[EC:2.7.8.37]	1,03726E-05	0	8,30537E-06
K13743_ko05100_Bacterialinvasionofepithelialcells_Humandiseases_Infectiousdiseases_ipgB2,proteinIpgB2;K13743_ko05131_Shigellosis_HumanDiseases_Infectiousdiseases_ipgB2,proteinIpgB2	0	0	1,66107E-05
K03896_ko00310_Lysinedegradation_Metabolism_Aminoacidmetabolism_iucB,acetylCoA:N6-hydroxylysineacetyltransferase[EC:2.3.1.102]	0	0	8,30537E-06
K02256_ko05010_Alzheimer'sdisease_HumanDiseases_Degenerativediseases_COX1,cytochromecoxidasesubunit1[EC:1.9.3.1];K02256_ko05016_Huntington'sdisease_HumanDiseases_Degenerativediseases_COX1,cytochromecoxidasesubunit1[EC:1.9.3.1];K02256_k	0	0	8,30537E-06
K00299_ko00920_Sulfurmetabolism_Metabolism_Energymetabolism_ssuE,FMNreductase[EC:1.5.1.38];K00299_ko00740_Riboflavinmetabolism_Metabolism_Metabolismofcofactorsandvitamins_ssuE,FMNreductase[EC:1.5.1.38]	0	1,5286E-05	0
K02402_ko02020_Two-componentsystem_Environmentalinformationprocessing_Signaltrasduction_flhC,flagellartranscriptionalactivatorFlhC;K02402_ko02040_Flagellarassembly_Organismalsystem_Cellmobility_flhC,flagellartranscriptionalactivatorFlhC	0	1,01907E-05	0
K03233_ko05134_Legionellosis_HumanDiseases_Infectiousdiseases_EEF1G,elongationfactor1-gamma	1,03726E-05	0	0
K00769_ko00230_Purinemetabolism_Metabolism_Nucleotidemetabolism_gpt,xanthinephosphoribosyltransferase[EC:2.4.2.22]	1,03726E-05	5,09533E-06	1,66107E-05
K10352_ko04530_Tightjunction_Cellgrowthanddeath_Cellularcommunity_MYH,myosinheavychain	2,07452E-05	0	0
K02637_ko00195_Photosynthesis_Metabolism_Energymetabolism_petD,cytochromeb6-fcomplexsubunit4	5,18629E-06	0	0
K14566_ko03008_Ribosomebiogenesisineukaryotes_GeneticinformationProcessing_Transcription_UTP24,FCF1,U3smallnucleolarRNA-associatedprotein24	5,18629E-06	0	0
K00189_ko00280_Valine,leucineandisoleucinedegradation_Metabolism_Aminoacidmetabolism_vorG,2-oxoisovaleratferredoxinoxidoreductase,gammasubunit[EC:1.2.7.7]	0	5,09533E-06	8,30537E-06
K02457_ko02010_Ctransporters_Environmentalinformationprocessing_Membranetransport_gspH,generalsecretionpathwayproteinH	0	5,09533E-06	0
K11906_ko02010_Ctransporters_Environmentalinformationprocessing_Membranetransport_vasD,lip,typeVIsecretionsystemproteinVasD	1,03726E-05	0	0
K02626_ko00330_Arginineandprolinemetabolism_Metabolism_Aminoacidmetabolism_pdaD,argininedecarboxylase[EC:4.1.1.19]	0	1,01907E-05	1,66107E-05
K03136_ko03022_Basaltranscriptionfactors_GeneticinformationProcessing_Transcription_TFIIE1,GTF2E1,TFA1,tfe,transcriptioninitiationfactorTFIIEsubunitalpha;K03136_ko05203_Viralcarcinogenesis_HumanDiseases_Cancers_TFIIE1,GTF2E1,TFA1,tfe,transcriptioni	5,18629E-06	0	0
K03191_ko05120_EpithelialcellsignalinginHelicobacterpyloriinfection_HumanDiseases_Infectiousdiseases_urel,acid-activatedureachannel	5,18629E-05	7,13347E-05	1,66107E-05
K01716_ko00061_Fattyacidbiosynthesis_Metabolism_Lipidmetabolism_fabA,3-hydroxyacyl-[acyl-carrierprotein]dehydratase/trans-2-decenoyl-[acyl-carrierprotein]isomerase[EC:4.2.1.595.3.3.14];K01716_ko01212_Fattyacidmetabolism_Metabolism_Overview_fab	1,03726E-05	0	0
K00922_ko04510_Focaladhesion_Cellgrowthanddeath_Cellularcommunity_PIK3C,phosphatidylinositol-4,5-bisphosphate3-kinase[EC:2.7.1.153];K00922_ko04550_Signalingpathwaysregulatingpluripotencyofstemcells_Cellgrowthanddeath_Cellularcommunity_PIK3C	0	0	1,66107E-05
K10606_ko04120_Ubiquitinmediatedproteolysis_GeneticInformationProcessing_Folding,sortinganddegradation_FANCL,PHF9,E3ubiquitin-proteinligaseFANCL[EC:6.3.2.19];K10606_ko03460_Fanconianemiapathway_GeneticinformationProcessing_ReplicationandRe	5,18629E-06	0	0
K02154_ko04142_Lysosome_CellularProcesses_Transportandcatabolism_ATPeV0A,ATP6N,V-typeH+-transportingATPasesubunita;K02154_ko04145_Phagosome_CellularProcesses_Transportandcatabolism_ATPeV0A,ATP6N,V-typeH+-transportingATPasesubunita;K(	0	0	8,30537E-06
K02636_ko00195_Photosynthesis_Metabolism_Energymetabolism_petC,cytochromeb6-fcomplexiron-sulfursubunit[EC:1.10.9.1]	0	1,01907E-05	0
K11422_ko00310_Lysinedegradation_Metabolism_Aminoacidmetabolism_SETD1,SET1,histone-lysineN-methyltransferaseSETD1[EC:2.1.1.43]	0	0	2,49161E-05
K14026_ko04141_Proteinprocessinginendoplasmicreticulum_GeneticInformationProcessing_Folding,sortinganddegradation_SEL1,SEL1L,SEL1protein	0	0	8,30537E-06
K05360_ko00480_Glutathionemetabolism_Metabolism_Metabolismofotheraminoacids_TXNDC12,protein-disulfidereductase(glutathione)[EC:1.8.4.2]	0	0	1,66107E-05
K02218_ko04340_Hedgehogsignalingpathway_Environmentalinformationprocessing_Signaltrasduction_CSNK1,CK1,caseinkinase1[EC:2.7.11.1]	1,03726E-05	0	0
K10984_ko02010_Ctransporters_Environmentalinformationprocessing_Membranetransport_PTS-Gam-EIIB,agaB,PTSsystem,galactosamine-specificIIBcomponent[EC:2.7.1.69];K10984_ko00052_Galactosemetabolism_Metabolism_Carbohydratemetabolism_PTS-Ga	5,18629E-06	0	0
K07432_ko00513_VariustypesofN-glycanbiosynthesis_Metabolism_Glycanbiosynthesisandmetabolism_ALG13,beta-1,4-N-acetylglucosaminyltransferase[EC:2.4.1.141];K07432_ko00513_VariustypesofN-glycanbiosynthesis_Metabolism_Glycanbiosynthesisandme	0	1,01907E-05	1,66107E-05
K10796_ko00330_Arginineandprolinemetabolism_Metabolism_Aminoacidmetabolism_prdE,D-prolinereductase(dithiol)PrdE[EC:1.21.4.1]	0	3,0572E-05	0
K08311_ko03018_RNAdegradation_GeneticInformationProcessing_Folding,sortinganddegradation_nudH,putative(di)nucleosidepolyphosphatehydrolase[EC:3.6.1.-]	0	0	1,66107E-05
K08773_ko02020_Two-componentsystem_Environmentalinformationprocessing_Signaltrasduction_RALBP1,RalA-bindingprotein1;K08773_ko05212_Pancreaticcancer_HumanDiseases_Cancers_RALBP1,RalA-bindingprotein1;K08773_ko05200_Pathwaysincancer_H	7,77944E-05	5,60487E-05	2,49161E-05
K05550_ko01220_Degradationofaromaticcompounds_Metabolism_Overview_benB-xylY,benzoate/toluate1,2-dioxygenasebetasubunit[EC:1.14.12.101.14.12.-];K05550_ko00362_Benzoatedegradation_Metabolism_Xenobioticsbiodegradationandmetabolism_benB-	5,18629E-06	0	0
K10212_ko00906_Carotenoidbiosynthesis_Metabolism_Metabolismofterpenoidsandpolyketides_K10212,crtO,glycosyl-4,4'-diaponeurosporenoateacyltransferase[EC:2.3.1.-]	5,18629E-06	1,01907E-05	0
K03130_ko03022_Basaltranscriptionfactors_GeneticinformationProcessing_Transcription_TAF5,transcriptioninitiationfactorTFIIDsubunit5;K03130_ko05168_Herpessimplexinfection_HumanDiseases_Infectiousdiseases_TAF5,transcriptioninitiationfactorTFIIDsubuni	0	0	1,66107E-05
K12296_ko02020_Two-componentsystem_Environmentalinformationprocessing_Signaltrasduction_comX1_2,competenceproteinComX	1,03726E-05	0	0
K05581_ko00190_Oxidativephosphorylation_Metabolism_Energymetabolism_ndhJ,NAD(P)H-quinoneoxidoreductasesubunitJ[EC:1.6.5.3]	0	0	1,66107E-05
K10599_ko04120_Ubiquitinmediatedproteolysis_GeneticInformationProcessing_Folding,sortinganddegradation_PRPF19,PRP19,pre-mRNA-processingfactor19[EC:6.3.2.19];K10599_ko03040_Spliceosome_GeneticinformationProcessing_Transcription_PRPF19,PRP1	5,18629E-06	5,09533E-06	0
K12733_ko03040_Spliceosome_GeneticinformationProcessing_Transcription_PPIL1,peptidyl-prolylcis-transisomerase-like1[EC:5.2.1.8]	5,18629E-06	0	0
K02568_ko00910_Nitrogenmetabolism_Metabolism_Energymetabolism_napB,cytochromec-typeproteinNapB	0	0	1,66107E-05
K03241_ko03013_RNAtransport_GeneticinformationProcessing_Transcription_EIF2B3,translationinitiationfactoreIF-2Bsubunitgamma	5,18629E-06	0	0
K14521_ko03008_Ribosomebiogenesisineukaryotes_GeneticinformationProcessing_Transcription_NAT10,KRE33,N-acetyltransferase10[EC:2.3.1.-]	5,18629E-06	0	0
K01496_ko00340_Histidinemetabolism_Metabolism_Aminoacidmetabolism_hisI,phosphoribosyl-AMPcyclohydrolase[EC:3.5.4.19];K01496_ko01230_Biosynthesisofaminoacids_Metabolism_Overview_hisI,phosphoribosyl-AMPcyclohydrolase[EC:3.5.4.19]	2,07452E-05	2,03813E-05	2,49161E-05
K00565_ko03015_mRNAsurveillancepathway_GeneticinformationProcessing_Transcription_RNMT,mRNA(guanine-N7-)-methyltransferase[EC:2.1.1.56]	0	0	8,30537E-06
K02734_ko03050_Proteasome_GeneticInformationProcessing_Folding,sortinganddegradation_PSMB2,20Sproteasomesubunitbeta4[EC:3.4.25.1]	0	0	8,30537E-06
K02940_ko03010_Ribosome_GeneticinformationProcessing_Transcription_RP-L9e,RPL9,largesubunitribosomalproteinL9e	0	0	8,30537E-06
K05546_ko04141_Proteinprocessinginendoplasmicreticulum_GeneticInformationProcessing_Folding,sortinganddegradation_GANAB,alpha1,3-glucosidase[EC:3.2.1.84];K05546_ko00513_VariustypesofN-glycanbiosynthesis_Metabolism_Glycanbiosynthesisandmet	1,03726E-05	0	0
K06166_ko00440_Phosphonateandphosphinatemetabolism_Metabolism_Metabolismofotheraminoacids_phnG,alpha-D-ribose1-methylphosphonate5-triphosphatesynthasesubunitPhnG[EC:2.7.8.37]	1,03726E-05	0	1,66107E-05
K03165_ko03460_Fanconianemiapathway_GeneticinformationProcessing_ReplicationandRepair_TOP3,DNAtopoisomeraseIII[EC:5.99.1.2];K03165_ko03440_Homologousrecombination_GeneticinformationProcessing_ReplicationandRepair_TOP3,DNAtopoisomeras	0	0	1,66107E-05
K10924_ko05111_Vibriocholeraepathogeniccycle_HumanDiseases_Infectiousdiseases_mshA,MSHApilinproteinMshA	0	5,09533E-06	0
K13766_ko00280_Valine,leucineandisoleucinedegradation_Metabolism_Aminoacidmetabolism_liuC,methylglutaconyl-CoAhydratase[EC:4.2.1.18]	0	5,09533E-06	0
K11204_ko00480_Glutathionemetabolism_Metabolism_Metabolismofotheraminoacids_GCLC,glutamate--cysteineligasecatalyticsubunit[EC:6.3.2.2]	5,18629E-06	0	0
K02781_ko02010_Ctransporters_Environmentalinformationprocessing_Membranetransport_PTS-Gut-EIIA,srlB,PTSsystem,glucitol/sorbitol-specificIIAcomponent[EC:2.7.1.69];K02781_ko00051_Fructoseandmannosemetabolism_Metabolism_Carbohydratemetaboli	3,11177E-05	3,0572E-05	0
K05338_ko02020_Two-componentsystem_Environmentalinformationprocessing_Signaltrasduction_lrgA,holin-likeprotein	1,03726E-05	0	0
K03197_ko02010_Ctransporters_Environmentalinformationprocessing_Membranetransport_virB2,lvhB2,typeIVsecretionsystemproteinVirB2;K03197_ko05134_Legionellosis_HumanDiseases_Infectiousdiseases_virB2,lvhB2,typeIVsecretionsystemproteinVirB2	5,18629E-06	3,56673E-05	0
K02210_ko04111_Cellcycle-yeast_CellularProcesses_Cellgrowthanddeath_MCM7,CDC47,DNAreplicationlicensingfactorMCM7[EC:3.6.4.12];K02210_ko04110_Cellcycle_CellularProcesses_Cellgrowthanddeath_MCM7,CDC47,DNAreplicationlicensingfactorMCM7[EC:	1,03726E-05	0	0
K00462_ko01220_Degradationofaromaticcompounds_Metabolism_Overview_bphC,biphenyl-2,3-diol1,2-dioxygenase[EC:1.13.11.39];K00462_ko00361_Chlorocyclohexaneandchlorobenzenedegradation_Metabolism_Xenobioticsbiodegradationandmetabolism_bph	5,18629E-06	1,01907E-05	0
K03953_ko05010_Alzheimer'sdisease_HumanDiseases_Degenerativediseases_NDUFA9,NADHdehydrogenase(ubiquinone)1alphasubcomplexsubunit9;K03953_ko05016_Huntington'sdisease_HumanDiseases_Degenerativediseases_NDUFA9,NADHdehydrogenase(ut	5,18629E-06	0	0
K01822_ko00140_Steroidhormonebiosynthesis_Metabolism_Lipidmetabolism_E5.3.3.1,steroiddelta-isomerase[EC:5.3.3.1];K01822_ko00984_Steroiddegradation_Metabolism_Xenobioticsbiodegradationandmetabolism_E5.3.3.1,steroiddelta-isomerase[EC:5.3.3.1]	5,18629E-06	5,09533E-06	0

K07235_ko04122_Sulfurrelaysystem_GeneticInformationProcessing_Folding,sortinganddegradation_tusD,dsrE,tRNA2-thiouridinesynthesizingproteinD[EC:2.8.1.-]	0	0	1,66107E-05
K12391_ko04142_Lysosome_CellularProcesses_Transportandcatabolism_AP1G1,AP-1complexsubunitgamma-1	1,03726E-05	0	0
K01900_ko00020_Citratecycle(TCAcycle)_Metabolism_Carbohydratemetabolism_LSC2,succinyl-CoAsynthetasebetasubunit[EC:6.2.1.46.2.1.5];K01900_ko00630_Glyoxylateanddicarboxylatemetabolism_Metabolism_Carbohydratemetabolism_LSC2,succinyl-CoAsynt	0	1,01907E-05	8,30537E-06
K06208_ko00400_Phenylalanine,tyrosineandtryptophanbiosynthesis_Metabolism_Aminoacidmetabolism_aroH,chorismatemutase[EC:5.4.99.5];K06208_ko01230_Biosynthesisofaminoacids_Metabolism_Overview_aroH,chorismatemutase[EC:5.4.99.5]	0	4,07627E-05	7,47483E-05
K12855_ko03040_Spliceosome_GeneticinformationProcessing_Transcription_PRPF6,PRP6,pre-mRNA-processingfactor6	0	5,09533E-06	0
K00247_ko02020_Two-componentsystem_Environmentalinformationprocessing_Signaltrasduction_frdD,fumaratereductasesubunitD;K00247_ko00020_Citratecycle(TCAcycle)_Metabolism_Carbohydratemetabolism_frdD,fumaratereductasesubunitD;K00247_ko0(	0	5,09533E-06	1,66107E-05
K11304_ko05166_HTLV-Iinfection_HumanDiseases_Infectiousdiseases_TIP60,KAT5,ESA1,histoneacetyltransferaseHTATIP[EC:2.3.1.48]	0	0	1,66107E-05
K12571_ko03018_RNAdegradation_GeneticInformationProcessing_Folding,sortinganddegradation_PAN2,PAB-dependentpoly(A)-specificribonucleasesubunit2[EC:3.1.13.4]	0	0	8,30537E-06
K02398_ko02040_Flagellarassembly_Organismalsystem_Cellmobility_flgM,negativeregulatorofflagellinsynthesisFlgM	3,6304E-05	2,54767E-05	5,81376E-05
K12814_ko03040_Spliceosome_GeneticinformationProcessing_Transcription_PRP2,pre-mRNA-splicingfactorATP-dependentRNAhelicase-likeproteinPRP2[EC:3.6.4.13]	0	5,09533E-06	0
K07122_ko02010_Ctransporters_Environmentalinformationprocessing_Membranetransport_mlaB,phospholipidtransportsystemtransporter-bindingprotein	1,03726E-05	0	0
K03236_ko03013_RNAtransport_GeneticinformationProcessing_Transcription_EIF1A,translationinitiationfactor1A	0	0	8,30537E-06
K03935_ko05010_Alzheimer'sdisease_HumanDiseases_Degenerativediseases_NDUFS2,NADHdehydrogenase(ubiquinone)Fe-Sprotein2[EC:1.6.5.31.6.99.3];K03935_ko05016_Huntington'sdisease_HumanDiseases_Degenerativediseases_NDUFS2,NADHdehydrogenas	0	0	1,66107E-05
K08794_ko04917_Prolactinsignalingpathway_Organismalsystem_Endocrinsystem_CAMK1,calcium/calmodulin-dependentproteinkinasel[EC:2.7.11.17]	0	0	8,30537E-06
K02009_ko02010_Ctransporters_Environmentalinformationprocessing_Membranetransport_cbiN,cobalt/nickeltransportprotein	4,66766E-05	1,01907E-05	0
K02786_ko02010_Ctransporters_Environmentalinformationprocessing_Membranetransport_PTS-Lac-EIIA,lacF,PTSsystem,lactose-specificIIAcomponent[EC:2.7.1.69];K02786_ko00052_Galactosemetabolism_Metabolism_Carbohydratemetabolism_PTS-Lac-EIIA,lacF	1,55589E-05	0	0
K02686_ko03440_Homologousrecombination_GeneticinformationProcessing_ReplicationandRepair_priB,primosomalreplicationproteinN	0	1,01907E-05	0
K02201_ko00770_PantothenateandCoAbiosynthesis_Metabolism_Metabolismofcofactorsandvitamins_E2.7.7.3B,pantetheine-phosphateadenylyltransferase[EC:2.7.7.3]	0	0	1,66107E-05
K10251_ko01040_Biosynthesisofunsaturatedfattyacids_Metabolism_Lipidmetabolism_HSD17B12,KAR,IFA38,17beta-estradiol17-dehydrogenase/very-long-chain3-oxoacyl-CoAreductase[EC:1.1.1.621.1.1.330];K10251_ko00062_fattyacidelongation_Metabolism_Lipi	5,18629E-06	0	0
K11254_ko05203_Viralcarcinogenesis_HumanDiseases_Cancers_H4,histoneH4;K11254_ko05322_Systemiclupuserythematosus_Humandiseases_Immunediseases_H4,histoneH4;K11254_ko05034_Alcoholism_HumanDiseases_SubstanceDependence_H4,histoneH4	0	1,01907E-05	0
K00171_ko00020_Citratecycle(TCAcycle)_Metabolism_Carbohydratemetabolism_porD,pyruvateferredoxinoxidoreductase,deltasubunit[EC:1.2.7.1];K00171_ko00010_Glycolysis/Gluconeogenesis_Metabolism_Carbohydratemetabolism_porD,pyruvateferredoxinoxi	4,66766E-05	5,09533E-06	2,49161E-05
K01110_ko04510_Focaladhesion_Cellgrowthanddeath_Cellularcommunity_PTEN,phosphatidylinositol-3,4,5-trisphosphate3-phosphataseanddual-specificityproteinphosphatasePTEN[EC:3.1.3.163.1.3.483.1.3.67];K01110_ko04530_Tightjunction_Cellgrowthanddeath	1,03726E-05	0	0
K12585_ko03018_RNAdegradation_GeneticInformationProcessing_Folding,sortinganddegradation_DIS3,RRP44,exosomecomplexexonucleaseDIS3/RRP44[EC:3.1.13.-]	5,18629E-06	0	0
K07237_ko04122_Sulfurrelaysystem_GeneticInformationProcessing_Folding,sortinganddegradation_tusB,dsrH,tRNA2-thiouridinesynthesizingproteinB	0,000383786	0,000825444	0,000855453
K03097_ko04520_Adherensjunction_Cellgrowthanddeath_Cellularcommunity_CSNK2A,caseinkinaseIIsubunitalpha[EC:2.7.11.1];K03097_ko04530_Tightjunction_Cellgrowthanddeath_Cellularcommunity_CSNK2A,caseinkinaseIIsubunitalpha[EC:2.7.11.1];K03097_ko(	0	5,09533E-06	0
K11227_ko02020_Two-componentsystem_Environmentalinformationprocessing_Signaltrasduction_PBS2,mitogen-activatedproteinkinasekinase[EC:2.7.12.2]	0	0	8,30537E-06
K08683_ko05010_Alzheimer'sdisease_HumanDiseases_Degenerativediseases_HSD17B10,3-hydroxyacyl-CoAdehydrogenase/3-hydroxy-2-methylbutyryl-CoAdehydrogenase[EC:1.1.1.351.1.1.178];K08683_ko00280_Valine,leucineandisoleucinedegradation_Metaboli	1,03726E-05	0	0
K02420_ko02040_Flagellarassembly_Organismalsystem_Cellmobility_fliQ,flagellarbiosyntheticproteinFliQ	2,07452E-05	0	3,32215E-05
K07590_ko03010_Ribosome_GeneticinformationProcessing_Transcription_RP-L7A,rplGB,largesubunitribosomalproteinL7A	1,03726E-05	0	0
K03198_ko02010_Ctransporters_Environmentalinformationprocessing_Membranetransport_virB3,lvhB3,typeIVsecretionsystemproteinVirB3	0	0	1,66107E-05
K02345_ko03030_DNAreplication_GeneticinformationProcessing_ReplicationandRepair_DPO3T,holE,DNApolymeraseIIIsubunittheta[EC:2.7.7.7];K02345_ko03440_Homologousrecombination_GeneticinformationProcessing_ReplicationandRepair_DPO3T,holE,DNA	1,55589E-05	0	0
K08762_ko04920_Adipocytokinesignalingpathway_Organismalsystem_Endocrinsystem_DBI,ACBP,diazepam-bindinginhibitor(GABAreceptormodulator,acyl-CoA-bindingprotein)	5,18629E-06	0	0
K14188_ko05150_Staphylococcusaureusinfection_HumanDiseases_Infectiousdiseases_dltC,D-alanine--poly(phosphoribitol)ligasesubunit2[EC:6.1.1.13];K14188_ko00473_D-Alaninemetabolism_Metabolism_Metabolismofotheraminoacids_dltC,D-alanine--poly(phos	0	1,5286E-05	8,30537E-06
K02196_ko02010_Ctransporters_Environmentalinformationprocessing_Membranetransport_ccmD,hemeexporterproteinD	1,03726E-05	0	0
K02896_ko03010_Ribosome_GeneticinformationProcessing_Transcription_RP-L24e,RPL24,largesubunitribosomalproteinL24e	1,03726E-05	1,01907E-05	0
K11258_ko00290_Valine,leucineandisoleucinebiosynthesis_Metabolism_Aminoacidmetabolism_ilvM,acetolactatesynthaseIIsmallsubunit[EC:2.2.1.6];K11258_ko00630_Glyoxylateanddicarboxylatemetabolism_Metabolism_Carbohydratemetabolism_ilvM,acetolacta	1,03726E-05	0	0
K12863_ko03040_Spliceosome_GeneticinformationProcessing_Transcription_CWC15,proteinCWC15	5,18629E-06	0	0
K02640_ko00195_Photosynthesis_Metabolism_Energymetabolism_petG,cytochromeb6-fcomplexsubunit5	0	0	2,49161E-05
K13793_ko05131_Shigellosis_HumanDiseases_Infectiousdiseases_ospE,espO,secretedeffectorOspE	1,03726E-05	0	0
	1	1	1

Supplementary Table 2S

List of identified analytes together with retention times in the two chromatographic dimensions (^1t_R and ^2t_R), experimental and tabulated linear retention indices (I^T_S), normalized 2D volume and relative standard deviation (RSD%) over three replicated analyses from each diet regimen sample.

Analytes	^1t_R (min)	^2t_R (s)	Exp I^T_s	Ref I^T_s	SD		L-Fr		S-Fr	
					Norm 2D Volume	RSD%	*Norm 2D Volume*	RSD%	*Norm 2D Volume*	RSD%
2-Butanone	5.02	0.517	-	900	5138694	11.3	5631898	7.1	5569975	0.6
Butanal	5.55	0.655	926	911	411362	8.9	271685	2.3	174077	9.3
3-Methylbutanal	6.02	0.828	960	-	654043	18.5	269406	9.8	463418	7.8
1-Methoxy-2-propanone	6.15	0.483	969	-	65635	6.1	54745	5.8	106606	6.3
1,1'-Oxybis-butane*	6.69	2.000	1003	-	235165	4.3	212164	3.3	253346	0.6
2-Pentanone	6.89	0.621	1013	1011	65431	16.1	-	-	-	-
Isoxazole	7.95	0.828	1061	-	265560	14.6	452941	15.7	199116	19.3
2,3-Pentanedione	8.55	0.931	1085	1076	884781	13.1	60210	17.2	-	-
Butyl acetate	8.89	1.448	1098	1100	21735	19.5	28854	17.3	32086	13.6
Hexanal	9.22	1.414	1110	1105	396840	12.7	173438	9.3	146149	1.3
2-Methyl-3-Hexanone	10.49	1.862	1155	-	25307	5.8	29376	6.0	34021	9.8
1-Butanol	11.09	0.724	1174	1175	1204294	11.7	401598	2.4	406819	5.9
2-Methylbutyl propanoate	11.09	2.449	1174	-	355481	8.2	1430224	1.9	1519475	4.6
3-Methyl-4-heptanone	11.29	2.345	1180	-	54378	1.4	63909	1.3	69875	2.8
3-Heptanone	11.42	1.897	1184	1167	31167	5.8	36638	10.2	29809	0.7
Heptanal	12.49	1.862	1216	1206	161709	16.0	95965	14.2	58851	9.3
2-Ethyl hexanal	12.55	2.414	1218	1216	351699	16.7	358964	8.0	332911	3.7
Pyridine	12.62	0.897	1220	-	6421261	10.4	73487	16.4	69223	6.9
Limonene	12.82	2.690	1226	1224	84920	16.1	465263	9.7	469188	8.2
3-Methyl-1-butanol	13.22	0.860	1238	1237	-	-	99615	4.0	118542	9.7
1,8-Cineole	13.35	2.862	1241	1245	43666	14.4	13611	0.3	-	-
1-(Chloromethoxy)-2-methyl-propane*	13.49	3.138	1245	-	38713	5.0	34792	17.2	50115	11.3
Butyl butanoate	13.62	2.517	1249	1243	7849331	4.5	8426060	7.3	9551280	4.9
Pentanol	14.82	0.897	1280	1274	24600	17.0	38194	2.0	28335	2.9

1-Butanol-3-methylpropanoate	15.09	1.483	1287	-	78221	20.5	84066	6.3	81943	0.7
Octanal	16.49	2.242	1324	1319	339710	15.3	89546	3.2	64821	11.2
2-Ethyl-2-hexenal	16.89	2.207	1334	1336	551382	13.2	565609	7.6	597980	5.9
6-Methyl-5-hepten-2-one	18.35	1.793	1371	1365	37763	7.6	43166	13.7	50728	0.4
Hexanol	18.89	1.000	1383	1386	636568	23.9	348981	2.2	290444	18.0
2-Propylhexanal	19.82	3.276	1405	-	87392	12.7	-	-	-	-
Nonanal	20.69	2.517	1429	1423	328418	22.0	393118	4.8	207225	1.3
1-Octen-3-ol	20.89	2.035	1434	1430	55234	14.9	59144	9.4	58307	10.6
2-Butoxy ethanol	20.95	1.069	1435	1435	18569	17.1	-	-	22972	13.5
1-Hepten-3-ol	22.82	1.207	1481	-	62592	13.1	55609	16.9	35653	7.4
Acetic acid	22.82	0.448	1481	1479	1279002	9.4	925652	17.8	770146	8.5
Heptanol	23.02	1.173	1486	1465	327093	19.6	297805	0.9	148568	14.0
2-Ethyl-1-hexanol	24.42	1.310	1522	1518	907920	19.4	1056351	12.5	815905	12.1
1H-Pyrrole	25.22	0.586	1543	1534	41440	8.0	69348	15.5	37818	3.9
Benzaldehyde	26.02	1.069	1563	1555	740857	27.5	99365	8.4	260884	20.3
Propanoic acid	26.29	0.517	1569	1564	135266	17.0	-	-	50900	14.8
Octanol	27.15	1.310	1591	1585	1121374	10.1	294466	6.4	224653	11.2
Butanoic acid	29.75	0.517	1659	1661	571958	19.8	77417	15.7	73686	15.1
Phenylacethaldehyde	30.55	1.104	1679	-	809122	7.4	462549	9.9	556029	8.4
Nonanol	31.15	1.414	1694	1695	574209	17.7	855342	1.4	465283	6.1
2-Propyl-1-heptanol	31.42	1.621	1700	-	1061702	20.1	19174	13.5	38284	13.0
2-Methyl butanoic acid	31.42	0.586	1700	1705	24362	16.5	-	-	-	-
3-(Methylthio)-1-propanol	33.15	0.793	1749	1744	65522	8.8	40929	15.0	30139	3.6
Pentanoic acid	33.95	0.586	1770	1768	18263	16.2	-	-	-	-
Decanol	34.95	1.517	1797	1781	68509	16.5	136539	4.5	107723	12.5
Hexanoic acid	37.75	0.621	1876	1873	42652	12.4	65044	12.3	49914	17.1
Butyl benzoate	38.55	1.790	1898	1903	1262029	13.1	1311705	18.8	1319326	3.3
Phenylethyl Alcohol	40.02	0.828	1943	1944	138203	17.6	97147	1.6	97156	10.5
6,10-Dimethyl-5,9-undecadien-2-ol*	41.69	1.724	1992	-	490283	16.8	123955	4.5	142311	4.7
Dodecanol	42.09	1.724	2004	-	62850	17.9	65189	0.9	54807	13.1
Phenol	43.02	0.586	2034	2026	56667	15.2	89277	1.7	107727	14.2
4-Methyl phenol	45.49	0.621	2109	2100	144082	4.8	124970	6.3	127323	8.3
Indole	56.02	0.724	2465	2460	192902	7.8	192077	4.2	82313	2.2

*Tentatively identified