# Extraction of Correlated Gene Clusters by Multiple Graph Comparison

Akihiro Nakaya	Susumu Goto	Minoru Kanehisa
nakaya@kuicr.kyoto-u.ac.jp	goto@kuicr.kyoto-u.ac.jp	kanehisa@kuicr.kyoto-u.ac.jp
Bioinformatics Center, Institute for Chemical Research, Kyoto University		, Kyoto University
	Uji, Kyoto 611-0011, Japan	

#### Abstract

This paper presents a new method to extract a set of correlated genes with respect to multiple biological features. Relationships among genes on a specific feature are encoded as a graph structure whose nodes correspond to genes. For example, the genome is a graph representing positional correlations of genes on the chromosome, the pathway is a graph representing functional correlations of gene products, and the expression profile is a graph representing gene expression similarities. When a set of genes are localized in a single graph, such as a gene cluster on the chromosome, an enzyme cluster in the metabolic pathway, or a set of coexpressed genes in the microarray gene expression profile, this may suggest a functional link among those genes. The functional link would become stronger when the clusters are correlated; namely, when a set of corresponding genes form clusters in multiple graphs. The newly introduced heuristic algorithm extracts such correlated gene *clusters* as isomorphic subgraphs in multiple graphs by using inter-graph links that are defined based on biological relevance. Using the method, we found *E. coli* correlated gene clusters in which genes are related with respect to the positions in the genome and the metabolic pathway, as well as the 3D structural similarity. We also analyzed protein-protein interaction data by two-hybrid experiments and gene coexpression data by microarrays in S. cerevisiae, and estimated the possibility of utilizing our method for screening the datasets that are likely to contain many false positive relations.

**Keywords:** correlated gene cluster, binary relationships, graph comparison, clustering

## 1 Introduction

**Correlated gene clusters.** The complete genome sequence contains the information about ordering of genes along the chromosome. Besides such *geometrical* relationships, other features characterize relationships among genes, including *similarity* relationships based on sequences or 3D structures of gene products, and *functional* relationships in metabolic/regulatory pathways. When multiple gene-gene relationships can be found on different attributes as above, it would be interesting to see whether or not a set of genes share their mutual relationships in relation to each attribute. For example, as reviewed by Erlandsen *et al.* [2], the enzymes in the glycolytic pathway (Fig. 1) commonly display  $\alpha/\beta$  folds, which is obtained by examining the relationships of enzymes with respect to their structural similarities and neighboring relationships in the pathway. This type of observation has been made for a specific set of genes. Here we examine all the sets of genes in a given organism that are correlated with respect to more than one attribute.

Gene-gene relationships on a specific attribute can be denoted by using a set of binary relationships in a general manner. For example, let a binary operator ' $\sim$ ' denote a binary relationship between two genes, and let  $g_1, g_2, g_3$ , and  $g_4$  be a series of genes arranged in this order in a genome sequence, their geometrical relationships are broken down into a set of binary relationships { $g_1 \sim g_2, g_2 \sim g_3, g_3 \sim g_4$ }. A set of binary relationships among genes forms a graph structure as a whole. Fig. 2 shows three graphs  $G_1$  (genome),  $G_2$  (pathway), and  $G_3$  (similarity), where each graph node corresponds to a



Figure 1: A series of enzymes in the glycolytic pathway display  $\alpha/\beta$  folds.

gene or a gene product. In a graph, two nodes are connected by an edge (expressed by a solid line) when they are related by a binary relationship. In a set of genes, if all or most of the genes reserve their mutual relationships in multiple graphs, like the light gray nodes and the dark gray nodes in Fig. 2, the biological relevance among those genes is considered to be supported at high possibility. We call such a set of genes a *correlated gene cluster* (or simply, *correlated cluster*), by which we can characterize, classify, and predict the activities of genes.

Hyperedges — Introduction of inter-graph links. Finding correlated gene clusters can be formalized as a subgraph isomorphism problem and has been proved to be NP-complete. Therefore, some heuristics are required to cope with this problem. To extract correlated gene clusters from two graphs, Ogata et al. [5] introduced a notion called FRECs (Functionally Related Enzyme Clusters). They also introduced a set of inter-graph links between two nodes that correspond to the same gene in each graph, and searched isomorphic subgraphs in the two graphs so that the nodes of the subgraphs are connected by the intergraph links. By comparing the genome and the metabolic pathway, they found that seven Escherichia coli genes catalyzing successive reaction steps in peptidoglycan biosynthesis pathway are located in close position also along the genome sequence, for instance.

We can extend the notion of FRECs by increasing the number of graphs so that the additional graphs provide

have clusnotion  $C_1$   $h_2$   $h_3$   $h_4$   $h_5$   $h_6$   $h_6$ 

 $G_2$ 

(Pathway)

 $C_{1}^{2}$ 

 $h_1$ 

 $G_1$ 

(Genome)

(Similarity)

Figure 2: Correlated gene clusters.

information about gene-gene relations that cannot be found by just two graphs. Fig. 2 shows an example of correlated gene clusters ( $C_1$  and  $C_2$ ) in three graphs  $G_1$ ,  $G_2$ , and  $G_3$ . Here, dashed lines represent linking of corresponding genes from three graphs and grouping them into a single category (same gene). We call this linkage a *hyperedge* and define a distance between two hyperedges so that it can reflect the distance (typically, the shortest path length) between their nodes in each graph. By gathering hyperedges based on this distance, we can find a set of nodes that are tightly coupled in the graphs, that is, a correlated gene cluster.

**Correlation among known and unknown genes.** Recent high-throughput experimental technologies provide huge and potentially interesting datasets, but they often contain unknown and hypothetical relationships as well as erroneous relationships. For example, coexpression relationships by microarrays/oligochips and protein-protein interactions by two-hybrid analysis might have such characteristics. Today's standard approaches to analyze such datasets include, for example, clustering the genes according to similarity of expression patterns, and extracting densely connected network components in a protein-protein network. When a set of known genes can be placed into the same category, such approaches may uncover functional links to unknown genes based on some biological features. Our method basically follows this strategy. One of the advantages of our method over the existing ones is that it makes it possible to automatically incorporate multiple features observed in multiple datasets. Even if relationships among genes cannot be explained in a single graph, it is possible to improve the sensitivity of data analysis by evaluating corresponding relationships in additional graphs.

As a practical application of our method, we will present the correlated gene clusters found in *Escherichia coli* datasets and *Saccharomyces cerevisiae* datasets. The latter includes the two-hybrid protein-protein interaction dataset by Ito *et al.* [3] and the coexpression dataset based on microarray experiments by DeRisi *et al.* [1].

### 2 Method

**Input datasets.** As input datasets, we use a set of n graphs  $G = \{G_1, \ldots, G_n\}$  and a set of m hyperedges  $H = \{h_1, \ldots, h_m\}$ . When n graphs are used, we denote a hyperedge with an n-tuple  $h_i = (x_{1,i_1}, \ldots, x_{n,i_n})$ . Here, the kth element  $h_i^k = x_{k,i_k}$  is  $G_k$ 's node that constitutes the hyperedge  $(1 \le k \le n)$ , and we assume that a hyperedge consists of exactly n nodes to make the problem simple.

**Distance between hyperedges.** Suppose that there are *n* graphs. Let  $C_1 = \{h_{s_1}, \ldots, h_{s_p}\}$  and  $C_2 = \{h_{t_1}, \ldots, h_{t_q}\}$  be sets of hyperedges, and let  $C_1^k = \{h_{s_1}^k, \ldots, h_{s_p}^k\}$  and  $C_2^k = \{h_{t_1}^k, \ldots, h_{t_q}^k\}$  be sets of the *k*th elements of hyperedges in  $C_1$  and  $C_2$ , respectively. We define the distance between two sets of hyperedges  $C_1$  and  $C_2$  as follows:

$$D(C_1, C_2) = \sum_{1 \le s \le n} dis(C_1^s, C_2^s),$$
(1)

where  $dis(C_1^s, C_2^s)$  is the distance between  $C_1^s$  and  $C_2^s$ . Here, for example,  $dis(C_1^s, C_2^s)$  is defined as  $max\{d(x, y)|x \in C_1^s, y \in C_2^s\}$ , <sup>1</sup> where d(x, y) is the length of the shortest path between nodes x and y in graph  $G_s$  (which can be calculated by Dijkstra's algorithm or Warshall-Floyd's algorithm).

In Fig. 2, let  $H = \{h_1, h_2, ..., h_9\}$  denote a set of hyperedges, and suppose that they are divided into two distinct sets  $C_1 = \{h_1, ..., h_4\}$  and  $C_2 = \{h_5, ..., h_9\}$ . Distance between these two sets is  $D(C_1, C_2) = \sum_{1 \le s \le 3} dis(C_1^s, C_2^s) = dis(C_1^1, C_2^1) + dis(C_1^2, C_2^2) + dis(C_1^3, C_2^3) = 10 + 8 + 8 = 26.$ 

**Clustering of hyperedges.** Using the distance D, we cluster the hyperedges. Let C be the initial set of clusters, each of which consists of a single hyperedge, i.e.,  $C = \{\{h_1\}, \ldots, \{h_m\}\}\}$ . Starting with C, we iterate the procedure to pick two clusters between which the distance is the smallest and to merge them into a new cluster (i.e., hierarchical clustering using the distance D). To avoid distant genes being merged into the same cluster, we use a threshold defined for each graph. Let  $p_i$  be the threshold for graph  $G_i$ . When the path length between two nodes x and y is greater than  $p_i$  in  $G_i$ , we change the value of d(x, y) to infinity, and leave the pairs of clusters whose distance is infinity untouched. When there are no cluster pairs whose distance is not infinity we stop the clustering procedure and thus obtain correlated gene clusters. Since two nodes within length  $p_i$  can be merged into the same cluster even if they are not directly connected, the parameter  $p_i$  makes it possible to find gene clusters that are not strictly conserved in the graphs.

### 3 Results

We implemented the algorithm by using the C++ language on a part of a SiliconGraphics Origin  $3800^2$  running under IRIX 6.5. Part of the program (e.g., calculation of N to N shortest paths using Dijkstra's algorithm) is parallelized by the POSIX thread library. We used this system to carry out multiple graph comparison and found correlated gene clusters in *E.coli* and *S.cerevisiae* datasets. Required computing resources depend on datasets. However, to estimate that the memory usage was feasible, we limited it to 512MB by the C shell limit command.

<sup>&</sup>lt;sup>1</sup>This definition carries out "complete linkage clustering". For "single linkage clustering", min is used instead of max. <sup>2</sup>256 MIPS R14000(500MHz) processors, 256GB main memory, and 8MB L2 cache for each processor.

#### 3.1 *E.coli* correlated gene clusters

We first searched correlated gene clusters in the three *E.coli* datasets, whose nodes correspond to *E.coli* genes or gene products. The *E.coli* genome dataset ( $G_1$ : 4,396 nodes and 4,396 edges) defines neighboring relationships among genes in the genome sequence. Two genes that are directly next to each other are connected by an edge. The *E.coli* pathway dataset ( $G_2$ : 761 nodes and 1,223 edges) defines positional relationships among gene products in the metabolic pathway.<sup>3</sup> The *E.coli* structure similarity dataset ( $G_3$ : 538 nodes and 3,823 edges) defines 3D structural similarities among proteins.<sup>4</sup> Two proteins in the same category are connected by an edge. We used a value 1 as the weight of each edge. Besides these three graphs, we used 917 hyperedges connecting genes and their products in the graphs. Note that since a single node can be contained in multiple hyperedges, the number of hyperedges can be greater than that of nodes of a graph.

By applying our algorithm with the threshold parameters  $p_1 = 2$ ,  $p_2 = 3$ , and  $p_3 = 0$  (execution time was 140 seconds), we found correlated gene clusters in the biotin metabolism pathway (Fig. 3(A)) and the tryptophan biosynthesis pathway (Fig. 3(B)). Table 1 shows the list of the *E.coli* genes constituting the correlated gene clusters in those pathways. Those clusters retain mutual relationships of genes with respect to positions in the genome sequence and structural similarity besides the relationships in the pathways. All the genes in the biotin pathway classified as "alpha and beta" ( $\alpha/\beta$ ), and the genes in the tryptophan pathway display TIM-barrel structures. We note, however, that these correlations are already known. Although the result confirms the validity of our method for multiple graph comparison, the addition of a third graph was too restrictive to uncover any new findings. Pairwise graph comparison is biologically more meaningful especially when the datasets do not appear to contain erroneous data.

(A) Biotin metabolism pathway

(B) Tryptophan biosynthesis pathway



Figure 3: *E.coli* correlated gene clusters.

(A) Biotin	metabolism
------------	------------

ase) [EC:2.3.1.47] [SP:BIOF_ECOLI]         b0778       bioD; dethiobiotin synthetase (dethiobiotin synthase) (dtb synthetase) (DTBS) [EC:6.3.3.3] [SP:BIOD_ECOLI]         (B) Tryptophan biosynthesis         b1260       trpA; tryptophan synthase alpha chain [EC:4.2.1.20] [SP:TRPA_ECOLI]         b1261       trpB; tryptophan synthase beta chain [EC:4.2.1.20] [SP:TRPB_ECOLI]		bioA; adenosylmethionine-8-amino-7-oxononanoate aminotransferase (7,8-diamino-pelargonic acid aminotransferase) (dapA amino-
ase) [EC:2.3.1.47] [SP:BIOF_ECOLI]         b0778       bioD; dethiobiotin synthetase (dethiobiotin synthase) (dtb synthetase) (DTBS) [EC:6.3.3.3] [SP:BIOD_ECOLI]         (B) Tryptophan biosynthesis         b1260       trpA; tryptophan synthase alpha chain [EC:4.2.1.20] [SP:TRPA_ECOLI]         b1261       trpB; tryptophan synthase beta chain [EC:4.2.1.20] [SP:TRPB_ECOLI]		transferase) [EC:2.6.1.62] [SP:BIOA_ECOLI]
b0778       bioD; dethiobiotin synthetase (dethiobiotin synthase) (dtb synthetase) (DTBS) [EC:6.3.3.3] [SP:BIOD_ECOLI]         (B)       Tryptophan biosynthesis         b1260       trpA; tryptophan synthase alpha chain [EC:4.2.1.20] [SP:TRPA_ECOLI]         b1261       trpB; tryptophan synthase beta chain [EC:4.2.1.20] [SP:TRPB_ECOLI]	b0776	bioF; 8-amino-7-oxononanoate synthase (7-keto-8-amino-pelargonic acid synthetase) (7-kap synthetase) (L-alanine-pimelyl CoA lig-
(B) Tryptophan biosynthesis b1260 trpA; tryptophan synthase alpha chain [EC:4.2.1.20] [SP:TRPA_ECOLI] b1261 trpB; tryptophan synthase beta chain [EC:4.2.1.20] [SP:TRPB_ECOLI]		ase) [EC:2.3.1.47] [SP:BIOF_ECOLI]
b1260 trpA; tryptophan synthase alpha chain [EC:4.2.1.20] [SP:TRPA_ECOLI] b1261 trpB; tryptophan synthase beta chain [EC:4.2.1.20] [SP:TRPB_ECOLI]	b0778	bioD; dethiobiotin synthetase (dethiobiotin synthase) (dtb synthetase) (DTBS) [EC:6.3.3.3] [SP:BIOD_ECOLI]
b1260 trpA; tryptophan synthase alpha chain [EC:4.2.1.20] [SP:TRPA_ECOLI] b1261 trpB; tryptophan synthase beta chain [EC:4.2.1.20] [SP:TRPB_ECOLI]		
b1261 trpB; tryptophan synthase beta chain [EC:4.2.1.20] [SP:TRPB_ECOLI]	(B) T	ryptophan biosynthesis
		i j propinali biobj infieste
	b1260	
b1262 trpC; indole-3-glycerol phosphate synthase (IGPS) / N-(5'-phospho-ribosyl)anthranilate isomerase (PRAI) [EC:4.1.1.48 5.3]		trpA; tryptophan synthase alpha chain [EC:4.2.1.20] [SP:TRPA_ECOLI]
[SP:TRPC-ECOLI]		trpA; tryptophan synthase alpha chain [EC:4.2.1.20] [SP:TRPA_ECOLI]
b1264 trpE; anthranilate synthase component I [EC:4.1.3.27] [SP:TRPE_ECOLI]	b1261	trpA; tryptophan synthase alpha chain [EC:4.2.1.20] [SP:TRPA_ECOLI] trpB; tryptophan synthase beta chain [EC:4.2.1.20] [SP:TRPB_ECOLI] trpC; indole-3-glycerol phosphate synthase (IGPS) / N-(5'-phospho-ribosyl)anthranilate isomerase (PRAI) [EC:4.1.1.48 5.3.1.24]

Table 1: E. coli genes constituting correlated gene clusters.

#### 3.2 S.cerevisiae correlated gene clusters

In this section, we present the results of screening the two-hybrid protein-protein interaction dataset. To evaluate whether or not protein-protein interactions in the dataset are significant, we searched correlated gene clusters. If an interaction or a relation is also observed in biological attributes other than protein-protein interactions, we judge the interaction is relevant.

As the target two-hybrid protein-protein interaction dataset, we used the one developed by Ito *et al.* [3]. This dataset (called "All data" in the original paper), used as the first graph  $G_1$ , includes

<sup>&</sup>lt;sup>3</sup>Compiled by Ogata *et al.* [5]. In this datasets, each node has a unique identifier, but it is related to genes by its EC number that is assigned as a "label", introducing redundancy.

<sup>&</sup>lt;sup>4</sup>Based on SCOP database release 1.50 [4].

See also "SCOP 3D-fold" from http://www.genome.ad.jp/kegg/kegg2.html.

3,280 genes (nodes) and 4,549 bait-prey interactions (edges). By calculating correlated gene clusters, we compared this dataset with the following datasets (as the second graph  $G_2$ ) that contain biological relationships: (1) *S.cerevisiae* coexpression dataset, (2) *S.cerevisiae* pathway dataset, and (3) *E.coli* genome dataset.

#### (1) S.cerevisiae two-hybrid v.s. S.cerevisiae coexpression

We used the coexpression dataset that was derived from the results of microarray analysis by DeRisi *et al.* [1]. This dataset consists of time-course measurements of gene expressions, and the similarities of chronological changes of expression patterns are compared among gene pairs by means of correlation coefficients.<sup>5</sup> We define a pair of genes are coexpressed when the correlation coefficient is not less than 0.97. Then the dataset consists of 3,307 genes (nodes) and 81,628 coexpressed gene pairs (edges). By using 1,547 hyperedges that connect the identical genes in the two-hybrid dataset and this coexpression dataset, we searched correlated gene clusters (execution time was 48 minutes).

It is interesting to note that these two datasets share only one gene-gene relationship (YGR148C -YLR295C). On the other hand, by including indirect gene-gene relationships through one intermediate gene (i.e., for the *i*th graph, setting the threshold  $p_i = 2$ ), we found a total of 249 correlated gene clusters. The cluster size ranges from two to nine. Table 2 lists examples of correlated gene clusters that consist of genes whose annotations contain keywords (A) "ribosomal protein", (B) "translation", and (C) "transcription".<sup>6</sup> The genes between two horizontal lines correspond to a correlated gene cluster.

Table 3 shows the correlated gene clusters consisting of the genes that are also referred to in Figure 3 of the original paper by Ito *et al.* [3]. By comparing their two-hybrid dataset with the coexpression dataset by DeRisi *et al.* [1], we found additional sixteen sets of putative gene-gene relationships with respect to (A) autophagy, (B) spindle pole body function, and (C) vesicular transport as shown in Table 3. The genes appear in the paper by Ito *et al.* are hilighted with bold fonts.

#### (2) S.cerevisiae two-hybrid v.s. S.cerevisiae pathway

The *S.cerevisiae* pathway dataset (574 nodes and 851 edges) defines positional relationships among gene products in the metabolic pathway.<sup>7</sup> Using 745 hyperedges, we searched correlated gene clusters that reserve their mutual relationships both in the two-hybrid dataset and this pathway dataset (execution time was 32 seconds). The genes that interact through one intermediate gene were included in the same cluster (i.e., for the *i*th graph, setting  $p_i = 2$ ). Table 4 shows a part of the resulting correlated gene clusters. In this table, we divided the correlated gene clusters into two categories according to whether each cluster contains (A) a single EC number or (B) multiple EC numbers.

In the first category with a single EC number, correlated gene clusters are mainly related to complexes. For example, the first two gene clusters (YJL140W~YOR210W) and (YJR063W and YDR156W) are related to RNA polymerases. On the other hand, in the category with multiple EC numbers, correlated gene clusters are located in close positions in a pathway. For example, YBR145W and YER073W (being more precise, two enzymes with EC numbers 1.1.1.1 and 1.2.1.3) are next to each other in the bile acids biosynthesis pathway, YFR047C and YLR209C (two enzymes with EC numbers 2.4.2.19, and 2.4.2.1) are next to each other through one intermediate node in the nicotinate and nicotinamide metabolism pathway.

(3) S.cerevisiae two-hybrid v.s. E.coli genome In the previous parts, we focused on a set of graphs defining the relationships among genes with respect to a single organism (E.coli or S.cerevisiae), and by using a set of hyperedges connecting the same genes or gene products in multiple graphs, we

<sup>&</sup>lt;sup>5</sup>See also KEGG/BRITE database at http://www.genome.ad.jp/brite/

and KEGG/EXPRESSION database from http://www.genome.ad.jp/kegg/kegg2.html.

<sup>&</sup>lt;sup>6</sup>A total list of the correlated gene clusters is obtained from http://web.kuicr.kyoto-u.ac.jp/~nakaya/pub/giw01/.

<sup>&</sup>lt;sup>7</sup>Compiled by Ogata *et al.*1 [5]. See also the footnote of section 3.1.

#### (A) Ribosomal protein

YNR037C40S ribosomal protein S15e [SP:YN8L_YEAST]YPL004CYPL004C; Lpa13pYNR071Csimilar to UDP-glucose 4-epimerase GAL10P [SP:YN9A_YEAST]YDL230WPTP1; protein-tyrosine phosphatase 1 (ptpase 1) [EC:3.1.3.48] [SP:PTP1_YEAST]YGL222Cunknown [SP:YGX2_YEAST]YJR119Cunknown [SP:YJ89_YEAST]YDR008CunknownYDR203WunknownYOR097Cunknown	
YNR071C       similar to UDP-glucose 4-epimerase GAL10P [SP:YN9A_YEAST]         YDL230W       PTP1; protein-tyrosine phosphatase 1 (ptpase 1) [EC:3.1.3.48] [SP:PTP1_YEAST]         YGL22C       unknown [SP:YGX2_YEAST]         YJR119C       unknown [SP:YJ89_YEAST]         YDR008C       unknown         YDR203W       unknown         YOR097C       unknown	
YDL230WPTP1; protein-tyrosine phosphatase 1 (ptpase 1) [EC:3.1.3.48] [SP:PTP1_YEAST]YGL222Cunknown [SP:YGX2_YEAST]YJR119Cunknown [SP:YJ89_YEAST]YDR008CunknownYDR203WunknownYOR097Cunknown	
YGL222C unknown [SP:YGX2_YEAST] YJR119C unknown [SP:YJ89_YEAST] YDR008C unknown YDR203W unknown YOR097C unknown	
YJR119C unknown [SP:YJ89_YEAST] YDR008C unknown YDR203W unknown YOR097C unknown	
YDR008C unknown YDR203W unknown YOR097C unknown	
YOR097C unknown	
YJR123W RPS5; 40S ribosomal protein S5e [SP:RS5_YEAST]	
YDL075W RPL31A; 60S ribosomal protein L31e [SP:RL31_YEAST]	
YHL033C RPL8A; 60S ribosomal protein L7Ae [SP:RL4A_YEAST]	
YDL208W NHP2; high mobility group-like nuclear protein [SP:NHP2_YEAST] YMR202W ERG2; C-8 sterol isomerase [SP:ERG2_YEAST]	
YNL16W unknown [SP:YNO6.YEAST]	
YBL072C RPS8A; 40S ribosomal protein S8e [SP:RS8_YEAST]	
YDL081C RPP1A: 60S acidic ribosomal protein LP1 [SP:RLA1-YEAST]	
YLR312C unknown	
YGL189C RPS26A; 40S ribosomal protein S26e [SP:R26A_YEAST]	
YGL030W RPL30; 60S ribosomal protein L30e [SP:RL30_YEAST]	
YDR529C QCR7; ubiquinol-cytochrome c reductase subunit 7 [EC:1.10.2.2] [SP:UCR7_YEAST]	
YOR167C RPS28A; 40S ribosomal protein S28e [SP:RS28_YEAST]	
YLR264W RPS28B; 40S ribosomal protein S28e [SP:RS28_YEAST]	
YLR340W RPP0; 60S acidic <b>ribosomal</b> protein LP0	
YDR382W     RPP2B; 60S acidic ribosomal protein LP2 [SP:RLA4_YEAST]       YGR085C     RPL11B; 60S ribosomal protein L11e [SP:RL11_YEAST]	
YJR048W CYC1; cytochrome c, iso-1 [SP:CYC1-YEAST]	
(B) Translation	
YPR016C CDC95; translation initiation factor 6 (eIF6)	
YDR012W RPL4B; 60S ribosomal protein L4e [SP:RL4B_YEAST]	
YFL037W TUB2; beta-tubulin [SP:TBB_YEAST]	
YBR143C SUP45, SUP1, SAL4; eukaryotic peptide chain release factor eRF subunit 1 [SP:ERF1_Y]	
YNL062C GCD10, TIF33; eukaryotic <b>translation</b> initiation factor eIF-3 gamma subunit [SP:IF33.]	
YIL066C RNR3; ribonucleoside-diphosphate reductase alpha chain [EC:1.17.4.1] [SP:RIR3_YEAST YGR204W ADE3; methylenetetrahydrofolate dehydrogenase (NADP+) /	
methenyltetrahydrofolate cyclohydrolase / formate-tetrahydrofolate ligase [EC:1.5.1.5 3.5]	496343 [SP-C1TC VEAST]
YPR041W TIF5: eukaryotic translation initiation factor eIF-5 [SP:IF5-YEAST]	.4.9 0.3.4.9 [51.0110_1EA51]
YDR224C HTB1; histone H2B.1 [SP:H2B1_YEAST]	
YGR222W PET54; mitochondrial splicing protein and translational activator [SP:PT54_YEAST]	
YAR042W SWH1; probable NH-terminus of OSH1/SWH1 [SP:SWH1_YEAST]	
YOL139C CDC33, TIF45; eukaryotic translation initiation factor eIF-4E [SP:IF4E_YEAST]	
YOR276W CAF20, CAP20; mRNA CAP-binding protein (eIF4F), 20K subunit [SP:IF43_YEAST]	
YPR163C TIF3, STM1; eukaryotic <b>translation</b> initiation factor eIF-4B [SP:IF4B_YEAST]	
YBR038W CHS2; chitin synthase 2 [EC:2.4.1.16] [SP:CHS2 YEAST]	
YBR038W         CHS2; chitin synthase 2 [EC:2.4.1.16] [SP:CHS2_YEAST]           YKR026C         GCN3, AAS2, TIF221; translation initiation factor eIF-2B alpha subunit [SP:E2BA_YE	AST]
YBR038W CHS2; chitin synthase 2 [EC:2.4.1.16] [SP:CHS2 YEAST]	AST]
YBR038W         CHS2; chitin synthase 2 [EC:2.4.1.16] [SP:CHS2_YEAST]           YKR026C         GCN3, AAS2, TIF221; translation initiation factor eIF-2B alpha subunit [SP:E2BA_YE           YPR033C         HTS1; histidyl-tRNA synthetase [EC:6.1.1.21] [SP:SYH_YEAST]	AST]
YBR038W       CHS2; chitin synthase 2 [EC:2.4.1.16] [SP:CHS2_YEAST]         YKR026C       GCN3, AAS2, TIF221; translation initiation factor eIF-2B alpha subunit [SP:E2BA_YE         YPR033C       HTS1; histidyl-tRNA synthetase [EC:6.1.1.21] [SP:SYH_YEAST]         (C) Transcription	AST]
YBR038W       CHS2; chitin synthase 2 [EC:2.4.1.16] [SP:CHS2_YEAST]         YKR026C       GCN3, AAS2, TIF221; translation initiation factor eIF-2B alpha subunit [SP:E2BA_YE         YPR033C       HTS1; histidyl-tRNA synthetase [EC:6.1.1.21] [SP:SYH_YEAST]         (C) Transcription	AST]
YBR038W         CHS2; chitin synthase 2 [EC:2.4.1.16] [SP:CHS2_YEAST]           YKR026C         GCN3, AAS2, TIF221; translation initiation factor eIF-2B alpha subunit [SP:E2BA_YE           YPR033C         HTS1; histidyl-tRNA synthetase [EC:6.1.1.21] [SP:SYH_YEAST]           (C) Transcription         YQR344C           YGR151C         unknown [SP:YG3N_YEAST]           YNL300W         unknown [SP:YN40_YEAST]	AST]
YBR038W       CHS2; chitin synthase 2 [EC:2.4.1.16] [SP:CHS2_YEAST]         YKR026C       GCN3, AAS2, TIF221; translation initiation factor eIF-2B alpha subunit [SP:E2BA_YE         YPR033C       HTS1; histidyl-tRNA synthetase [EC:6.1.1.21] [SP:SYH_YEAST]         (C) Transcription         YOR344C       TYE7, SGC1; basic helix-loop-helix transcription factor [SP:TYE7_YEAST]         YGR151C       unknown [SP:YG3N_YEAST]         YNL300W       unknown [SP:YN40_YEAST]         YOR062C       unknown	AST]
YBR038W         CHS2; chitin synthase 2 [EC:2.4.1.16] [SP:CHS2_YEAST]           YKR026C         GCN3, AAS2, TIF221; translation initiation factor eIF-2B alpha subunit [SP:E2BA_YE           YPR033C         HTS1; histidyl-tRNA synthetase [EC:6.1.1.21] [SP:SYH_YEAST]           (C) Transcription         YOR344C         TYE7, SGC1; basic helix-loop-helix transcription factor [SP:TYE7_YEAST]           YGR151C         unknown [SP:YG3N_YEAST]         unknown [SP:YN40_YEAST]           YOR062C         unknown         SP:YN40_YEAST]           YMR039C         SUB1, TSP1; transcriptional coactivator [SP:SUB1_YEAST]	AST]
YBR038W       CHS2; chitin synthase 2 [EC:2.4.1.16] [SP:CHS2_YEAST]         YKR026C       GCN3, AAS2, TIF221; translation initiation factor eIF-2B alpha subunit [SP:E2BA_YE         YPR033C       HTS1; histidyl-tRNA synthetase [EC:6.1.1.21] [SP:SYH_YEAST]         (C) Transcription       TYE7, SGC1; basic helix-loop-helix transcription factor [SP:TYE7_YEAST]         YOR344C       TYE7, SGC1; basic helix-loop-helix transcription factor [SP:TYE7_YEAST]         YNL300W       unknown [SP:YG3N_YEAST]         YNL300W       unknown [SP:YN40_YEAST]         YOR062C       unknown         YMR039C       SUB1, TSP1; transcriptional coactivator [SP:SUB1_YEAST]         YIL004C       BET1; protein transport protein [SP:BET1_YEAST]	AST]
YBR038W       CHS2; chitin synthase 2 [EC:2.4.1.16] [SP:CHS2_YEAST]         YKR026C       GCN3, AAS2, TIF221; translation initiation factor eIF-2B alpha subunit [SP:E2BA_YE         YPR033C       HTS1; histidyl-tRNA synthetase [EC:6.1.1.21] [SP:SYH_YEAST]         (C) Transcription       TYE7, SGC1; basic helix-loop-helix transcription factor [SP:TYE7_YEAST]         YGR151C       unknown [SP:YG3N_YEAST]         YNL300W       unknown [SP:YM40_YEAST]         YOR062C       unknown         YHR039C       SUB1, TSP1; transcriptional coactivator [SP:SUB1_YEAST]         YIL004C       BET1; protein transport protein [SP:BET1_YEAST]         YIL005W       protein disulfide-isomerase [EC:5.3.4.1] [SP:YIA5_YEAST]	AST]
YBR038W       CHS2; chitin synthase 2 [EC:2.4.1.16] [SP:CHS2_YEAST]         YKR026C       GCN3, AAS2, TIF221; translation initiation factor eIF-2B alpha subunit [SP:E2BA_YE         YPR033C       HTS1; histidyl-tRNA synthetase [EC:6.1.1.21] [SP:SYH_YEAST]         (C) Transcription         YOR344C       TYE7, SGC1; basic helix-loop-helix transcription factor [SP:TYE7_YEAST]         YOR151C       unknown [SP:YG3N_YEAST]         YOR062C       unknown [SP:YN40_YEAST]         YOR062C       unknown         YMR039C       SUB1, TSP1; transcriptional coactivator [SP:SUB1_YEAST]         YIL004C       BET1; protein transport protein [SP:BET1_YEAST]         YIL005W       protein disulfide-isomerase [EC:5.3.4.1] [SP:YIA5_YEAST]         YIR017C       MET28; transcriptional activator of sulfur amino acid metabolism [SP:MT28_YEAST]	AST]
YBR038W       CHS2; chitin synthase 2 [EC:2.4.1.16] [SP:CHS2_YEAST]         YKR026C       GCN3, AAS2, TIF221; translation initiation factor eIF-2B alpha subunit [SP:E2BA_YE         YPR033C       HTS1; histidyl-tRNA synthetase [EC:6.1.1.21] [SP:SYH_YEAST]         (C) Transcription       TYE7, SGC1; basic helix-loop-helix transcription factor [SP:TYE7_YEAST]         YGR151C       unknown [SP:YG3N_YEAST]         YNL300W       unknown [SP:YM40_YEAST]         YOR062C       unknown         YHL004C       SUB1, TSP1; transcriptional coactivator [SP:SUB1_YEAST]         YIL005W       protein disulfide-isomerase [EC:5.3.4.1] [SP:YIA5_YEAST]	AST]
YBR038W         CHS2; chitin synthase 2 [EC:2.4.1.16] [SP:CHS2_YEAST]           YKR026C         GCN3, AAS2, TIF221; translation initiation factor eIF-2B alpha subunit [SP:E2BA_YE           YPR033C         HTS1; histidyl-tRNA synthetase [EC:6.1.1.21] [SP:SYH_YEAST]           (C) Transcription         TYE7, SGC1; basic helix-loop-helix transcription factor [SP:TYE7_YEAST]           YOR344C         unknown [SP:YG3N_YEAST]           YNL300W         unknown [SP:YG3N_YEAST]           YNR009C         SUB1, TSP1; transcriptional coactivator [SP:SUB1_YEAST]           YIL004C         BET1; protein transport protein [SP:BET1_YEAST]           YIR017C         MET28; transcriptional activator of sulfur amino acid metabolism [SP:MT28_YEAST]           YIR017C         MET28; transcriptional activator of sulfur amino acid metabolism [SP:MT28_YEAST]	AST]
YBR038W       CHS2; chitin synthase 2 [EC:2.4.1.16] [SP:CHS2_YEAST]         YKR026C       GCN3, AAS2, TIF221; translation initiation factor eIF-2B alpha subunit [SP:E2BA_YE         YPR033C       HTS1; histidyl-tRNA synthetase [EC:6.1.1.21] [SP:SYH_YEAST]         (C) Transcription       TYE7, SGC1; basic helix-loop-helix transcription factor [SP:TYE7_YEAST]         YOR344C       unknown [SP:YG3N_YEAST]         YNL300W       unknown [SP:YM40_YEAST]         YOR062C       unknown [SP:YN40_YEAST]         YMR030C       SUB1, TSP1; transcriptional coactivator [SP:SUB1_YEAST]         YIL004C       BET1; protein transport protein [SP:BET1_YEAST]         YIR017C       MET28; transcriptional activator of suffur amino actid metabolism [SP:MT28_YEAST]         YKR101W       SIR1; silencing regulatory protein [SP:SIR1_YEAST]         YIL025C       unknown [SP:YIC5_YEAST]         YGL112C       TAF60; transcription initiation factor [SP:T2D5_YEAST]         YGL122C       NAB2; nuclear polyadenylated RNA-binding protein [SP:NAB2_YEAST]	AST]
YBR038W       CHS2; chitin synthase 2 [EC:2.4.1.16] [SP:CHS2_YEAST]         YKR026C       GCN3, AAS2, TIF221; translation initiation factor eIF-2B alpha subunit [SP:E2BA_YE         YPR033C       HTS1; histidyl-tRNA synthetase [EC:6.1.1.21] [SP:SYH_YEAST]         (C) Transcription       TYE7, SGC1; basic helix-loop-helix transcription factor [SP:TYE7_YEAST]         YOR344C       TYE7, SGC1; basic helix-loop-helix transcription factor [SP:TYE7_YEAST]         YOR050C       unknown [SP:YG3N_YEAST]         YNL300W       unknown [SP:YG4N_YEAST]         YOR062C       unknown [SP:YN40_YEAST]         YIL004C       BET1; protein transport protein [SP:BET1_YEAST]         YIL005W       protein disulfide-isomerase [EC:5.3.4.1] [SP:YIA5_YEAST]         YIR017C       MET28; transcriptional activator of sulfur amino acid metabolism [SP:MT28_YEAST]         YIL025C       unknown [SP:YIC5_YEAST]         YIL025C       unknown [SP:YIC5_YEAST]         YGL112C       TAF60; transcription initiation factor [SP:T2D5_YEAST]         YGL112C       NAB2; nuclear polyadenylated RNA-binding protein [SP:NAB2_YEAST]         YKL109W       HAP4; transcriptional activator [SP:HAP4_YEAST]	AST]
YBR038WCHS2; chitin synthase 2 [EC:2.4.1.16] [SP:CHS2_YEAST]YKR026CGCN3, AAS2, TIF221; translation initiation factor eIF-2B alpha subunit [SP:E2BA_YEYPR033CHTS1; histidyl-tRNA synthetase [EC:6.1.1.21] [SP:SYH_YEAST](C) TranscriptionYOR344CTYE7, SGC1; basic helix-loop-helix transcription factor [SP:TYE7_YEAST]YGR151Cunknown [SP:YG3N_YEAST]YNL300Wunknown [SP:YM40_YEAST]YOR062CunknownYMR039CSUB1, TSP1; transcriptional coactivator [SP:SUB1_YEAST]YIL004CBET1; protein transport protein [SP:BET1_YEAST]YIR017CMET28; transcriptional activator of sulfur amino acid metabolism [SP:MT28_YEAST]YKR101WSIR1; silencing regulatory protein [SP:SIR1_YEAST]YIL025Cunknown [SP:YIC5_YEAST]YGL112CTAF60; transcription initiation factor [SP:T2D5_YEAST]YGL122CNAB2; nuclear polyadenylated RNA-binding protein [SP:NAB2_YEAST]YKL109WHAP4; transcriptional activator [SP:HAP4_YEAST]YGL236Cunknown [SP:YG4Z_YEAST]	AST]
YBR038W       CHS2; chitin synthase 2 [EC:2.4.1.16] [SP:CHS2_YEAST]         YKR026C       GCN3, AAS2, TIF221; translation initiation factor eIF-2B alpha subunit [SP:E2BA_YE         YPR033C       HTS1; histidyl-tRNA synthetase [EC:6.1.1.21] [SP:SYH_YEAST]         (C)       Transcription         YOR344C       TYE7, SGC1; basic helix-loop-helix transcription factor [SP:TYE7_YEAST]         YOR151C       unknown [SP:YG3N_YEAST]         YNL300W       unknown [SP:YN40_YEAST]         YOR062C       unknown         YPT, soc1; transcriptional coactivator [SP:SUB1_YEAST]         YIL004C       BET1; protein transport protein [SP:BET1_YEAST]         YIL005W       protein disulfide-isomerase [EC:5.3.4.1] [SP:YIA5_YEAST]         YKR101W       SIR1; silencing regulatory protein [SP:SIR1_YEAST]         YKR101W       SIR1; silencing regulatory protein [SP:SIR1_YEAST]         YGL122C       NAB2; nuclear polyadenylated RNA-binding protein [SP:NAB2_YEAST]         YGL122C       NAB2; nuclear polyadenylated RNA-binding protein [SP:NAB2_YEAST]         YGL122C       NAB2; nuclear polyadenylated RNA-binding protein [SP:NAB2_YEAST]         YGR250C       YAP6; transcriptional activator [SP:HAP4_YEAST]         YGR250C       YAP6; transcription factor of a fungal-specific family of bzip proteins	
YBR038W       CHS2; chitin synthase 2 [EC:2.4.1.16] [SP:CHS2_YEAST]         YKR026C       GCN3, AAS2, TIF221; translation initiation factor eIF-2B alpha subunit [SP:E2BA_YE         YPR033C       HTS1; histidyl-tRNA synthetase [EC:6.1.1.21] [SP:SYH_YEAST]         (C) Transcription       TYE7, SGC1; basic helix-loop-helix transcription factor [SP:TYE7_YEAST]         YOR344C       unknown [SP:YG3N_YEAST]         YNL300W       unknown [SP:YG3N_YEAST]         YNL00W       unknown [SP:YN40_YEAST]         YOR062C       unknown [SP:YN40_YEAST]         YIL004C       BET1; protein transport protein [SP:BET1_YEAST]         YIR017C       MET28; transcriptional activator of sulfur amino acid metabolism [SP:MT28_YEAST]         YIL025C       unknown [SP:YIC5_YEAST]         YIL025C       unknown [SP:YIC5_YEAST]         YGL112C       TAF60; transcriptional activator [SP:SIR1_YEAST]         YGL122C       NAB2; nuclear polyadenylated RNA-binding protein [SP:NAB2_YEAST]         YKL109W       HAP4; transcriptional activator [SP:HAP4_YEAST]         YGR236C       unknown [SP:YG4Z_YEAST]         YGR236C       unknown [SP:YG4Z_YE	
YBR038WCHS2; chitin synthase 2 [EC:2.4.1.16] [SP:CHS2_YEAST]YKR026CGCN3, AAS2, TIF221; translation initiation factor eIF-2B alpha subunit [SP:E2BA_YEYPR033CHTS1; histidyl-tRNA synthetase [EC:6.1.1.21] [SP:SYH_YEAST](C) TranscriptionTYE7, SGC1; basic helix-loop-helix transcription factor [SP:TYE7_YEAST]YGR151Cunknown [SP:YG3N_YEAST]YNL300Wunknown [SP:YN40_YEAST]YOR062CunknownYHL004CBET1; protein transport protein [SP:BET1_YEAST]YIL005Wprotein disulfide-isomerase [EC:5.3.4.1] [SP:YIA5_YEAST]YIR017CMET28; transcriptional activator of sulfur amino acid metabolism [SP:MT28_YEAST]YIL025Cunknown [SP:YIC5_YEAST]YGL112CTAF60; transcriptional initiation factor [SP:T2D5_YEAST]YGL12CYAF6; transcriptional activator [SP:T2D5_YEAST]YGL12CYAF6; transcriptional activator [SP:HAP4_YEAST]YGL12CYAF6; transcription factor [SP:HAP4_YEAST]YKL109WHAP4; transcription factor [SP:HAP4_YEAST]YGR236Cunknown [SP:YG4Z_YEAST]YDR259CYAP6; transcription factor of a fungal-specific family of bzip proteinsYMR11CSuccinate dehydrogenase (ubiquinone) cytochrome b subunit precursor [EC:1.3.5.1] [SP:YYIL084CSDS3; transcriptional regulator [SP:SDS3_YEAST]	
YBR038W       CHS2; chitin synthase 2 [EC:2.4.1.16] [SP:CHS2_YEAST]         YKR026C       GCN3, AAS2, TIF221; translation initiation factor eIF-2B alpha subunit [SP:E2BA_YE         YPR033C       HTS1; histidyl-tRNA synthetase [EC:6.1.1.21] [SP:SYH_YEAST]         (C) Transcription	
YBR038WCHS2; chitin synthase 2 [EC:2.4.1.16] [SP:CHS2_YEAST]YKR026CGCN3, AAS2, TIF221; translation initiation factor eIF-2B alpha subunit [SP:E2BA_YEYPR033CHTS1; histidyl-tRNA synthetase [EC:6.1.1.21] [SP:SYH_YEAST](C) TranscriptionYOR344CTYE7, SGC1; basic helix-loop-helix transcription factor [SP:TYE7_YEAST]YOR341Cunknown [SP:YG3N_YEAST]YNL300Wunknown [SP:YM40_YEAST]YNL300Wunknown [SP:YN40_YEAST]YNL300Wunknown [SP:YN40_YEAST]YIL004CBET1; protein transport protein [SP:BET1_YEAST]YIL005Wprotein disulfide-isomerase [EC:5.3.4.1] [SP:YIA5_YEAST]YIR017CMET28; transcriptional activator of sulfur amino acid metabolism [SP:MT28_YEAST]YIK101WSIR1; silencing regulatory protein [SP:SIR1_YEAST]YGL112CNAB2; nuclear polyadenylated RNA-binding protein [SP:NAB2_YEAST]YKR100WHAP4; transcriptional activator [SP:HAP4_YEAST]YGR236Cunknown [SP:YG4Z_YEAST]YDR259CYAP6; transcriptional factor of a fungal-specific family of bzip proteinsYMR118Csuccinate dehydrogenase (ubiquinone) cytochrome b subunit precursor [EC:1.3.5.1] [SP:YYIL084CSDS3; transcriptional regulator [SP:SDS3_YEAST]YNL202WSPS19; peroxisomal 2,4-diencyl-CoA reductase [SP:SP19_YEAST]YOR358WHAP5; transcriptional activator [SP:HAP5_YEAST]	
YBR038WCHS2; chitin synthase 2 [EC:2.4.1.16] [SP:CHS2_YEAST]YKR026CGCN3, AAS2, TIF221; translation initiation factor eIF-2B alpha subunit [SP:E2BA_YEYPR033CHTS1; histidyl-tRNA synthetase [EC:6.1.1.21] [SP:SYH_YEAST](C) TranscriptionYOR344CTYE7, SGC1; basic helix-loop-helix transcription factor [SP:TYE7_YEAST]YOR341Cunknown [SP:YG3N_YEAST]YNL300Wunknown [SP:YG3N_YEAST]YNL300Wunknown [SP:YY40_YEAST]YMR039CSUB1, TSP1; transcriptional coactivator [SP:SUB1_YEAST]YIL004CBET1; protein transport protein [SP:BET1_YEAST]YIR017CMET28; transcriptional activator of sulfur amino acid metabolism [SP:MT28_YEAST]YIL025Cunknown [SP:YIC5_YEAST]YGL112CTAF60; transcriptional activator [SP:T2D5_YEAST]YGL122CNAB2; nuclear polyadenylated RNA-binding protein [SP:NAB2_YEAST]YKL109WHAP4; transcriptional activator [SP:T2D5_YEAST]YGR236Cunknown [SP:YG4Z_YEAST]YGR236Cunknown [SP:YG4Z_YEAST]YMR18Csuccinate dehydrogenase (ubiquinone) cytochrome b subunit precursor [EC:1.3.5.1] [SP:YYIL084CSDS3; transcriptional regulator [SP:SDS3_YEAST]YNL202WSPS19; peroxisomal 2,4-dienoyl-CoA reductase [SP:SP19_YEAST]YDR257CMTH1; repressor of hexose transport genes [SP:MTH1_YEAST]	
YBR038WCHS2; chitin synthase 2 [EC:2.4.1.16] [SP:CHS2_YEAST]YKR026CGCN3, AAS2, TIF221; translation initiation factor eIF-2B alpha subunit [SP:E2BA_YEYPR033CHTS1; histidyl-tRNA synthetase [EC:6.1.1.21] [SP:SYH_YEAST](C) TranscriptionYOR344CTYE7, SGC1; basic helix-loop-helix transcription factor [SP:TYE7_YEAST]YOR341Cunknown [SP:YG3N_YEAST]YNL300Wunknown [SP:YG3N_YEAST]YNL300Wunknown [SP:YY40_YEAST]YMR039CSUB1, TSP1; transcriptional coactivator [SP:SUB1_YEAST]YIL004CBET1; protein transport protein [SP:BET1_YEAST]YIR017CMET28; transcriptional activator of sulfur amino acid metabolism [SP:MT28_YEAST]YIL025Cunknown [SP:YIC5_YEAST]YGL112CTAF60; transcriptional activator [SP:T2D5_YEAST]YGL12CNAB2; nuclear polyadenylated RNA-binding protein [SP:NAB2_YEAST]YGR236Cunknown [SP:YG4Z_YEAST]YGR236Cunknown [SP:YG4Z_YEAST]YDR259CYAP6; transcription al activator of a fungal-specific family of bzip proteinsYMR118Csuccinate dehydrogenase (ubiquinone) cytochrome b subunit precursor [EC:1.3.5.1] [SP:YYIL084CSDS3; transcriptional regulator [SP:SDS3_YEAST]YNL202WSPS19; peroxisomal 2,4-dienoyl-CoA reductase [SP:SP19_YEAST]YDR277CMTH1; repressor of hexose transport genes [SP:MTH1_YEAST]	
YBR038WCHS2; chitin synthase 2 [EC:2.4.1.16] [SP:CHS2_YEAST]YKR026CGCN3, AAS2, TIF221; translation initiation factor eIF-2B alpha subunit [SP:E2BA_YEYPR033CHTS1; histidyl-tRNA synthetase [EC:6.1.1.21] [SP:SYH_YEAST](C) TranscriptionYOR344CTYE7, SGC1; basic helix-loop-helix transcription factor [SP:TYE7_YEAST]YOR341Cunknown [SP:YG3N_YEAST]YNL300Wunknown [SP:YM0_YEAST]YOR062CunknownYPT07_VGR02CSUB1, TSP1; transcriptional coactivator [SP:SUB1_YEAST]YIL004CBET1; protein transport protein [SP:BET1_YEAST]YIL005Wprotein disulfide-isomerase [EC:5.3.4.1] [SP:YIA5_YEAST]YIR017CMET28; transcriptional activator of sulfur amino acid metabolism [SP:MT28_YEAST]YKR101WSIR1; silencing regulatory protein [SP:SIR1_YEAST]YGL122Cunknown [SP:YIC5_YEAST]YGL122CNAB2; nuclear polyadenylated RNA-binding protein [SP:NAB2_YEAST]YKL09WHAP4; transcriptional activator [SP:HAP4_YEAST]YGR259CYAP6; transcriptional regulator [SP:SD3_YEAST]YLL084CSDS3; transcriptional regulator [SP:SD3_YEAST]YNL202WSPS19; peroxisomal 2,4-dienoyl-COA reductase [SP:SP19_YEAST]YOR358WHAP5; transcriptional activator [SP:HAP5_YEAST]YOR250CCIN5; transcriptional activator [SP:HAP5_YEAST]YOR250CCIN5; transcriptional activator [SP:HAP5_YEAST]YOR358WHAP5; transcriptional activator [SP:HAP5_YEAST]YOR358WHAP5; transcriptional activator [SP:HAP5_YEAST]YOR250CYS1; errosional 2,4-dienoyl-COA reductase [SP:SP19_YEAS	
YBR038WCHS2; chitin synthase 2 [EC:2.4.1.16] [SP:CHS2_YEAST]YKR026CGCN3, AAS2, TIF221; translation initiation factor eIF-2B alpha subunit [SP:E2BA_YEYPR033CHTS1; histidyl-tRNA synthetase [EC:6.1.1.21] [SP:SYH_YEAST](C) TranscriptionYOR344CTYE7, SGC1; basic helix-loop-helix transcription factor [SP:TYE7_YEAST]YOR341Cunknown [SP:YG3N_YEAST]YNL300Wunknown [SP:YM40_YEAST]YOR062CunknownWMR039CSUB1, TSP1; transcriptional coactivator [SP:SUB1_YEAST]YIL004CBET1; protein transport protein [SP:BET1_YEAST]YIL005Wprotein disulfide-isomerase [EC:5.3.4.1] [SP:YIA5_YEAST]YIR017CMET28; transcriptional activator of sulfur amino acid metabolism [SP:MT28_YEAST]YKR101WSIR1; silencing regulatory protein [SP:SIR1_YEAST]YGL112CNAB2; nuclear polyadenylated RNA-binding protein [SP:NAB2_YEAST]YGL12CNAB2; nuclear polyadenylated RNA-binding protein [SP:NAB2_YEAST]YGL12CNAB2; nuclear polyadenylated RNA-binding protein [SP:NAB2_YEAST]YGR259CYAP6; transcriptional activator [SP:HAP4_YEAST]YGR259CYAP6; transcriptional regulator [SP:SD3_YEAST]YNL202WSPS19; peroxisomal 2,4-dienoyl-CoA reductase [SP:SP19_YEAST]YOR358WHAP5; transcriptional activator [SP:HAP5_YEAST]YOR358WHAP5; transcriptional activator [SP:HAP5_YEAST]YOR028CCIN5; transcriptional activator [SP:HAP5_YEAST]YOR028CCIN5; transcriptional activator [SP:HAP5_YEAST]YOR028CCIN5; transcriptional activator [SP:CIN5_YEAST]YOR167WC	
YBR038WCHS2; chitin synthase 2 [EC:2.4.1.16] [SP:CHS2_YEAST]YKR026CGCN3, AAS2, TIF221; translation initiation factor eIF-2B alpha subunit [SP:E2BA_YEYPR033CHTS1; histidyl-tRNA synthetase [EC:6.1.1.21] [SP:SYH_YEAST](C) TranscriptionYOR344CTYE7, SGC1; basic helix-loop-helix transcription factor [SP:TYE7_YEAST]YOR051Cunknown [SP:YG3N_YEAST]YNL300Wunknown [SP:YN40_YEAST]YOR062Cunknown [SP:YN40_YEAST]YIL004CBET1; protein transcriptional coactivator [SP:SUB1_YEAST]YIL005Wprotein disulfide-isomerase [EC:5.3.4.1] [SP:YIA5_YEAST]YKR101WSIR1; silencing regulatory protein [SP:SIR1_YEAST]YKR101WSIR1; silencing regulatory protein [SP:SIR1_YEAST]YGL122CNAB2; nuclear polyadenylated RNA-binding protein [SP:NAB2_YEAST]YKL109WHAP4; transcriptional activator [SP:HAP4_YEAST]YGR256Cunknown [SP:YG4Z_YEAST]YGR256Cunknown [SP:YG4Z_YEAST]YGR266unknown [SP:YG4Z_YEAST]YGR267YAP6; transcriptional activator [SP:SD3_YEAST]YMR118Csuccinate dehydrogenase (ubiquinone) cytochrome b subunit precursor [EC:1.3.5.1] [SP:YYIL084CSDS3; transcriptional activator [SP:SD3_YEAST]YOR358WHAP5; transcriptional activator [SP:HAP5_YEAST]YOR358WHAP5; transcriptional activator [SP:HAP5_YEAST]YOR358WHAP5; transcriptional activator [SP:HAP5_YEAST]YOR358WHAP5; transcriptional activator [SP:HAP5_YEAST]YOR358WHAP5; transcriptional activator [SP:CN5_YEAST]YOR358WHAP5; transcriptional acti	
YBR038W       CHS2; chitin synthase 2 [EC:2.4.1.16] [SP:CHS2_YEAST]         YKR026C       GCN3, AAS2, TIF221; translation initiation factor eIF-2B alpha subunit [SP:E2BA-YE         YPR033C       HTS1; histidyl-tRNA synthetase [EC:6.1.1.21] [SP:SYH_YEAST]         (C)       Transcription         YOR34C       TYE7, SGC1; basic helix-loop-helix transcription factor [SP:TYE7_YEAST]         YOR34C       TWE7, SGC1; basic helix-loop-helix transcription factor [SP:TYE7_YEAST]         YOR026C       unknown [SP:YG3N_YEAST]         YOR040C       unknown [SP:YM0.YEAST]         YOR030C       SUB1, TSP1; transcriptional coactivator [SP:SUB1_YEAST]         YIL004C       BET1; protein transport protein [SP:BET1_YEAST]         YIL005W       protein disulfide-isomerase [EC:5.3.4.1] [SP:YIA5_YEAST]         YIR017C       MET28; transcriptional activator of sufur amino acid metabolism [SP:MT28_YEAST]         YIL004C       BET1; silencing regulatory protein [SP:SIR1_YEAST]         YIL020W       Unknown [SP:YIC5_YEAST]         YGL122C       TAF60; transcription initiation factor [SP:T2D5_YEAST]         YGL226C       unknown [SP:YG4Z_YEAST]         YGR236C       unknown [SP:YG4Z_YEAST]         YGR236C       unknown [SP:YG4Z_YEAST]         YGR236C       unknown [SP:YG4Z_YEAST]         YDR259C       YAP6; transcriptional activator [SP:SD3_YEAST]	
YBR038WCHS2; chitin synthase 2 [EC:2.4.1.16] [SP:CHS2_YEAST]YKR026CGCN3, AAS2, TIF221; translation initiation factor eIF-2B alpha subunit [SP:E2BA-YEYPR033CHTS1; histidyl-tRNA synthetase [EC:6.1.1.21] [SP:SYH_YEAST](C) TranscriptionYOR344CTYE7, SGC1; basic helix-loop-helix transcription factor [SP:TYE7_YEAST]YGR151Cunknown [SP:YG3N_YEAST]YNL300Wunknown [SP:YM0_YEAST]YOR062CunknownYPT07062CunknownYPT0707CBET1; protein transport protein [SP:BET1_YEAST]YIL004CBET1; protein transport protein [SP:BET1_YEAST]YIL005Wprotein disulfide-isomerase [EC:5.3.4.1] [SP:YIA5_YEAST]YKR101WSIR1; silencing regulatory protein [SP:SIR1_YEAST]YKL1025Cunknown [SP:YIC5_YEAST]YGL122CTAF60; transcriptional activator [SP:T2D5_YEAST]YGL122CNAB2; nuclear polyadenylated RNA-binding protein [SP:NAB2_YEAST]YGL122CNAB2; nuclear polyadenylated RNA-binding protein [SP:NAB2_YEAST]YGR236Cunknown [SP:YG4Z_YEAST]YGR236Cunknown [SP:YG4Z_YEAST]YL084CSDS3; transcriptional activator [SP:SDS3_YEAST]YNL202WSPS19; peroxisomal 2,4-dienoyl-CoA reductase [SP:SP19_YEAST]YNL202WSPS19; peroxisomal 2,4-dienoyl-CoA reductase [SP:SP19_YEAST]YOR038CCIN5; transcriptional activator [SP:CIN5_YEAST]YOR038CCIN5; transcriptional activator [SP:CIN5_YEAST]YOR028CCIN5; transcriptional activator [SP:CAD1_YEAST]YOR028CCIN5; transcriptional activator [SP:CAD1_YEAST]YOR028CCI	
YBR038W       CH52; chitin synthase 2 [EC:2.4.1.16] [SP:CHS2_YEAST]         YKR026C       GCN3, AAS2, TIF221; translation initiation factor [I-2B alpha subunit [SP:E2BA_YE         YPR033C       HTS1; histidyl-tRNA synthetase [EC:6.1.1.21] [SP:SYH_YEAST]         (C)       Transcription         YOR344C       TYE7, SGC1; basic helix-loop-helix transcription factor [SP:TYE7_YEAST]         YGR151C       unknown [SP:YG3N_YEAST]         YOR062C       unknown         YMR039C       SUB1, TSP1; transcriptional coactivator [SP:SUB1_YEAST]         YIL004C       BET1; protein transport protein [SP:BET1_YEAST]         YIR017C       MET28; transcriptional activator of sulfur amino acid metabolism [SP:MT28_YEAST]         YIL025C       unknown [SP:YIC5_YEAST]         YGL112C       TAF60; transcription initiation factor [SP:T2D5_YEAST]         YGL12C       TAF60; transcription al activator [SP:HAP4_YEAST]         YGR236C       unknown [SP:YIC5_YEAST]         YGR236C       unknown [SP:YG4Z_YEAST]         YGR	
YBR038W       CH52; chitin synthase 2 [EC:2.4.1.16] [SP:CHS2,YEAST]         YKR026C       GCN3, AAS2, TIF221; translation initiation factor [GF-2B alpha subunit [SP:E2BA-YE         YPR033C       HTS1; histidyl-IRNA synthetase [EC:6.1.1.21] [SP:SYH_YEAST]         (C)       Transcription         YR0834C       TYE7, SGC1; basic helix-loop-helix transcription factor [SP:TYE7_YEAST]         YNL300W       unknown [SP:YG3N_YEAST]         YNL300W       unknown         YWR039C       SUB1, TSP1; transcriptional coactivator [SP:SUB1_YEAST]         YIL004C       BET1; protein transport protein [SP:BET1_YEAST]         YIL005W       protein disulfide-isomerase [EC:5.3.4.1] [SP:YIA5_YEAST]         YKR107C       MET28; transcriptional activator of sulfur amino acid metabolism [SP:MT28_YEAST]         YKR101W       SIR1; silencing regulatory protein [SP:BET1_YEAST]         YGL122C       NAB2; nuclear polyadenylated RNA-binding protein [SP:MA82_YEAST]         YGL22C       nuknown [SP:YIC5_YEAST]         YGR236C       unknown [SP:YG4Z_YEAST]         YGR236C       unknown [SP:YG4Z_YEAST]         YGR236C       unknown [SP:YG4Z_YEAST]         YGR236C       unknown [SP:YG4Z_YEAST]         YGL22C       NAB2; nuclear polyadenylated RNA-binding protein [SP:MA82_YEAST]         YGR236C       unknown [SP:YG4Z_YEAST] <td< td=""><td></td></td<>	
YBR038W       CHS2; chitin synthase 2 [EC:2.4.1.16] [SP:CHS2.YEAST]         YKR026C       GCN3, AAS2, TIF221; translation initiation factor eIF-2B alpha subunit [SP:E2BA.YE         HTS1; histidyl-tRNA synthetase [EC:6.1.21] [SP:SYH_YEAST]         (C)       Transcription         YOR344C       TYE7, SGC1; basic helix-loop-helix transcription factor [SP:TYE7_YEAST]         YOR30C       Unknown [SP:YG3N_YEAST]         YOR062C       unknown         YNL300W       unknown         YMR039C       SUB1, TSP1; transcriptional coactivator [SP:SUB1_YEAST]         YIL004C       BET1; protein transport protein [SP:BET1_YEAST]         YIR017C       MET28; transcriptional activator of sulfur amino acid metabolism [SP:MT28_YEAST]         YIR017C       MET28; transcriptional activator [SP:SIR1_YEAST]         YGL112C       NAB2; nuclear polyadenylated RNA-binding protein [SP:NAB2_YEAST]         YGL22C       NAB2; nuclear polyadenylated RNA-binding protein [SP:NAB2_YEAST]         YGR236C       Unknown [SP:YG4Z_YEAST]         YGR236C       Suscinate dehydrogenase (ubiquinone) cytochrome b subunit precursor [EC:1.3.5.1] [SP:Y         YIL084C       SDS3; transcriptional activator [SP:CID5_YEAST]         YNL2024W       SPS1; peroxisomal 2,4-dienoyl-CoA reductase [SP:SP19_YEAST]         YOR358W       HAP5; transcriptional activator [SP:CID5_YEAST]         YOR026C<	
YBR038W       CH52; chitin synthase 2 [EC:2.4.1.16] [SP:CHS2,YEAST]         YKR026C       GCN3, AAS2, TIF221; translation initiation factor [GF-2B alpha subunit [SP:E2BA-YE         YPR033C       HTS1; histidyl-IRNA synthetase [EC:6.1.1.21] [SP:SYH_YEAST]         (C)       Transcription         YR0834C       TYE7, SGC1; basic helix-loop-helix transcription factor [SP:TYE7_YEAST]         YNL300W       unknown [SP:YG3N_YEAST]         YNL300W       unknown         YWR039C       SUB1, TSP1; transcriptional coactivator [SP:SUB1_YEAST]         YIL004C       BET1; protein transport protein [SP:BET1_YEAST]         YIL005W       protein disulfide-isomerase [EC:5.3.4.1] [SP:YIA5_YEAST]         YKR107C       MET28; transcriptional activator of sulfur amino acid metabolism [SP:MT28_YEAST]         YKR101W       SIR1; silencing regulatory protein [SP:BET1_YEAST]         YGL122C       NAB2; nuclear polyadenylated RNA-binding protein [SP:MA82_YEAST]         YGL22C       nuknown [SP:YIC5_YEAST]         YGR236C       unknown [SP:YG4Z_YEAST]         YGR236C       unknown [SP:YG4Z_YEAST]         YGR236C       unknown [SP:YG4Z_YEAST]         YGR236C       unknown [SP:YG4Z_YEAST]         YGL22C       NAB2; nuclear polyadenylated RNA-binding protein [SP:MA82_YEAST]         YGR236C       unknown [SP:YG4Z_YEAST] <td< td=""><td></td></td<>	

Table 2: Correlated gene clusters related to "ribosomal", "translation", and "transcription".

(A) Autophagy		
YMR159C	<b>APG16</b> ; similar to human Sin3 complex component SAP18, possible coiled-coil protein [SP:YM34_YEAST]	
YJR025C	BNA1, HAD1; 3-hydroxyanthranilate 3,4-dioxygenase [EC:1.13.11.6] [SP:3HAO_YEAST]	
(B) Spindl	e pole body function	
YKR037C	SPC34; spindle pole body protein [SP:YK17 YEAST]	
YCR082W	unknown [SP:YCX2_YEAST]	
YLR423C	unknown	
YMR124W	unknown [SP:YM11_YEAST]	
YIL144W	TID3; Dmc1p interacting protein [SP:YIO4_YEAST]	
YOR089C	VPS21, YPT51; GTP-binding protein [SP:YP51_YEAST]	
(C) Vesicu	lar transport	
YBL050W	SEC17; vesicular-fusion protein [SP:SC17_YEAST]	
YDR178W	SDH4; succinate dehydrogenase membrane anchor subunit [EC:1.3.5.1] [SP:SDH4_YEAST]	
YMR197C	VTI1; vesicle transport V-snare protein VTI1 [SP:VTI1_YEAST]	
YOR036W	PEP12; syntaxin (T-SNARE), vacuolar [SP:PE12_YEAST]	
YDR468C	<b>TLG1</b> ; tSNARE that affects a late Golgi compartment	
YGL044C	RNA15; component of the cleavage and polyadenylation factor CF I involved in pre-mRNA 3'-end processing [SP:RN15_YEAST]	
YBL102W	SFT2; SFT2 protein [SP:SFT2_YEAST]	
YNL133C	unknown [SP:YNN3_YEAST]	
YOR220W	unknown	
YIL004C	BET1; protein transport protein [SP:BET1_YEAST]	
YIL005W	protein disulfide-isomerase [EC:5.3.4.1] [SP:YIA5_YEAST]	
YMR039C	SUB1, TSP1; transcriptional coactivator [SP:SUB1_YEAST]	
YLR324W	unknown	
YDR453C	YDR453C; probable thiol-specific antioxidant protein 2 [SP:TSA2_YEAST]	
YNL044W	YIP3; unknown [SP:YIPC.YEAST]	
YGR192C	TDH3, GPD3; glyceraldehyde 3-phosphate dehydrogenase [EC:1.2.1.12] [SP:G3P3_YEAST]	
YJL052W	TDH1, GPD1, SSS2; glyceraldehyde 3-phosphate dehydrogenase [EC:1.2.1.12] [SP:G3P1_YEAST]	
YDR313C	PIB1; phosphatidylinositol(3)-phosphate binding protein	
YGR042W	unknown [SP:YGIT,YEAST]	
YGL198W	unknown [SP:YGU8.YEAST]	
YNL216W	RAP1, GRF1; DNA-binding protein with repressor and activator activity [SP:RAP1_YEAST]	
YJL036W	SNX4; unknown [SP:YJD6,YEAST]	
YDR473C YKR014C	PRP3; essential splicing factor <b>YPT52</b> ; GTP-binding protein of the rab family [SP:YP52_YEAST]	
YKR014C YKL035W	YP152; G1P-binding protein of the rab family [SP:YP52,YEAS1] UGP1: UTP-glucose-1-phosphate uridylyltransferase [EC:2.7.7.9] [SP:UDPG_YEAST]	
YFL054C	URANOW [SP:YFF4.YEAST]	
YFL054C YDR425W	unknown [SF:YFF4_YEAST] unknown	
YPL280W	unknown	
1 F L280 W	unknown	

Table 3: Correlated gene clusters related to the genes listed in Ito et al. [3].

extracted correlated gene clusters. In this section, we extend the hyperedges so that they can contain datasets from multiple organisms. G

It is well known that in prokaryotic genomes, such as in E.coli, functionally related genes are often located continuously on the chromosome constituting an operon. Unfortunately, this is not usually the case for eukaryotic genomes including S.cerevisiae. However, if we can define functional identity of genes between the two species, the operon information in E.coli may be utilized for identifying functional links in S.cerevisiae.

Fig. 4 shows a schematic picture. To connect two organisms, we introduce a mapping from a set of genes in one organism to another based on the sequence similarities (orthologous relationships) as follows:

$$F_{SS}: S(G_1) \to S(G_2) \tag{2}$$

where  $S(G_1)$  and  $S(G_2)$  denote the sets of genes in the graphs  $G_1$  and  $G_2$  corresponding to two organisms, respectively. We use the criterion of bidirectional best hits to define orthologs when two genomes are compared by the Smith-Waterman algorithm

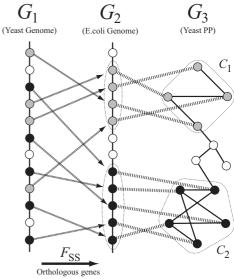


Figure 4: Mapping of genes.

at the amino acid sequence level with the threshold similarity score of 70. To characterize genes of an organism, its genes  $S(G_1)$  are once mapped to the nodes of the graph  $G_2$  that encodes functional orthologs in another organism. After that, we compare  $G_2$  and an additional graph  $G_3$  of the original organism instead of comparing  $G_1$  and  $G_3$  directly.

Suppose that  $G_1$  and  $G_3$  are the binary relationships among *S. cerevisiae* genes with respect to

<ul> <li>YLL140W RPB4: DNA-directed RNA polymerase II 32 RD polypeptide [EC2.7.7.6] [SP:RPD4_YEAST]</li> <li>YKL1440 RPC5, YKL1, UNF; DNA-directed RNA polymerase II 13 rate abuaut [EC2.7.7.6] [SP:RPC1_YEAST]</li> <li>YUR05W RPA14; DNA-directed RNA polymerase II 13 rate abuaut [EC2.7.7.6] [SP:RPC1_YEAST]</li> <li>YUR05W RPA14; DNA-directed RNA polymerase II 13 rate abuaut [EC2.7.7.6] [SP:RPA2_YEAST]</li> <li>YUR05W RPA14; DNA-directed RNA polymerase II 14 rate abuaut [EC2.7.7.6] [SP:RPA3_YEAST]</li> <li>YUR05W RPA14; DNA-directed RNA polymerase II 14 rate polymerate [EC2.7.7.6] [SP:RPA3_YEAST]</li> <li>YUR05W RPA14; DNA-directed RNA polymerase II 14 rate polymerate [EC2.7.7.6] [SP:RPA3_YEAST]</li> <li>YUR05W RPA14; DNA-directed RNA polymerase II 14 rate polymerate [EC2.7.7.6] [SP:RPA3_YEAST]</li> <li>YUR05W RPA14; DNA-directed RNA polymerase [EC2.7.7.7] [SP:DPB3_YEAST]</li> <li>YUR07W DPB5; DNA polymerase geliated [SC2.7.7.7] [SP:GB1_YEAST]</li> <li>YUR07W DPB5; DNA polymerase geliated [SC2.7.7.6] [SP:GB1_YEAST]</li> <li>YUR07W DPB5; DNA dolymerase [EC2.7.7.6] [SP:CB1_YEAST]</li> <li>YUR07W DPB5; DNA dolymerase [EC2.7.7.6] [SP:CB1_YEAST]</li> <li>YUR07W DFR; Ladavjate Kinase [EC2.7.4.3] [SP:AD1_YEAST]</li> <li>YUR07W ADK1; adavjate kinase [EC2.7.4.3] [SP:AD1_YEAST]</li> <li>YUR07W ADK1; adavjate kinase [EC2.7.4.3] [SP:RAD1_YEAST]</li> <li>YOR07W CTT1; exhalase [EC1.1.1.6] [SP:CAT1_YEAST]</li> <li>YOR08W CTT1; exhalase [EC1.1.1.6] [SP:CAT1_YEAST]</li> <li>YOR08W CTT1; exhalase [EC2.1.1.1] [SP:RAD2_YEAST]</li> <li>YOR07W CTB1; exhalase [EC2.1.1.1] [SP:RAD2_YEAST]</li> <li>YOR07W CTB1; exhalase [EC2.1.1.1] [SP:RAD2_YEAST]</li> <li>YOR07W CTB1; exhalase [EC2.1.1.1.6] [SP:CAT1_YEAST]</li> <li>YOR07W CTB1; exhalase [EC2.1.1.1.6] [SP:CAT1_YEAST]</li> <li>YOR07W CTB1; exhalase [EC2.1.1.1.6] [SP:RAD2_YEAST]</li> <li>YOR07W CTB1; exhalase [EC2.1.1.6] [SP:RAD2_YEAST]</li> <li>YOR07W CTB1; exhalase [EC2.1.1.6] [SP:CAT1_YE</li></ul>
<ul> <li>YOR116C RP031, RPC1, RPC160; DNA-directed RNA polymerase II 1 argst stubint [EC2.7.7.6] [SP:RPCX,YEAST]</li> <li>YOR2063W RPA12, RR44; DNA-directed RNA polymerase II 37 kD polypeptide [EC2.7.7.6] [SP:RPAX,YEAST]</li> <li>YOR1663W RPA12, RR44; DNA-directed RNA polymerase II 37 kD polypeptide [EC2.7.7.6] [SP:RPAX,YEAST]</li> <li>YOR1670W P101; acd phosphatase [EC3.1.33] [SP:PPCA.YEAST]</li> <li>YOR1670W P101; acd phosphatase [EC3.1.33] [SP:PPCA.YEAST]</li> <li>YOR1670W P101; acd phosphatase [EC3.1.33] [SP:PPCA.YEAST]</li> <li>YOR1670W P101; acd phosphatase [EC3.1.1.14] [SP:DPD4XFAST]</li> <li>YOR1670W P101; Specific dehydrogenase (NADP+1), mitochordnal [EC3.1.1.24] [SP:IDHP.YEAST]</li> <li>YOR1670W P17; Isolaritad elaydrogenase (attaliatione) / long-chain alcohol dehydrogenase [EC1.2.1.1.1.1] [SP:FADH_YEAST]</li> <li>YOR1680W ADH3; alcohol dehydrogenase [EC1.1.1.14] [SP:ADH3.YEAST]</li> <li>YOR1680W ADH3; alcohol dehydrogenase [EC1.1.1.14] [SP:ADH3.YEAST]</li> <li>YOR1680W CT11; catalase [EC1.11.1.0] [SP:CAT1.YEAST]</li> <li>YOR170C RP38; DNA-directed RNA polymerase II 14.2 kD polymepiate [EC2.7.7.6] [SP:RPB.YEAST]</li> <li>YOR170C RP38; DNA-directed RNA polymerase II 14.2 kD polymepiate [EC2.7.7.6] [SP:RPB.YEAST]</li> <li>YOR260C CTN1; catalase [EC1.11.1.6] [SP:CAT1.YEAST]</li> <li>YOR270C RP38; DNA-directed RNA polymerase II 14.2 kD polymepiate [EC2.7.7.6] [SP:RPB.YEAST]</li> <li>YOR270C RP38; DNA-directed RNA polymerase II 14.2 kD polymepiate [EC2.7.7.6] [SP:RPB.YEAST]</li> <li>YOR270C RP38; DNA-directed RNA polymerase II 14.2 kD polymepiate [EC2.7.7.6] [SP:RPB.YEAST]</li> <li>YOR270C RP38; DNA-directed</li></ul>
<ul> <li>YOR210W RPB10; DNA-directed RNA polymerses 1.1, Land III 8.3 kD polypeptide [EC:2.7.7.6] [SP:RPAX_YEAST]</li> <li>YDR05W RPA14; DNA-directed RNA polymerses 113 xD polypeptide [EC:2.7.7.6] [SP:RPAX_YEAST]</li> <li>YDR07W RPA14; DNA-directed RNA polymerses 113 xD polypeptide [EC:2.7.7.6] [SP:RPAX_YEAST]</li> <li>YDR07W RPA14; DNA-directed RNA polymerses [DS:2.1.7.1] [SP:DDP3,YEAST]</li> <li>YDR07W RPA14; DNA-directed RNA polymerses [DS:2.1.7.1] [SP:DDP3,YEAST]</li> <li>YDR07W DDP3; DDP polymerses equation, submit C [DC:2.7.7.7] [SP:DDP3,YEAST]</li> <li>YDR07W IDP1; isocitrate delydrogenase [Cutathione) / Iong-chain alcohol delydrogenase [EC:1.1.1.1]</li> <li>YDR07W DDP3; DNA and edupting and an experimental statistical statis</li></ul>
YRI663W RPA12, RRM; DNA-directed RNA polymerase 11.37 KD polypepidde [EC:27.7.6] [SP:RPAS.YEAST] YRI615W RPA14, DNA-directed RNA polymerase 11.4 KD polypepidde [EC:27.7.6] [SP:RPAS.YEAST] YRI71W PHO12; acid phosphatase [EC:3.1.32] [SP:PPAC.YEAST] YRI728W DPB3; DNA polymerase (DE:22.7.7] [SP:DPAC.YEAST] YRI728W DPB3; DNA polymerase (DE:22.7.7] [SP:DPAC.YEAST] YRI71W DPHO12; acid phosphatase [EC:2.1.3.1] [SP:PPAC.YEAST] YRI71W DPHO12; acid phosphatase [DE:22.7.7] [SP:DPAC.YEAST] YRI71W DPHO12; acid phosphatase [DE:22.7.7] [SP:DPAC.YEAST] YRI71W DPHO12; acid phosphatase [DE:22.7.7] [SP:DPAC.YEAST] YRI71W DPHO12; acid phosphatase [DE:27.7.4] [SP:ADHAYEAST] YDI73W DPHO12; acid phosphatase [DE:27.7.4] [SP:ADHAYEAST] YDI73W DPHO12; acid phosphatase [DE:27.7.4] [SP:ADHAYEAST] YDI73W ADK1; aconylate kinase [C:2.7.4.3] [SP:KAD1.YEAST] YDR236W CTT1; catalase [DE:1.1.1.6] [SP:CAT.YEAST] YGR036W CTT1; catalase [DE:1.1.1.6] [SP:CAT.YEAST] YGR026W PFK1; Gpinosphoftwickhinase [EC:2.7.1.1] [SP:K6P1YEAST] YGR026W PFK1; Gpinosphoftwickhinase [EC:2.7.1.1] [SP:K6P1YEAST] YGR027W PFK1; Gpinosphoftwickhinase [EC:2.7.1.1] [SP:K6P1YEAST] YGR027W PFK1; Gpinosphoftwickhinase [EC:2.7.1.1] [SP:K6P1YEAST] YGR047W SER3; D-3-phosphoftwickhinase [EC:2.7.1.1] [SP:K6P2YEAST] YGR047W SER3; D-3-phosphoftwickhinase [EC:2.7.1.1] [SP:K6P1YEAST] YGR047W SER3; D-3-phosphoftwickhinase [EC:2.7.1
<ul> <li>VDR106W RPA14; DNA-directed RNA polymerase 1.14 kD polymeptide [EC2.7.7.6] [SP:RPAS,YEAST]</li> <li>VR071W PHO11; acid phosphatase [BC3.1.3.2] [SP:PPAB,YEAST]</li> <li>VR071W PHO12; acid phosphatase [BC3.1.3.2] [SP:PPAB,YEAST]</li> <li>VR074W SPA1; formaldelyde delydrogenase [Cu1.1.11, [SP:ADB1,YEAST]</li> <li>VR074W SPA1; formaldelyde delydrogenase [Cu1.1.11, [SP:ADB1,YEAST]</li> <li>VR074W ADK1; adenylate kinase [EC2.7.4.3] [SP:KAD1,YEAST]</li> <li>VR076W ADK1; adenylate kinase [EC2.7.4.3] [SP:KAD1,YEAST]</li> <li>VR076W ADK1; adenylate kinase [EC2.7.4.3] [SP:KAD1,YEAST]</li> <li>VGR086W CT11; catalase [EC1.1.1.16] [SP:CAT1,YEAST]</li> <li>VGR086W CT11; catalase [EC1.1.1.16] [SP:CAT3,YEAST]</li> <li>VGR086W CT11; catalase [EC1.1.1.16] [SP:CAT3,YEAST]</li> <li>VGR070C RFB8; DNA-directed RNA polymerase II 1.0.10 polymeptide [EC2.7.7.6] [SP:RPB9,YEAST]</li> <li>VGR070C TD13, GFD3; glyocarddelyde 3-phosphate delydrogenase [EC1.2.1.12] [SP:G3P3,YEAST]</li> <li>VGR070C PFK; 6-phosphofructokinase [EC2.7.1.11] [SP:K6P1,YEAST]</li> <li>VGR070C PFK; 6-phosphofructokinase [EC2.7.1.13] [SP:STCYEAST]</li> <li>VGR070C PFK; 6-phosphofructokin</li></ul>
<ul> <li>YHR01W PHO11; acid phosphatase [EC3.1.3.2] [SP:PPAC.VEAST]</li> <li>YHR21SW DPB3; DNA polymerase [EC3.1.3.2] [SP:PPAC.VEAST]</li> <li>YCR014C POL4; DNA polymerase [EC3.1.3.2] [SP:PPAC.VEAST]</li> <li>YCR014C POL4; DNA polymerase [EC3.1.3.2] [SP:PPAC.VEAST]</li> <li>YUD066W DP1; isocitrate daydrogenase [KADP+4), mitochondrial [EC1.1.1.42] [SP:DD1+YEAST]</li> <li>YDD067W DP1; isocitrate daydrogenase [C2.1.1.1.4] [SP:CB1+YEAST]</li> <li>YDD078W ADB3; alcohol dehydrogenase [C2.1.1.1.4] [SP:CB1+YEAST]</li> <li>YDR226W ADB1; alcohol dehydrogenase [C2.1.1.1.4] [SP:ADB3/YEAST]</li> <li>YDR226W ADB1; alcohol dehydrogenase [C2.1.1.1.4] [SP:ADB3/YEAST]</li> <li>YDR267W ADB2; PAK3; alemplate kinase [C2.1.1.1.4] [SP:ADB3/YEAST]</li> <li>YDR267W ADB2; PAK3; alemplate kinase [C2.1.1.1.4] [SP:ADB2,YEAST]</li> <li>YDR267W ADB2; PAK3; alemplate kinase [C2.1.1.1.4] [SP:CAT7,YEAST]</li> <li>YGR070C CTA1; catalase [C2.1.1.1.6] [SP:CAT7,YEAST]</li> <li>YGR070C RPB9; DNA-directed RNA polymerase 1.1.4; HD adyapeptide [EC2.7.7.6] [SP:RPB4,YEAST]</li> <li>YOR224C RPB8; DNA-directed RNA polymerase 1.1.4; HD 6X subunit [EC2.7.7.6] [SP:RPB4,YEAST]</li> <li>YUG070W TDB1; GPD1; SSS2; gloceradehydrogenase [EC1.1.1.6] [SP:CAT2,YEAST]</li> <li>YUL074C SEB33; D-3-phosphoglycerate dehydrogenase [EC1.1.1.6] [SP:CAT2,YEAST]</li> <li>YUL074C SEB33; D-3-phosphoglycerate dehydrogenase [EC1.1.1.6] [SP:SR7X,YEAST]</li> <li>YUL074C SEB33; D-3-phosphoglycerate dehydrogenase [EC1.1.1.6] [SP:CAT2,T.6] [SP:RPB8,YEAST]</li> <li>YUL074C SEB33; D-3-phosphoglycerate dehydrogenase [EC3.1.1.1] [SP:K6P2,YEAST]</li> <li>YUL074C SEB33; D-3-phosphoglycerate dehydrogenase [EC1.1.1.6] [SP:STR2,YEAST]</li> <li>YUL074C SEB33; D-3-phosphoglycerate dehydrogenase [EC3.1.1.3] [SP:STR2,YEAST]</li> <li>YUL074C SEB33; D-3-phosphoglycerate dehydrogenase [EC3.1.1.3] [SP:STR2,YEAST]</li> <li>YUL074C MSP1; Anseparaginase [EC3.3.1.1] [SP:ASG2,YEAST]</li> <li>YUL074C MSP3; Anse</li></ul>
<ul> <li>YHR215W PH012; acid phosphatase [EC:3.1.32] [SP:PPACXEAST]</li> <li>YBR278W DFB3; DNA polymerase IV [EC:2.7.7.7] [SP:DPB3,YEAST]</li> <li>YCR014C POL4; DNA polymerase IV [EC:2.7.7.7] [SP:DPALYEAST]</li> <li>YDL066W IDP1; isocirate dehydrogenase (RADP1, mitochondrial [EC:1.1.1.42] [SP:IDHP,YEAST]</li> <li>YND178W HYR1; glutathione peroxidase [EC:1.1.1.9] [SP:GSN1,YEAST]</li> <li>YDL168W ADB3; alcohol dehydrogenase (RADP1, MADD1,YEAST]</li> <li>YDR266W ADB3; alcohol dehydrogenase (EC:1.1.1.1] [SP:ADH3,YEAST]</li> <li>YDR266W CTT1; catalase [EC:1.1.1.6] [SP:CATA,YEAST]</li> <li>YOR266W CTT1; catalase [EC:1.1.6] [SP:CATA,YEAST]</li> <li>YOR266W CTT1; catalase [EC:1.1.6] [SP:CATA,YEAST]</li> <li>YOR266W CTT1; catalase [EC:1.1.6] [SP:CATA,YEAST]</li> <li>YOR267C RPB9; DNA-directed RNA polymerase II 142 kD polyneptide [EC:2.7.6] [SP:RPB0,YEAST]</li> <li>YOR267C RPB9; DNA-directed RNA polymerase II 142 kD polyneptide [EC:2.7.6] [SP:RPB0,YEAST]</li> <li>YOR260C TDB3, GPD3; glyceraldehyde 3-phosphate dehydrogenase [EC:1.2.1.12] [SP:GS1P3,YEAST]</li> <li>YUL052W TDB1, GPD3; glyceraldehyde 3-phosphate dehydrogenase [EC:1.2.1.12] [SP:GS1P3,YEAST]</li> <li>YGR20C PFK1; 6-phosphofructokinase [EC:2.1.11] [SP:KP2YEAST]</li> <li>YHR205C PFK2; 6-phosphofructokinase [EC:1.1.1.6] [SP:CATA,YEAST]</li> <li>YUL072W SER3; D-3-phosphoglycerate dehydrogenase [EC:1.1.1.6] [SP:CATA,YEAST]</li> <li>YUL074W SER3; D-3-phosphoglycerate dehydrogenase [EC:1.1.1.6] [SP:RP1P4,YEAST]</li> <li>YUR340C RP443, RRN12; DNA-dependent RNA polymerase 1.1.13] [SP:SERX,YEAST]</li> <li>YUR340C RP443, RRN12; DNA-dependent RNA polymerase 36 D polyneptide [EC:2.7.6] [SP:RP44,YEAST]</li> <li>YUR340C RP443, RRN12; DNA-dependent RNA polymerase 36 D polyneptide [EC:2.7.6] [SP:RP44,YEAST]</li> <li>YUR340C RP443, RRN12; DNA-dependent RNA polymerase 36 D polyneptide [EC:2.7.6] [SP:RP44,YEAST]</li> <li>YUR340C RP443, RRN12; DNA-dependent RNA polymerase 36 D polynepti</li></ul>
<ul> <li>YBR278W DPB3; DNA jobymerase epailon, subunit C [EC:27.7.7] [SP:DPB3; YEAST]</li> <li>YCR014C POL4; DNA jobymerase (PSI-DAVEAST]</li> <li>YDL066W IDP1; isocitrate dehydrogenase (RMDP+), mitochondrial [EC:1.1.1.42] [SP:DHP,YEAST]</li> <li>YIR037W MYR1; jattahione percovadase [EC:1.1.1.9] [SP:CSH1; YEAST]</li> <li>YDL068W SFA1; formaldehyde dehydrogenase (glutathione) / long-chain alcohol dehydrogenase [EC:1.1.1.4]</li> <li>YDL078W ADR1; adenylate kinase [EC:27.4.3] [SP:KAD1; YEAST]</li> <li>YDR078W ADR1; adenylate kinase [EC:27.4.3] [SP:KAD2; YEAST]</li> <li>YDR226C CTA1; catalase [EC:1.1.1.6] [SP:CATA, YEAST]</li> <li>YDR226C CTD13; catalase [EC:1.1.1.6] [SP:CATA, YEAST]</li> <li>YOR226C REPB8; DNA-directed RNA polymerase 1.11, 111 [SP:K0F1; YEAST]</li> <li>YOR226C PFK1; G-bosphofructokinase [EC:27.1.1] [SP:K0F2; YEAST]</li> <li>YUR050C PFK1; G-bosphofructokinase [EC:27.1.1] [SP:K0F2; YEAST]</li> <li>YUR050C PFK1; G-bosphofructokinase [EC:3.1.1.1] [SP:K0F2; YEAST]</li> <li>YUR050C PFK2; G-phosphofructokinase [EC:3.1.1.1] [SP:K0F2; YEAST]</li> <li>YUR050C PFK2; G-phosphofructokinase [EC:3.1.1.1] [SP:K0F2; YEAST]</li> <li>YUR070C RP483; DNA-directed RNA polymerase [EC:1.1.1.36] [SP:SETA, YEAST]</li> <li>YUR070C RP443; RRN12; DNA-dependent RNA polymerase 36 DD polypeptide [EC:2.7.7.6] [SP:RP44; YEAST]</li> <li>YUR070C RP443; RRN12; DNA-dependent RNA polymerase 36 DD polypeptide [EC:2.7.7.6] [SP:RP44; YEAST]</li> <li>YUR070C RP443; RRN12; DNA-dependent RNA polymerase 36 DD polypeptide [EC:2.7.7.6] [SP:RP44; YEAST]</li> <li>YUR070C RP443; RRN12; DNA-dependent RNA polymerase 36 DD polypeptide [EC:2.7.7.6] [SP:RP44; YEAST]</li> <li>YUR070C RP443; RRN12; DNA-dependent RNA polymerase 36 DD polypeptide [EC:2.7.7.6] [SP:RP44; YEAST]</li></ul>
YCR014C POL4: DNA polymerase IV [EC:27.7.7] [SF:DPO4-YEAST] YDL066W IDP1; isocitrate dehydrogenase (RADP4), mitochondrai [EC:1.1.1.42] [SF:DHP-YEAST] YR083W ADR1; aduchol dehydrogenase [EC:1.1.1.9] [SP-GSR1_YEAST] YDL168W ADR1; aduchol dehydrogenase [EC:1.1.1.1] [SP-KAD1-YEAST] YDR028W ADR1; aduchol dehydrogenase [EC:1.1.1.1] [SP-KAD1-YEAST] YDR028W ADR1; aduchol dehydrogenase [EC:1.1.1.1] [SP-KAD1-YEAST] YDR028W CTT1; crainase [EC:1.1.1.6] [SP-CATTY-YEAST] YGR038W CTT1; crainase [EC:1.1.1.6] [SP-CATTY-YEAST] YGR028W CTT1; crainase [EC:1.1.1.6] [SP-CATTY-YEAST] YGR028W CTT1; crainase [EC:1.1.1.6] [SP-CATTY-YEAST] YGR028W CTT1; crainase [EC:1.1.1.6] [SP-CATTY-YEAST] YGR026W CTT1; crainase [EC:1.1.1.6] [SP-CATTY-YEAST] YGR026W CTT1; crainase [EC:1.1.1.6] [SP-CATTY-YEAST] YGR026W CTT1; crainase [EC:1.1.1.6] [SP-CATTY-YEAST] YGR026W CTT1; crainase [EC:1.1.1.1] [SP-K6P1-YEAST] YGR026W CTT1; crainase [EC:1.1.1.1] [SP-K6P1-YEAST] YGR026W CTT1; crainase [EC:1.1.1.1] [SP-K6P1-YEAST] YGR026W CTT1; crainase [EC:1.1.1.1] [SP-K6P1-YEAST] YGR026W CPFR3; c-phosphofructokinase [EC:2.7.1.1] [SP-K6P1-YEAST] YGR026W CPFR3; c-phosphofructokinase [EC:3.1.1.1] [SP-K6P1-YEAST] YGR030W SER3; D-3-phosphoglycerate dehydrogenase [EC:1.1.1.0] [SP-SERX-YEAST] YHR030W SER3; D-3-phosphoglycerate dehydrogenase [EC:1.1.1.6] YGR031W ASP1; 1-asparaginase [EC:3.5.1.1] [SP-X622-YEAST] YHR030W SER3; D-3-phosphoglycerate dehydrogenase [EC:1.1.1.6] YGR04C RPA3; RIN12; DNA-digapediat RNA PI, I.1.11 Have 26 AD polyneptide [EC:2.7.7.6] [SP-RPA4-YEAST] YHR030W ASP1; 1-asparaginase [EC:3.5.1.1] [SP-X622-YEAST] YHR030W SF1; threonyl-tRNA synthetase, mitochondrial [EC:6.1.3] [SP-SYNT-YEAST] YHR030W SF1; threonyl-tRNA synthetase, critochondrial [EC:6.1.3] [SP-SYNT-YEAST] YHR030W ASP1; 1-asparaginase [EC:3.5.1.1] [SP-X61+YEAST] YHR030W ASP1; 1-asparaginase [EC:3.5.1.1] [SP-X61+YEAST] YHR030W ASP1; 1-asparaginase [EC:3.5.1.1] [SP-X61+YEAST] YHR030W ASP1; 1-asparaginase [EC:3.5.1.1] [SP-X61+YEAST] YHR030W ASP1; 1-asparaginase [EC
<ul> <li>YDL066W IDP1; isocitrate delydrogenase (NADF+), mitochondrial [EC:1.1.1.42] [SP:EDHP-YEAST]</li> <li>YIR037W HYR1; gittahione percosidase [EC:1.1.1.6] [SP:GSILYEAST]</li> <li>YDL068W SFA1; formaldelyde delydrogenase (gittathione) / long-chain alcohol delydrogenase [EC:1.2.1.1.1.1.1] [SP:FADH_YEAST]</li> <li>YDR226W ADR1; adenylate kinase [EC:2.7.43] [SP:KADLYEAST]</li> <li>YDR226W ADR1; adenylate kinase [EC:2.7.43] [SP:KADLYEAST]</li> <li>YDR226W CTT1; catalase [EC:1.1.1.6] [SP:CATA_YEAST]</li> <li>YGR036W CTT1; catalase [EC:1.1.1.6] [SP:CATA_YEAST]</li> <li>YGR0406W CTD1; catalase [EC:1.1.1.6] [SP:CATA_YEAST]</li> <li>YGR0406W CTD1; catalase [EC:1.1.1.6] [SP:CATA_YEAST]</li> <li>YGR0406W CTD1; catalase [EC:1.1.1.6] [SP:CATA_YEAST]</li> <li>YGR0406 CFFR1; chosphofructokinase [EC:2.7.1.1] [SP:K6P1/YEAST]</li> <li>YHR050C PFFR1; chosphofructokinase [EC:2.7.1.1] [SP:K6P1/YEAST]</li> <li>YHR050C PFFR1; chosphofructokinase [EC:2.7.1.1] [SP:K6P2/YEAST]</li> <li>YGR340C PFFR1; chosphofructokinase [EC:3.1.1.1] [SP:ASC2.YEAST]</li> <li>YGR340C RP433; 3-phosphoglycerate delydrogenase [EC:1.1.1.95] [SP:SERX_YEAST]</li> <li>YGR340C RP433; RN12; DNA-dependent RNA polymerase 36 kD polypeptide [EC:2.7.6] [SP:RP44_YEAST]</li> <li>YGR340C RP433; RN12; DNA-dependent RNA polymerase 36 kD polypeptide [EC:2.7.6] [SP:RP44_YEAST]</li> <li>YGR340C MSP1; threonyl-tINA synthetase, ritochoming [EC:6.1.1.3] [SP:SYTM_YEAST]</li> <li>YGR340C SAH1; adparaginase [EC:3.1.1] [SP:ASG1-YEAST]</li> <li>YGR340C MSP1; threonyl-tINA synthetase, ritochoming [EC:6.1.3.3] [SP:SYTM_YEAST]</li> <li>YGR340C SAH1; adparaginase [EC:3.1.1] [SP:ASG1-YEAST]</li> <li>YGR340C MSP1; threonyl-tINA synthetase, r</li></ul>
<ul> <li>YDL066W IDP1; isocitrate delydrogenase (NADF+), mitochondrial [EC:1.1.1.42] [SP:EDHP-YEAST]</li> <li>YIR037W HYR1; gittahione percosidase [EC:1.1.1.6] [SP:GSILYEAST]</li> <li>YDL068W SFA1; formaldelyde delydrogenase (gittathione) / long-chain alcohol delydrogenase [EC:1.2.1.1.1.1.1] [SP:FADH_YEAST]</li> <li>YDR226W ADR1; adenylate kinase [EC:2.7.43] [SP:KADLYEAST]</li> <li>YDR226W ADR1; adenylate kinase [EC:2.7.43] [SP:KADLYEAST]</li> <li>YDR226W CTT1; catalase [EC:1.1.1.6] [SP:CATA_YEAST]</li> <li>YGR036W CTT1; catalase [EC:1.1.1.6] [SP:CATA_YEAST]</li> <li>YGR0406W CTD1; catalase [EC:1.1.1.6] [SP:CATA_YEAST]</li> <li>YGR0406W CTD1; catalase [EC:1.1.1.6] [SP:CATA_YEAST]</li> <li>YGR0406W CTD1; catalase [EC:1.1.1.6] [SP:CATA_YEAST]</li> <li>YGR0406 CFFR1; chosphofructokinase [EC:2.7.1.1] [SP:K6P1/YEAST]</li> <li>YHR050C PFFR1; chosphofructokinase [EC:2.7.1.1] [SP:K6P1/YEAST]</li> <li>YHR050C PFFR1; chosphofructokinase [EC:2.7.1.1] [SP:K6P2/YEAST]</li> <li>YGR340C PFFR1; chosphofructokinase [EC:3.1.1.1] [SP:ASC2.YEAST]</li> <li>YGR340C RP433; 3-phosphoglycerate delydrogenase [EC:1.1.1.95] [SP:SERX_YEAST]</li> <li>YGR340C RP433; RN12; DNA-dependent RNA polymerase 36 kD polypeptide [EC:2.7.6] [SP:RP44_YEAST]</li> <li>YGR340C RP433; RN12; DNA-dependent RNA polymerase 36 kD polypeptide [EC:2.7.6] [SP:RP44_YEAST]</li> <li>YGR340C MSP1; threonyl-tINA synthetase, ritochoming [EC:6.1.1.3] [SP:SYTM_YEAST]</li> <li>YGR340C SAH1; adparaginase [EC:3.1.1] [SP:ASG1-YEAST]</li> <li>YGR340C MSP1; threonyl-tINA synthetase, ritochoming [EC:6.1.3.3] [SP:SYTM_YEAST]</li> <li>YGR340C SAH1; adparaginase [EC:3.1.1] [SP:ASG1-YEAST]</li> <li>YGR340C MSP1; threonyl-tINA synthetase, r</li></ul>
<ul> <li>YIR037W HYR1; glutathione peroxidase [EC:1.11.16] [SP-GSHJ_YEAST]</li> <li>YDL168W SFA1; formaldehyd edhydrogenase [EC:1.1.1.1] [SP:ADH3.YEAST]</li> <li>YMR038W ADH3; alcohol dehydrogenase [EC:1.1.1.1] [SP:ADH3.YEAST]</li> <li>YMR038W ADK1; adenylate kinase [EC:1.1.1.16] [SP:CATA_YEAST]</li> <li>YDR236W CT1; catalase [EC:1.11.16] [SP:CATA_YEAST]</li> <li>YGR076W CT1; catalase [EC:1.11.16] [SP:CATA_YEAST]</li> <li>YGR070C CT1; catalase [EC:1.11.16] [SP:CATA_YEAST]</li> <li>YGR070C CT1; catalase [EC:1.11.16] [SP:CATA_YEAST]</li> <li>YGR070C TDH3; GPD3; glyceraldehyde 3-phosphate dehydrogenase [EC:2.7.7.6] [SP:RPB9.YEAST]</li> <li>YGR070C TDH3; GPD3; glyceraldehyde 3-phosphate dehydrogenase [EC:1.2.1.12] [SP:G3P1.YEAST]</li> <li>YGR070C PTN1; GPD3; glyceraldehyde 3-phosphate dehydrogenase [EC:1.2.1.12] [SP:G3P1.YEAST]</li> <li>YGR070C SF3; GybonsphogProtextoknase [EC:2.7.1.11] [SP:K6P1.YEAST]</li> <li>YGR070C SF3; GPD3; glyceraldehyde 3-phosphogProtextoknase [EC:3.1.13] [SP:S4P2.YEAST]</li> <li>YVR15C ASP3-2; L-separaginase [EC:3.1.11] [SP:ASG2.YEAST]</li> <li>YVR15C ASP3-2; L-separaginase [EC:3.1.11] [SP:ASG2.YEAST]</li> <li>YUR35C RP43, RN12; DNA-dependent RNA polymerase 1. H. H0 KD subunit [EC:2.7.7.6] [SP:RP48.YEAST]</li> <li>YUR35C RP43, RN12; DNA-dependent RNA polymerase 3. GD Oplypeptide [EC:2.7.7.6] [SP:RP48.YEAST]</li> <li>YUR324W RP43, RN12; DNA-dependent RNA polymerase 3. GD Oplypeptide [EC:2.7.7.6] [SP:RP48.YEAST]</li> <li>YUR324W RP43, L-separaginase [EC:3.1.11] [SP:ASG1-YEAST]</li> <li>YUR324W ASP1; L-separaginase [EC:3.1.13] [SP:S4T1.YEAST]</li> <li>YUR324W RP43, L-separaginase [EC:3.1.11] [SP:ASG2.YEA</li></ul>
YDL168W       SFA1; formaldelyde dehydrogenase [EC:1.1.1] [SP:ABA:YEAST]         YMR038W       ADH3; adenylate kinase [EC:2.7.43] [SP:KADL;YEAST]         YBR226W       ADK; adenylate kinase [EC:2.7.43] [SP:KADL;YEAST]         YBR226W       ADK; adenylate kinase [EC:1.7.43] [SP:KADL;YEAST]         YGR038W       CTT1; catalase [EC:1.11.1.6] [SP:CATA.YEAST]         YGR038W       CTT1; catalase [EC:1.11.1.6] [SP:CATA.YEAST]         YGR038W       CTT1; catalase [EC:1.11.1.6] [SP:CATA.YEAST]         YGR02C       TDB3, GPD3; glyceraldelyde 3-phosphate dehydrogenase [EC:1.2.1.12] [SP:G3P1.YEAST]         YGR032W       TDB3, GPD3; glyceraldelyde 3-phosphate dehydrogenase [EC:1.2.1.12] [SP:G3P3.YEAST]         YGR04C       PFK2; 6-hosphofructokinase [EC:2.7.1.11] [SP:K6P1.YEAST]         YMR030C       SER3; D-3-phosphoglycerate dehydrogenase [EC:1.1.1.36] [SP:SERX.YEAST]         YIL074C       SER3; 3-3-phosphoglycerate dehydrogenase [EC:1.1.1.6] [SP:SERX.YEAST]         YUR74C       ASP3-2; L-asparaginase [EC:3.5.1.1] [SP:ASG2.YEAST]         YUR740C       RP43; RN12; DNA-dependent RNA polymerase 0.4D polypeptide [EC:2.7.7.6] [SP:RP4.YEAST]         YUR74C       ASP3-2; L-asparaginase plec:3.5.1.1] [SP:ASG2.YEAST]         YUR74C       ASP3-2; L-asparaginase plec:3.5.1.1] [SP:ASG2.YEAST]         YUR74C       RP43; RN12; DNA-dependent RNA polymerase 0.5 Do ploppide [EC:2.7.7.6] [SP:RP4.YEAST]         YUR74C
YMR083W ADB3; alcohol dehydrogenase [EC:1.1.1] [SP:ADB3.YEAST] YDR226W ADK1; adenylate kinase [EC:2.7.4.3] [SP:KAD1_YEAST] YDR256C CTA1; catalase [EC:1.1.1.6] [SP:CATT.YEAST] YGR070C CTA1; catalase [EC:1.1.1.6] [SP:CATT.YEAST] YGR070C RPB9; DNA-directed RNA polymerase II 14.2 kD polypeptide [EC:2.7.7.6] [SP:RPB9.YEAST] YOR224C RPB8; DNA-directed RNA polymerase II 14.2 kD polypeptide [EC:2.7.7.6] [SP:RPB9.YEAST] YOR224C PD83; gyceraldehyde 3-phosphate dehydrogenase [EC:1.2.1.12] [SP:G3P1_YEAST] YJGR070C PFK1; 6-phosphofructokinase [EC:2.7.1.11] [SP:K6P1_YEAST] YHR070C PFK1; 6-phosphofructokinase [EC:2.7.1.11] [SP:K6P1_YEAST] YHR070C PFK1; 6-phosphofructokinase [EC:2.7.1.11] [SP:K6P1_YEAST] YHR070C PFK1; 6-phosphofructokinase [EC:2.7.1.11] [SP:K6P2_YEAST] YHR070C PFK1; 6-phosphofructokinase [EC:2.7.1.1] [SP:K6P2_YEAST] YHR070C PFK1; 6-phosphofructokinase [EC:3.7.1.1] [SP:K6P2_YEAST] YHR070C SPS3; L-asparaginase [EC:3.5.1.1] [SP:ASG2_YEAST] YHR070C RP88; DNA-directed RNA polymerase 30 kD polypeptide [EC:2.7.7.6] [SP:RPB8_YEAST] YOR24C RP88; DNA-directed RNA polymerase 30 kD polypeptide [EC:2.7.7.6] [SP:RP44_YEAST] YHL078W THS1; threonyl-tRNA synthetase, cytoplasmic [EC:6.1.1.3] [SP:SYTC_YEAST] YHL078W THS1; threonyl-tRNA synthetase, cytoplasmic [EC:6.1.1.3] [SP:SYTC_YEAST] YHL078W ASP1; L-asparaginase [EC:3.5.1.1] [SP:ASG1_YEAST] YHR05W ASP1; L-asparaginase [EC:3.5.1.1]
YDR226W ADK1; adenylate kinase [EC:2.7.4.3] [SP:KAD1;YEAST] YER170W ADK2, PAK3; adenylate kinase [EC:2.7.4.3] [SP:KAD2;YEAST] YGR088W CTT1; catalase [EC:1.11.6] [SP:CAT,YEAST] YGR088W CTT1; catalase [EC:1.11.6] [SP:CAT,YEAST] YGR026C RPB9; DNA-directed RNA polymerase II 14.2 kD polypeptide [EC:2.7.7.6] [SP:RPB3,YEAST] YOR224C RPB8; DNA-directed RNA polymerase II, 14.2 kD polypeptide [EC:2.7.7.6] [SP:RPB3,YEAST] YGR026C TDH3, GPD3; glyceraldehyde 3-phosphate dehydrogenase [EC:1.2.1.12] [SP:G3P1,YEAST] YGR026C PFK1; 6-phosphofructokinase [EC:2.7.1.11] [SP:K6P1,YEAST] YMR206C PFK2; 6-phosphofructokinase [EC:2.7.1.11] [SP:K6P2,YEAST] YHR031W SER3; D-3-phosphoglycerate dehydrogenase [EC:1.1.1.95] YLR157C ASP3-2; L-asparaginase [EC:3.5.1.1] [SP:ASG2,YEAST] YLR157C MSP3-2; L-asparaginase mitochondrail [EC:6.1.1.3] [SP:SYTG.YEAST] YLR157C MSP3-2; L-asparaginase mitochondrail [EC:6.1.1.3] [SP:SYTG.YEAST] YLR158C MSP1: L-asparaginase mitochondrail [EC:6.1.1.3] [SP:SYTG.YEAST] YLR158C MSP1: L-asparaginase glass chaine [C:6.1.1.1] [SP:ASG1,YEAST] YLR158C MSP1: L-asparaginase glass chaine [SP:AST] YLR158C MSP1: L-asparaginase glass chaine [SP:AST] YER058C M12; adenoydi dehydrogenase [EC:1.1.1] [SP:ASG1,YEAST] YER058C M12; adenoydi dehydrogenase [EC:1.2.1.3] [SP:PTNY,YEAST] YER058C M12; adenoydi dehydrogenase [EC:1.2.1.3] [SP:PTNY,YEAST] YER057C M24557 YER057C M245577 YER057C M
YER170W         ADK2, PAK3; adenylate kinase [EC:27.4.3] [SP:KAD2,ÝEAST]           YDR256C         CTA1; catalase [EC:1.11.1.6] [SP:CATT,YEAST]           YGR070C         RPB8; DNA-directed RNA polymerase II.4.2 kD polypeptide [EC:2.7.7.6] [SP:RPB8,YEAST]           YOR224C         RPB8; DNA-directed RNA polymerase II.4.2 kD polypeptide [EC:2.7.7.6] [SP:RPB8,YEAST]           YGR072         TDH3, GPD3, glyceraldehyde 3-phosphate dehydrogenase [EC:1.2.1.12] [SP:G3P1,YEAST]           YGR070         PFK1; 6-phosphofructokinase [EC:2.7.1.11] [SP:K6P1,YEAST]           YR208C         PFK1; 6-phosphofructokinase [EC:2.7.1.11] [SP:K6P1,YEAST]           YLR074C         SER33, 3-phosphoglycerate dehydrogenase [EC:1.1.05] [SP:SERX.YEAST]           YLR074C         SER33, 3-phosphoglycerate dehydrogenase [EC:1.1.1.95] [SP:SERX.YEAST]           YUR154C         ASP3-3; L-asparaginase [EC:3.5.1.1] [SP:ASG2,YEAST]           YUR340C         RPP8; DNA-directed RNA polymerase 36 kD polypeptide [EC:2.7.6] [SP:RP4.YEAST]           YUL078W         THS1; threonyl-tRNA synthetase, pitoplasnic [EC:6.1.1.3] [SP:SYTC,YEAST]           YUL078W         YBK1; threonyl-tRNA synthetase, pitoplasnic [EC:6.1.1.3] [SP:SYTC,YEAST]           YR145W         ASP1; L-separaginase [EC:3.1.1.1] [SP:ASG1,YEAST]           YR1078W         YBK1; separaginase [EC:3.1.1.1] [SP:ASG1,YEAST]           YR1078W         YBK1; threonyl-tRNA synthetase, pitoplasnic [EC:6.3.1.3] [SP:SYTC,YEAST]
Y DR256C CTA1; catalase [EC:111.16] [SF-CATA,YEÅST] YGR088W CTT1; catalase [EC:11.16] [SF-CATA,YEÅST] YGR02C RPB9; DNA-directed RNA polymerase II 14.2 kD polypeptide [EC:2.7.7.6] [SF:RPB9,YEAST] YOR24C RPB9; DNA-directed RNA polymerase II 1.1 II 6 KD subunit [EC:2.7.7.6] [SF:RPB8,YEAST] YGR02C TDH3, GPD3; glyceraldehyde 3-phosphate dehydrogenase [EC:12.1.12] [SF:G3P3,YEAST] YGR240C PFK1; 6-phosphofructokinase [EC:7.1.11] [SF:K6P1,YEAST] YMR205C PFK2; 6-phosphofructokinase [EC:7.1.11] [SF:K6P2,YEAST] YHR02C PFK1; 6-phosphofructokinase [EC:7.1.11] [SF:K6P2,YEAST] YHR02C PFK1; 6-phosphofructokinase [EC:7.1.11] [SF:K6P2,YEAST] YLL074C SER33; 3-phosphoglycerate dehydrogenase [EC:1.1.1.95] YLL074C SER33; 3-phosphoglycerate dehydrogenase [EC:1.1.1.95] YLR157C ASP3-2; L-asparaginase [EC:3.5.1.1] [SF:ASG2,YEAST] YOR240C RP43; I-asparaginase [EC:3.5.1.1] [SF:ASG2,YEAST] YOR240C RP43; RN12; DNA-directed RNA polymerase 1, II, III 16 KD aubunit [EC:2.7.7.6] [SF:RP8,YEAST] YOR240C RP43; RN12; DNA-directed RNA polymerase 36 kD polypeptide [EC:2.7.7.6] [SF:RP4A,YEAST] YLR157C MSP3-2; L-asparaginase [EC:3.5.1.1] [SF:ASG1,YEAST] YKL194C MST1; threonyl-tRNA synthetase, cytoplasmic [EC:6.1.3] [SF:SYTA,YEAST] YKL194C MST1; threonyl-tRNA synthetase, cytoplasmic [EC:6.3.5.4] [SF:SYTA,YEAST] YLR058W LN1; threonyl-tRNA synthetase, Cytoplasmic [EC:6.3.5.4] [SF:SYTA,YEAST] YLR058W LN1; threonine dehydrogenase [EC:3.1.1] [SF:ASG1,YEAST] YEK038W ASP1; asparaginase [EC:3.1.1] [SF:ASG1,YEAST] YEK038W ASP1; asparaginase [EC:3.1.1] [SF:ASG1,YEAST] YEK043C SAH1; adenosylhomocysteinase [EC:3.1.1] [SF:ASG1,YEAST] YEK043C SAH1; adenosylhomocysteinase [EC:3.1.1] [SF:ASG1,YEAST] YKL020C FR82; phenylalanyl-tRNA synthetase alpha chain [EC:6.1.2.0] [SF:SYFB,YEAST] YKL020C FR82; phenylalanyl-tRNA synthetase alpha chain [EC:1.7.4.1] [SF:NR1,YEAST] YKL020C FR82; phenylalanyl-tRNA synthetase alpha chain [EC:1.7.4.1] [SF:NR1,YEAST] YKL020C FR82; phenylalanyl-tRNA synthetase alpha chain [EC:1.7.4.1] [SF:NR1,YEAST] YKL020C FR82; Al
YGL070C       RPB9, DNA-directed RNA polymerase II 14.2 kD polypeptide [EC:2.7.7.6] [SP:RPB9.YEAST]         YGL070C       RPB9, DNA-directed RNA polymerase II, I, III 16 KD subunit [EC:2.7.7.6] [SP:RPB8.YEAST]         YGR192C       TDB1, GPD3; glyceraldehyde 3-phosphate dehydrogenase [EC:1.2.1.12] [SP:G3P3.YEAST]         YGR20C       PFR1; 6-phosphofuctokinase [EC:2.7.1.11] [SP:K6P1.YEAST]         YGR30C       PFR1; 6-phosphofuctokinase [EC:2.7.1.11] [SP:K6P1.YEAST]         YGR30C       PFR2; 6-phosphofuctokinase [EC:3.7.1.1] [SP:K6P1.YEAST]         YL1074C       SER3; D-3-phosphoglycerate dehydrogenase [EC:1.1.1.05]         YL1074C       SER3; J-1-asparaginase [EC:3.5.1.1] [SP:ASC3.YEAST]         YL1074C       RP43; AR112; DNA-directed RNA polymerase (1, 1, 111 16 KD subunit [EC:2.7.7.6] [SP:RPA4.YEAST]         YOR340C       RP44; AR112; DNA-directed RNA polymerase [EC:6.1.1.3] [SP:SYTM.YEAST]         YKL194C       MST1; threonyl-tRNA synthetase, entochonding [EC:6.3.5.4] [SP:SYTM.YEAST]         YR1078W       TB1; threonyl-tRNA synthetase, entochonding [EC:6.3.5.4] [SP:ASN1.YEAST]         YKL194C       MST1; threonyl-tRNA synthetase, entochonding [EC:6.3.5.4] [SP:SYSN1.YEAST]         YR145W <t< td=""></t<>
YGL070C       RPB9; DNA-directed RNA polymerase I, II, II 16 KD submit [EC:2.7.7.6] [SP:RPB8,YEAST]         YGR242C       RPB8; DNA-directed RNA polymerase I, II, III 16 KD submit [EC:2.7.7.6] [SP:RPB8,YEAST]         YJL052W       TDH1, GPD1, SSS2; glyceraldehyde 3-phosphate dehydrogenase [EC:1.2.1.12] [SP:G3P3,YEAST]         YGR240C       PFK1; 6-phosphofructokinase [EC:2.7.1.11] [SP:K6P1,YEAST]         YMR205C       PFK2; 6-phosphofructokinase [EC:2.7.1.11] [SP:K6P1,YEAST]         YL072W       SER3; 3-phosphogiveerate dehydrogenase [EC:1.1.1.95]         YLR157C       ASP3-2; L-asparaginase [EC:3.5.1.1] [SP:ASG2,YEAST]         YLR157C       ASP3-2; L-asparaginase [EC:3.5.1.1] [SP:ASG2,YEAST]         YOR240C       RP48; DNA-directed RNA polymerase 1, II, III 16 KD submit [EC:2.7.7.6] [SP:RP8,YEAST]         YOR240C       RP48; DNA-directed RNA polymerase 36 kD polypeptide [EC:2.7.7.6] [SP:RP4,YEAST]         YOR240C       RP48; DNA-directed RNA polymerase 36 kD polypeptide [EC:2.7.7.6] [SP:RP4,YEAST]         YOR240C       RP48; DNA-directed RNA polymerase 36 kD polypeptide [EC:2.7.7.6] [SP:RP4,YEAST]         YKL194C       MS1; threonyl-tRNA synthetase, cytoplasmic [EC:6.1.1.3] [SP:SYTG,YEAST]         YKL194C       MS1; threonyl-tRNA synthetase, cytoplasmic [EC:6.1.3.8] [SP:SN1_YEAST]         YBR321W       ASP1; L-asparaginase [EC:3.5.1.1] [SP:ASG1_YEAST]         YER080W       IAN; thrononine detalyndycanase [EC:2.1.1.1] [SP:ASH5_YEAST]
YOR224C         RPB8: DNA-directed RNA polymerase 1, II, III 16 KD submit [EC:12.7.7.6] [SP:RPB8.YEAST]           YGR192C         TDB1, GPD3; glyceraldehyde 3-phosphate dehydrogenase [EC:12.1.12] [SP:G3P3.YEAST]           YGR240C         PFK1; 6-phosphofructokinase [EC:2.7.1.11] [SP:K6P1.YEAST]           YMR205C         PFK2; 6-phosphofructokinase [EC:2.7.1.11] [SP:K6P2.YEAST]           YER081W         SER3; 3-phosphoglycerate dehydrogenase [EC:1.1.1.05] [SP:SERX.YEAST]           YLR157C         ASP3-2; L-asparaginase [EC:3.5.1.1] [SP:ASC2.YEAST]           YUR157C         ASP3-2; L-asparaginase [EC:3.5.1.1] [SP:ASC2.YEAST]           YOR240C         RPA43, L-asparaginase [EC:3.5.1.1] [SP:ASC2.YEAST]           YOR240C         RPA43, RN12; DNA-dependent RNA polymerase 36 kD polypeptide [EC:2.7.7.6] [SP:RP44.YEAST]           YOR240C         RPA43, RN12; DNA-dependent RNA polymerase 36 kD polypeptide [EC:2.7.7.6] [SP:RP44.YEAST]           YKL194C         MST1; threonyl-tRNA synthetase, ortoplasmic [EC:6.1.1.3] [SP:SYTM.YEAST]           YKL194C         MST1; threonyl-tRNA synthetase, entiochondrial [EC:6.1.1.3] [SP:SYTM.YEAST]           YPR145W         MST1; threonyl-tRNA synthetase, entiochondrial [EC:6.3.5.4] [SP:ASN1.YEAST]           YPR145W         ASP1; L-asparaginase [EC:3.5.1.1] [SP:ASG1.YEAST]           YPR145W         ASP1; L-asparaginase [EC:3.5.1.1] [SP:ASG1.YEAST]           YPR145W         ASP1; L-asparaginase [EC:3.5.1.1.1] [SP:ASG1.YEAST]
YGR192C       TDH3, GPD3; glyceraldebyde 3-phosphate dehydrogenase [EC:1.2.1.12] [SP:G3P3,YEAST]         YJL052W       TDH1, GPD1, SS22; glyceraldebyde 3-phosphate dehydrogenase [EC:1.2.1.12] [SP:G3P1,YEAST]         YMR206C       PFK1; 6-phosphofructokinase [EC:2.7.1.11] [SP:K6P1,YEAST]         YMR205C       PFK2; 6-phosphofructokinase [EC:2.7.1.11] [SP:K6P1,YEAST]         YLR157C       ASP3.2; L-asparaginase [EC:3.1.1.135]         YLR157C       ASP3.3; L-asparaginase [EC:3.1.1] [SP:ASC2,YEAST]         YOR240C       RPB8; DNA-directed RNA polymerase 1, H, H1 6 KD subunit [EC:2.7.7.6] [SP:RPB8,YEAST]         YOR340C       RPA43, RRN12; DNA-directed RNA polymerase 1, H, H1 6 KD subunit [EC:2.7.7.6] [SP:RP44,YEAST]         YUL078W       THS1; threonyl-tRNA synthetase, cytoplasmic [EC:6.1.1.3] [SP:SYTC,YEAST]         YKL194C       MST1; threonyl-tRNA synthetase, cytoplasmic [EC:6.1.1.3] [SP:SN1_YEAST]         YBR32W       ASP1; L-asparaginase [EC:3.1.1] [SP:ASC1.2]         YPR421W       ASP1; L-asparaginase [EC:3.1.1] [SP:ASC1.2]         YBR42W       ASP1; L-asparaginase [EC:3.1.1.1] [SP:ASC1.2]         YBR42W       ASP1; L-asparaginase [EC:3.1.1.1] [SP:ASC1.2]         YBR43W       AD45; alcohol dehyd
YJL052W       TDH1, GPD1, SSS2; glyceriadeliyde 3-phosphate debydrogenase [Ec:1.2.1.12] [SP:G3P1-YEAST]         YGR240C       PFK1; 6-phosphofructokinase [Ec:2.7.1.1] [SP:K6P1-YEAST]         YMR205C       PFK2; 6-phosphofructokinase [Ec:2.7.1.1] [SP:K6P2-YEAST]         YHL074C       SER33, 3-phosphoglycerate dehydrogenase [Ec:1.1.1.95]         YLR157C       ASP5-2; L-asparaginase [EC:3.5.1.1] [SP:ASG2-YEAST]         YR157C       ASP5-2; L-asparaginase [EC:3.5.1.1] [SP:ASG2-YEAST]         YOR244C       RPB8; DNA-directed RNA polymerase 1, II, III 16 KD subunit [EC:2.7.7.6] [SP:RPA4-YEAST]         YOR24C       RPB8; DNA-directed RNA polymerase 36 KD polypeptide [EC:2.7.7.6] [SP:RPA4-YEAST]         YIL078W       THS1; threonyl-tRNA synthetase, cytoplasmic [EC:6.1.1.3] [SP:SYTC.YEAST]         YKL194C       MST1; threonyl-tRNA synthetase, cytoplasmic [EC:6.3.5.4] [SP:ASN1_YEAST]         YBR21W       ASP1; L-asparaginase [EC:3.5.1.1] [SP:ASG1_YEAST]         YPR21W       ASP1; L-asparaginase [EC:3.5.1.1] [SP:ASG1_YEAST]         YPR21W       ASP1; L-asparaginase [EC:3.1.1.1] [SP:ABH5_YEAST]         YPR21W       ASP1; L-asparaginase [EC:3.5.1.1] [SP:ASG1_YEAST]         YPR21W       ASP1; L-asparaginase [EC:3.5.1.1] [SP:ASH1_YEAST]         YPR05W       ADS1; aldehyde dehydrase [EC:4.2.1.6] [SP:HDH_YEAST]         YPR05W       ADS1; aldehyde dehydragenase [EC:1.2.1.3] [SP:SHAH_YEAST]         YPR045C
YGR240C       PFK1; 6-phosphofructokinase [EC:2.7.1.1] [SP:K6P1/YEAST]         YMR205C       PFK2; 6-phosphofyterate dehydrogenase [EC:1.1.1.95] [SP:SERX.YEAST]         YLR07C       SER3; 3-phosphoglycerate dehydrogenase [EC:1.1.1.95]         YLR07C       SER3; 3-phosphoglycerate dehydrogenase [EC:1.1.1.95]         YLR15C       ASP3-2; L-asparaginase [EC:3.5.1.1] [SP:ASG2.YEAST]         YOR240C       RPB8; DNA-directed RNA polymerase I, II, III 16 KD subunit [EC:2.7.7.6] [SP:RPB8.YEAST]         YOR340C       RPA43, RRN12; DNA-directed RNA polymerase 36 kD polypeptide [EC:2.7.7.6] [SP:RP44-YEAST]         YUL078W       THS1; threonyl-tRNA synthetase, cytoplasmic [EC:6.1.1.3] [SP:SYTCY_YEAST]         YDR321W       ASP1; L-asparaginase [EC:3.5.11] [SP:ASGLYEAST]         YER036W       ILV1; threonint edhydratase [EC:4.2.1.6] [SP:THDFLYEAST]         YER043C       SAH1; adenosylhomocysteinase [EC:3.1.1] [SP:ASHLYEAST]         YER043C       SAH1; adenosylhomocysteinase [EC:3.1.1] [SP:ASHLYEAST]         YER043C       SAH1; adenosylhomocysteinase [EC:3.6.1.1] [SP:ASHLYEAST]         YFR047C       nictaine-nuclocide pyrophosphyrlase (carboxylating) [EC:4.2.19] [SP:NADC_YEAST]         YFR047C
YMR205C         PFK2; 6-phosphofructokinase         EC:2.1.11         [PFK2:66P2.VEAST]           YER081W         SER3; 3-phosphoglycerate dehydrogenase         [EC:1.1.1.95]         [SP:SERX.YEAST]           YLR15C         ASP3-2; L-asparaginase         [EC:3.1.1]         [SP:ASG2.YEAST]           YLR158C         ASP3-2; L-asparaginase         [EC:3.1.1]         [SP:ASG2.YEAST]           YOR240C         RP443, RNN1; DNA-dependent RNA polymerase 36 kD polypeptide         [EC:2.7.7.6]         [SP:RPB8_YEAST]           YIL078W         THS1; threonyl-tRNA synthetase, cytoplasmic [EC:6.1.1.3]         [SP:SYTC.YEAST]           YKL194C         MST1; threonyl-tRNA synthetase, mitochondrial [EC:6.1.1.3]         [SP:SYTC.YEAST]           YBR321W         ASP1; L-asparagines [EC:3.5.1.1]         [SP:ASG1.YEAST]           YER086W         ILN1; threonine dehydratase [EC:4.2.1.16]         [SP:STMT.YEAST]           YER045W         ADH5; alcohol dehydrogenase [EC:1.1.1]         [SP:ABL5.YEAST]           YER047C         SAH1; adenosylhomocysteinase [EC:3.5.1.1]         [SP:SAH1.YEAST]           YER047W         ADD3; alcehyde dehydrogenase [EC:1.1.1.3]         [SP:SYBA.YEAST]           YER047C         SAH1; adenosylhomocysteinase [EC:3.5.1.4]         [SP:ABL5.YEAST]           YER047C         SAH1; adenosylhomocysteinase [EC:4.2.1.6]         [SP:ABL7.YEAST]
YER081W       SER3; D-3-phosphoglycerate dehydrogenase [EC:1.1.1.95] [SF:SERX.YEAST]         YIL074C       SER3; 3-phosphoglycerate dehydrogenase [EC:1.1.1.95]         YLR157C       ASP3-2; L-asparaginase [EC:3.5.1.1] [SP:ASG2.YEAST]         YLR158C       ASP3-3; L-asparaginase [EC:3.5.1.1] [SP:ASG2.YEAST]         YOR224C       RPB8; DNA-directed RNA oplymerase 1, II, III 16 KD subunit [EC:2.7.7.6] [SP:RPB8_YEAST]         YOR24C       RPA43, RRN12; DNA-dependent RNA polymerase 36 kD polypeptide [EC:2.7.7.6] [SP:RP44_YEAST]         YIL078C       MST1; threonyl-tRNA synthetase, cytoplasmic [EC:6.1.1.3] [SP:SYTC_YEAST]         YKL194C       MST1; threonyl-tRNA synthetase, cytoplasmic [EC:6.1.1.3] [SP:SYTM_YEAST]         YPR145W       ASN1; asparaginase [EC:3.5.1.1] [SP:ASG1_YEAST]         YPR145W       ASN1; asparaginase [EC:1.1.1.1] [SP:ADH5-YEAST]         YPR145W       ASN1; asparaginase [EC:1.1.1.1] [SP:ADH5-YEAST]         YPR145W       ADM3; aldehydrogenase [EC:1.1.1.3] [SP:DH5.YEAST]         YER045W       Cash1; algenosylhomocysteinase [EC:3.1.1] [SP:ADH5-YEAST]         YER045C       SAH1; adenosylhomocysteinase [EC:3.1.1] [SP:ATH.YEAST]         YER045W       cystathionine beta-lyase [EC:4.4.1.8] [SP:METC_YEAST]         YFL022C       FRS2; phenylalanyl-tRNA synthetase alpha chain [EC:1.1.2.0] [SP:SYFB_YEAST]         YFL022C       FRS2; phenylalanyl-tRNA synthetase alpha chain [EC:1.1.2.0] [SP:NADC_YEAST]
YIL074C       SER33; 3-phosphoglycerate dehydrogenase [EC:1.11.95]       Y         YLR157C       ASP3-2; L-asparaginase [EC:3.5.1.1] [SP:ASG2.YEAST]         YQR24C       RPB8; DNA-directed RNA polymerase 0; AD polymerase 0; AD polymeptide [EC:2.7.7.6] [SP:RPB8,YEAST]         YQR340C       RPA43, RRN12; DNA-dependent RNA polymerase 0; AD polymeptide [EC:2.7.7.6] [SP:RP44-YEAST]         YUO78W       THS1; threonyl-tRNA synthetase, cytoplasmic [EC:6.1.1.3] [SP:YTC.YEAST]         YKL194C       MST1; threonyl-tRNA synthetase, mitochondrial [EC:6.1.1.3] [SP:SYTM_YEAST]         YDR321W       ASP1; L-asparaginase [EC:3.5.1.1] [SP:ASG1.YEAST]         YPR15W       ASP1; L-asparagine synthase (glutamine-hydrolysing) [EC:6.3.5.4] [SP:SYTM_YEAST]         YPR047C       MSN1; threonine dehydratase [EC:4.2.1.6] [SP:THDH_YEAST]         YBR045W       ADD5; alcohol dehydrogenase [EC:3.3.1.1] [SP:ADH5_YEAST]         YER0472W       ALD3; aldehyde dehydrogenase [EC:3.3.1.1] [SP:SAHH_YEAST]         YFR045C       rice taminotransferase [EC:2.4.2.10] [SP:SYFB_YEAST]         YFR047C       nicotinate-nucleotide phyrophosphorylase (carboxylating) [EC:2.4.2.10] [SP:RNAC_YEAST]         YFR047C       nicotinate-nucleotide prophosphorylase (carboxylating) [EC:2.4.2.10] [SP:RNA2YEAST]         YR0406C       RNR3; ribonucleoside-diphosphate reductase alpha chain [EC:2.1.7.6] [SP:RNA2YEAST]         YR0407C       nicotinate-nucleoside phosphorylase [EC:2.4.1.1] [SP:RIR3_YEAST]
TLR157C       ASP3-2; L-asparaginase [EC:3.5.1.1]       [SP:ASC2,YEAST]         YLR158C       ASP3-3; L-asparaginase [EC:3.5.1.1]       [SP:ASC2,YEAST]         YOR224C       RPB8; DNA-directed RNA polymerase 1, II, III 16 KD subunit [EC:2.7.7.6]       [SP:RPB8,YEAST]         YOR340C       RPA43, RRN12; DNA-dependent RNA polymerase 36 kD polypeptide [EC:2.7.7.6]       [SP:RPB4,YEAST]         YIL078W       THS1; threonyl-tRNA synthetase, cytoplasmic [EC:6.1.1.3]       [SP:SYTM_YEAST]         (B) Correlated gene clusters with multiple EC numbers         YDR321W       ASP1; L-asparaginase [EC:3.5.1.1]       [SP:ASG1,YEAST]         YBR145W       ADS1; alcohol dehydrogenase [EC:1.1.13]       [SP:ASN1,YEAST]         YBR145W       ADB1; alcohol dehydrogenase [EC:1.1.13]       [SP:DHA5,YEAST]         YER043C       SAH1; alenosylhomocysteinase [EC:3.5.1]       [SP:SHB4,YEAST]         YER043C       SAH1; alenosylhomocysteinase [EC:3.5.1]       [SP:SATH,YEAST]         YER043C       SAH1; alenosylhomocysteinase [EC:3.5.1]       [SP:SHB4,YEAST]         YER043C       SAH1; alenosylhomocysteinase [EC:2.6.1.1]       [SP:NADC,YEAST]         YER043C       richate-nucleotide pyrophosphorylase [C:2.4.1.1]       [SP:NADC,YEAST]         YER043C       richate-nucleotide pyrophosphorylase [EC:2.4.1.1]       [SP:NADC,YEAST]         YL020C       YEAST       YE
YLR158C       ASP3-3; L-asparaginase [EC:3.5.1.1] [SP:ASG2_YEAST]         YOR224C       RPB8; DNA-directed RNA polymerase I, II, III 16 KD subunit [EC:2.7.7.6] [SP:RPB8,YEAST]         YOR340C       RPA43, RNN12; DNA-dependent RNA polymerase 36 kD polypoptide [EC:2.7.7.6] [SP:RPB8,YEAST]         YLL078W       THS1; threonyl-tRNA synthetase, cytoplasmic [EC:6.1.1.3] [SP:SYTC_YEAST]         YKL194C       MST1; threonyl-tRNA synthetase, cytoplasmic [EC:6.1.1.3] [SP:SYTC_YEAST]         YDR321W       ASP1; L-asparaginase [EC:3.5.1.1] [SP:ASG1.YEAST]         YDR145W       ASP1; L-asparaginase [EC:3.5.1.1] [SP:ASG1.YEAST]         YER048W       ASN1; asparagine synthase (glutamine-hydrolysing) [EC:6.3.5.4] [SP:ASN1.YEAST]         YER043W       ADB5; alcohol dehydrogenase [EC:1.1.1.6] [SP:THD4.YEAST]         YER043C       SAH1; adenosylhomocysteinase [EC:1.1.3] [SP:DA5.YEAST]         YER043C       SAH1; adenosylhomocysteinase [EC:2.4.1.8] [SP:METC_YEAST]         YFL05W       cystathionine beta-lyase [EC:4.4.1.8] [SP:METC_YEAST]         YFL06W       AAT1; asparate aminotransferase [EC:2.6.1.1] [SP:AATM_YEAST]         YL106W       AAT1; asparate eminoransferase [EC:2.6.1.1] [SP:AATM_YEAST]         YL106W       AAT1; asparate eminoransferase [EC:2.4.1.4] [SP:NETC_YEAST]         YL106W       RNR3; ribonucleoside phophorylase [EC:2.4.2.19] [SP:NADC_YEAST]         YL106W       RNR3; ribonucleoside Apholymerase III, 34 KD subunit [EC:2.1.7
YOR224C       RPB8; DNA-directed RNA polymerase I, II, III 16 KD subuit [EC:2.7.7.6] [SP:RPB8,YEAST]         YOR340C       RPA43, RRN12; DNA-dependent RNA polymerase 36 kD polypeptide [EC:2.7.7.6] [SP:RPA4.YEAST]         YILO78W       THS1; threonyl-tRNA synthetase, oxtoplasmic [EC:6.1.1.3] [SP:SYTC.YEAST]         YKL194C       MST1; threonyl-tRNA synthetase, mitochondrial [EC:6.1.1.3] [SP:SYTM.YEAST]         YDR321W       ASP1; L-asparaginase [EC:3.5.1.1] [SP:ASG1.YEAST]         YDR31W       ASP1; L-asparaginase [EC:3.5.1.1] [SP:ASG1.YEAST]         YPR145W       ASN1; asparagine synthase (glutamine-hydrolysing) [EC:6.3.5.4] [SP:ASN1.YEAST]         YBR086W       ILV1; threonine dehydratase [EC:4.2.1.16] [SP:THDH_YEAST]         YBR073W       ALD3; aldehyde dehydrogenase [EC:1.1.1] [SP:ABH5.YEAST]         YER073W       ALD3; aldehyde dehydrogenase [EC:3.3.1.1] [SP:SAHH.YEAST]         YFR045C       CSAtthionine beta-lyase [EC:4.4.1.8] [SP:METC.YEAST]         YFR047C       nicotinate-nucleotide pyrophosphorylase (carboxylating) [EC:2.4.2.19] [SP:NADC.YEAST]         YLL066C       RNR3; ribonucleoside-diphosphate reductase alpha chain [EC:2.1.7.4] [SP:RNPH_YEAST]         YR1030C       RPC34; DNA-directed RNA polymerase III, 34 KD subunit [EC:2.7.7.6] [SP:RPC6.YEAST]         YLL066C       RNR3; ribonucleoside-diphosphate reductase alpha chain [EC:1.1.7.4] [SP:RIR3.YEAST]         YR1046C       RNR3; ribonucleoside-diphosphate reductase alpha chain [EC:2.1.7.6] [SP:
YOR224C       RPB8; DNA-directed RNA polymerase I, II, III 16 KD subuit [EC:2.7.7.6] [SP:RPB8,YEAST]         YOR340C       RPA43, RRN12; DNA-dependent RNA polymerase 36 kD polypeptide [EC:2.7.7.6] [SP:RPA4.YEAST]         YILO78W       THS1; threonyl-tRNA synthetase, oxtoplasmic [EC:6.1.1.3] [SP:SYTC.YEAST]         YKL194C       MST1; threonyl-tRNA synthetase, mitochondrial [EC:6.1.1.3] [SP:SYTM.YEAST]         YDR321W       ASP1; L-asparaginase [EC:3.5.1.1] [SP:ASG1.YEAST]         YDR31W       ASP1; L-asparaginase [EC:3.5.1.1] [SP:ASG1.YEAST]         YPR145W       ASN1; asparagine synthase (glutamine-hydrolysing) [EC:6.3.5.4] [SP:ASN1.YEAST]         YBR086W       ILV1; threonine dehydratase [EC:4.2.1.16] [SP:THDH_YEAST]         YBR073W       ALD3; aldehyde dehydrogenase [EC:1.1.1] [SP:ABH5.YEAST]         YER073W       ALD3; aldehyde dehydrogenase [EC:3.3.1.1] [SP:SAHH.YEAST]         YFR045C       CSAtthionine beta-lyase [EC:4.4.1.8] [SP:METC.YEAST]         YFR047C       nicotinate-nucleotide pyrophosphorylase (carboxylating) [EC:2.4.2.19] [SP:NADC.YEAST]         YLL066C       RNR3; ribonucleoside-diphosphate reductase alpha chain [EC:2.1.7.4] [SP:RNPH_YEAST]         YR1030C       RPC34; DNA-directed RNA polymerase III, 34 KD subunit [EC:2.7.7.6] [SP:RPC6.YEAST]         YLL066C       RNR3; ribonucleoside-diphosphate reductase alpha chain [EC:1.1.7.4] [SP:RIR3.YEAST]         YR1046C       RNR3; ribonucleoside-diphosphate reductase alpha chain [EC:2.1.7.6] [SP:
YOR340C         RPA43, RRN12; DNA-dependent RNA polymerase 36 kD polypeptide [EC:2.7.7.6] [SP:RPA4.YEAST]           YIL1078W         THS1; threonyl-tRNA synthetase, cytoplasmic [EC:6.1.1.3] [SP:SYTM.YEAST]           YKL194C         MST1; threonyl-tRNA synthetase, mitochondrial [EC:6.1.1.3] [SP:SYTM.YEAST]           YDR321W         ASP1; L-asparaginase [EC:3.5.1.1] [SP:ASG1.YEAST]           YDR145W         ASN1; asparagine synthase (glutamine-hydrolysing) [EC:6.3.5.4] [SP:ASN1.YEAST]           YBR145W         AD15; alcohol dehydrogenase [EC:1.1.16] [SP:THDH.YEAST]           YBR045W         AD45; alcohol dehydrogenase [EC:1.2.1.3] [SP:SDHA5.YEAST]           YER043C         SAH1; adenosylhomocysteinase [EC:3.5.1.1] [SP:SAHH.YEAST]           YER043C         SAH1; adenosylhomocysteinase [EC:3.5.1.1] [SP:SAHH.YEAST]           YER043C         SAH1; adenosylhomocysteinase [EC:3.5.1.1] [SP:SAHH.YEAST]           YER043C         FRS2; phenylalanyl-tRNA synthetase alpha chain [EC:6.1.20] [SP:SYFB_YEAST]           YHL06W         AAT1; aspartate aminotransferase [EC:2.6.1.1] [SP:AATM.YEAST]           YL106W         ALT1; aspartate aminotransferase [EC:2.6.1.1] [SP:PNPH_YEAST]           YL106W         RNR3; ribonucleoside-diphosphate reductase alpha chain [EC:1.17.4.1] [SP:RPG.YEAST]           YL106W         RNR3; ribonucleoside-diphosphate reductase alpha chain [EC:1.17.4.1] [SP:RPG.YEAST]           YL106W         RNR3; ribonucleoside-diphosphate reductase alpha chain [EC:1.17.4
YIL078W       THS1; threonyl-tRNA synthetase, cytoplasmic [EC:6.1.1.3] [SP:SYTC.YEAST]         YKL194C       MST1; threonyl-tRNA synthetase, mitochondrial [EC:6.1.1.3] [SP:SYTM.YEAST]         (B) Correlated gene clusters with multiple EC numbers         YDR321W       ASP1; L-asparaginase [EC:3.5.1.1] [SP:ASG1.YEAST]         YPR145W       ASN1; asparagine synthase (glutamine-hydrolysing) [EC:6.3.5.4] [SP:ASN1.YEAST]         YBR145W       ADB5; alcohol dehydrogenase [EC:1.1.1.1] [SP:ADH5.YEAST]         YER073W       ALD3; aldehyde dehydrogenase [EC:1.1.1.1] [SP:ADH5.YEAST]         YER043C       SAH1; adenosylhomocysteinase [EC:3.1.1] [SP:ADH5.YEAST]         YER043C       SAH1; adenosylhomocysteinase [EC:2.6.1.1] [SP:ADH5.YEAST]         YFR045W       cystathionine beta-lyase [EC:4.4.1.8] [SP:METC.YEAST]         YKL100W       AAT1; aspartate aminotransferase [EC:2.6.1.1]         YFR047C       nicotinate-nucleotide pyrophosphorylase (carboxylating) [EC:2.4.2.19] [SP:NADC.YEAST]         YLR006C       RNR3; ribonucleoside-diphosphate reductase alpha chain [EC:1.17.4.1] [SP:RIR3.YEAST]         YNR003C       RPC34; DNA-directed RNA polymerase III, 34 KD subunit [EC:2.7.6.6] [SP:PRPLYEAST]         YNL066C       RNR3; ribonucleoside-diphosphate reductase alpha chain [EC:1.17.4.1] [SP:RIR3.YEAST]         YNR003C       RPC34; DNA-directed RNA polymerase III, 34 KD subunit [EC:2.7.7.6] [SP:RPC6.YEAST]         YNL066C       RNR3; ribonucleoside-d
YKL194C       MST1; threonyl-tRNA synthetase, mitochondrial [EC:6.1.1.3] [SP:SYTM_YEAST]         (B) Correlated gene clusters with multiple EC numbers         YDR321W       ASP1; L-asparaginase [EC:3.5.1.1] [SP:ASG1.YEAST]         YPR145W       ASN1; asparagine synthase (glutamine-hydrolysing) [EC:6.3.5.4] [SP:ASN1_YEAST]         YBR145W       ADH5; alcohol dehydrogenase [EC:1.1.1.6] [SP:TTDH_YEAST]         YBR05W       ALD3; aldehyde dehydrogenase [EC:1.2.1.3] [SP:DHA5.YEAST]         YER043C       SAH1; adenosylhomocysteinase [EC:3.3.1.1] [SP:ADH5.YEAST]         YFR055W       cystathionine beta-lyase [EC:4.4.1.8] [SP:METC_YEAST]         YFR052W       cystathionine beta-lyase [EC:4.4.1.8] [SP:METC_YEAST]         YFR047C       nicotinate-nucleotide pyrophosphorylase [EC:2.4.2.1] [SP:NADC_YEAST]         YL106W       AAT1; aspartate aminotransferase [EC:2.6.1.1] [SP:AATM_YEAST]         YLR209C; probable purine nucleoside phosphorylase [EC:2.4.2.1] [SP:NPH_YEAST]         YLR050C       ribonable purine nucleoside phosphorylase [EC:2.4.2.1] [SP:NPH_YEAST]         YLR060C       RNR3; ribonucleoside-diphosphate reductase alpha chain [EC:1.17.4.1] [SP:RIB3.YEAST]         YR003C       RPC34; DNA-directed RNA polymerase III, 34 KD subunit [EC:2.7.7.6] [SP:RPC6.YEAST]         YR1066C       RNR3; ribonucleoside-diphosphate reductase alpha chain [EC:1.17.4.1] [SP:RIB3.YEAST]         YR0037       YRC23; abparadiphosphate reductase alpha chain [EC:1.17.4.1
(B) Correlated gene clusters with multiple EC numbers         YDR321W       ASP1; L-asparaginase [EC:3.5.1.1] [SP:ASG1.YEAST]         YPR145W       ASN1; asparagine synthase (glutamine-hydrolysing) [EC:6.3.5.4] [SP:ASN1.YEAST]         YER086W       ILV1; threonine dehydratase [EC:4.2.1.16] [SP:THDH_YEAST]         YBR145W       ADH5; alcohol dehydrogenase [EC:1.1.1.1] [SP:ADH5.YEAST]         YER073W       ALD3; aldehyde dehydrogenase [EC:3.3.1.1] [SP:SAHH_YEAST]         YER043C       SAH1; adenosylhomccysteinase [EC:3.3.1.1] [SP:SAHH_YEAST]         YFR055W       cystathionine beta-lyase [EC:4.4.1.8] [SP:METC.YEAST]         YFR043C       FR32; phenylalanyl-tRNA synthetase alpha chain [EC:6.1.1.20] [SP:SYFB_YEAST]         YKL06W       AAT1; aspartate aminotransferase [EC:2.6.1.1] [SP:ATM_YEAST]         YFR047C       nicotinate-nucleotide pyrophosphorylase [CC:2.4.2.1] [SP:NADC_YEAST]         YLR209C       YLR209C; probable purine nucleoside phosphorylase [CC:2.4.2.1] [SP:NADC_YEAST]         YN003C       RPC34; DNA-directed RNA polymerase III, 34 KD subunit [EC:2.7.7.6] [SP:RPC6_YEAST]         YN003C       RPC34; DNA-directed RNA polymerase III, 34 KD subunit [EC:2.7.7.6] [SP:RR3_YEAST]         YOR074C       CDC21; thymidylate synthase (TS) [EC:2.1.1.4] [SP:TYSY_YEAST]         YOR074C       CDC21; thymidylate synthase (SI [SC:2.2.1.1] [SP:AATM_YEAST]         YDR148C       KGD2; 2-oxoglutarate dehydrogenase EC:2.2.1.1] [SP:A
YDR321WASP1; L-asparaginase [EC:3.5.1.1] [SP:ASG1.YEAST]YPR145WASN1; asparagine synthase (glutamine-hydrolysing) [EC:6.3.5.4] [SP:ASN1.YEAST]YER08WILV1; threonine dehydrogenase [EC:4.2.1.16] [SP:THDH_YEAST]YBR145WADH5; alcohol dehydrogenase [EC:1.2.1.3] [SP:DHA5.YEAST]YER073WALD3; aldehyde dehydrogenase [EC:3.1.1] [SP:ADH5.YEAST]YER042CSAH1; adenosylhomocysteinase [EC:3.3.1.1] [SP:AHH.YEAST]YFR055Wcystathionine beta-lyase [EC:4.4.1.8] [SP:METC_YEAST]YFL022CFK52; phenylalanyl-tRNA synthetase alpha chain [EC:6.1.1.20] [SP:SYFB_YEAST]YKL06WAAT1; aspartate aminotransferase [EC:2.6.1.1] [SP:AATM_YEAST]YFR047Cnicotinate-nucleotide pyrophosphorylase (carboxylating) [EC:2.4.2.1] [SP:NADC_YEAST]YLR209CYLR209C; probable purine nucleoside phosphorylase [EC:2.4.2.1] [SP:PNPH_YEAST]YLR003CRPC34; DNA-directed RNA polymerase III, 34 KD subunit [EC:1.7.4.1] [SP:RIR3.YEAST]YOR074CCDC21; thymidylate synthase (EC:2.6.1.1] [SP:AATM_YEAST]YOR374WALD4; aldehyde dehydrogenase [EC:2.1.1.4] [SP:TYSY_YEAST]YDR148CKGD2; 2-oxoglutarate dehydrogenase [EC:1.1.3] [SP:DHA4.YEAST]YOR374WALD4; aldehyde dehydrogenase [EC:1.2.1.3] [SP:DHA4.YEAST]YFL018CLPD1, DHLP1; dihydrolipoamide dehydrogenase [EC:1.8.1.4] [SP:TDLH_YEAST]YFR055Wcystathionine beta-lyase [EC:4.4.1.8] [SP:TYSY_YEAST]YGL070CRPB9; DNA-directed RNA polymerase II 1.4.2 kD polypeptide [EC:2.7.7.6] [SP:RB9_YEAST]YGL070CRPB9; DNA-directed RNA polymerase [EC:2.6.1.1] [SP:DLDH_YEAST]YFL018CLPD1, DHLP1; dihydrolipoamide dehydrogenase [E
YDR321WASP1; L-asparaginase [EC:3.5.1.1] [SP:ASG1.YEAST]YPR145WASN1; asparagine synthase (glutamine-hydrolysing) [EC:6.3.5.4] [SP:ASN1.YEAST]YER08WILV1; threonine dehydrogenase [EC:4.2.1.16] [SP:THDH_YEAST]YBR145WADH5; alcohol dehydrogenase [EC:1.2.1.3] [SP:DHA5.YEAST]YER073WALD3; aldehyde dehydrogenase [EC:3.1.1] [SP:ADH5.YEAST]YER042CSAH1; adenosylhomocysteinase [EC:3.3.1.1] [SP:AHH.YEAST]YFR055Wcystathionine beta-lyase [EC:4.4.1.8] [SP:METC_YEAST]YFL022CFK52; phenylalanyl-tRNA synthetase alpha chain [EC:6.1.1.20] [SP:SYFB_YEAST]YKL06WAAT1; aspartate aminotransferase [EC:2.6.1.1] [SP:AATM_YEAST]YFR047Cnicotinate-nucleotide pyrophosphorylase (carboxylating) [EC:2.4.2.1] [SP:NADC_YEAST]YLR209CYLR209C; probable purine nucleoside phosphorylase [EC:2.4.2.1] [SP:PNPH_YEAST]YLR003CRPC34; DNA-directed RNA polymerase III, 34 KD subunit [EC:1.7.4.1] [SP:RIR3.YEAST]YOR074CCDC21; thymidylate synthase (EC:2.6.1.1] [SP:AATM_YEAST]YOR374WALD4; aldehyde dehydrogenase [EC:2.1.1.4] [SP:TYSY_YEAST]YDR148CKGD2; 2-oxoglutarate dehydrogenase [EC:1.1.3] [SP:DHA4.YEAST]YOR374WALD4; aldehyde dehydrogenase [EC:1.2.1.3] [SP:DHA4.YEAST]YFL018CLPD1, DHLP1; dihydrolipoamide dehydrogenase [EC:1.8.1.4] [SP:TDLH_YEAST]YFR055Wcystathionine beta-lyase [EC:4.4.1.8] [SP:TYSY_YEAST]YGL070CRPB9; DNA-directed RNA polymerase II 1.4.2 kD polypeptide [EC:2.7.7.6] [SP:RB9_YEAST]YGL070CRPB9; DNA-directed RNA polymerase [EC:2.6.1.1] [SP:DLDH_YEAST]YFL018CLPD1, DHLP1; dihydrolipoamide dehydrogenase [E
YPR145WASN1; asparagine synthase (glutamine-hydrolysing) [EC:6.3.5.4] [SP:ASN1.YEAST]YER086WILV1; threonine dehydratase [EC:4.2.1.16] [SP:THDH_YEAST]YBR145WADB5; alcohol dehydrogenase [EC:1.1.1.1] [SP:ADH5.YEAST]YER073WALD3; aldehyde dehydrogenase [EC:1.2.1.3] [SP:DHA5.YEAST]YER073WALD3; aldehyde dehydrogenase [EC:3.3.1.1] [SP:ADH5.YEAST]YER05Wcystathionine beta-lyase [EC:4.4.1.8] [SP:METC-YEAST]YFR052Wcystathionine beta-lyase [EC:4.4.1.8] [SP:METC-YEAST]YFL022CFRS2; phenylalanyl-tRNA synthetase alpha chain [EC:6.1.1.20] [SP:SYFB_YEAST]YKL106WAAT1; aspartate aminotransferase [EC:2.6.1.1] [SP:AATM_YEAST]YLR09CYLR209C; probable purine nucleoside phosphorylase [EC:2.4.2.19] [SP:NADC_YEAST]YLR09CRNR3; ribonucleoside-diphosphate reductase alpha chain [EC:1.17.4.1] [SP:RIR3_YEAST]YL066CRNR3; ribonucleoside-diphosphate reductase alpha chain [EC:1.17.4.1] [SP:RR3_YEAST]YOR074CCDC21; thymidylate synthase (TS) [EC:2.1.1.45] [SP:TYSY_YEAST]YOR374WALD4; aldehydr genase [EC:1.1.1.3] [SP:DHA4_YEAST]YOR374WALD4; aldehydr genase [EC:1.2.1.3] [SP:DHA4_YEAST]YOR374WALD4; aldehydr genase [EC:4.4.1.8] [SP:METC_YEAST]YFR055Wcystathionine beta-lyase [EC:4.4.1.8] [SP:MA4_YEAST]YGL070CRPB9; DNA-directed RNA polymerase II 14.2 kD polypeptide [EC:2.7.7.6] [SP:RPB9_YEAST]YGL070CRPB9; DNA-directed RNA polymerase II 14.2 kD polypeptide [EC:2.7.7.6] [SP:RPB9_YEAST]YGL070CRPB9; DNA-directed RNA polymerase [EC:2.6.4.4] [SP:DLDH_YEAST]YFR055Wcystathionine beta-lyase [EC:4.4.1.8] [SP:METC_Y
YER086WILV1; threonine dehydratase [EC:4.2.1.16] [SP:THDH_YEAST]YBR145WADH5; alcohol dehydrogenase [EC:1.1.1] [SP:ADH5_YEAST]YER043CSAH1; adenosylhomocysteinase [EC:3.3.1.1] [SP:SAHH_YEAST]YER043CSAH1; adenosylhomocysteinase [EC:4.1.8] [SP:METC_YEAST]YFR055Wcystathionine beta-lyase [EC:4.4.1.8] [SP:METC_YEAST]YFL022CFRS2; phenylalanyl-tRNA synthetase alpha chain [EC:6.1.1.20] [SP:SYFB_YEAST]YKL106WAAT1; aspartate aminotransferase [EC:2.6.1.1] [SP:AATM_YEAST]YLR209CYLR209C; probable purine nucleoside phosphorylase [EC:2.4.2.1] [SP:PNPH_YEAST]YLR209CYLR209C; probable purine nucleoside phosphorylase [EC:2.4.2.1] [SP:PNPH_YEAST]YNR03CRPC34; DNA-directed RNA polymerase III, 34 KD subunit [EC:1.17.4.1] [SP:RIR3_YEAST]YNR03CRPC34; DNA-directed RNA polymerase III, 34 KD subunit [EC:1.17.4.1] [SP:RR3_YEAST]YOR074CCDC21; thymidylate synthase (TS) [EC:2.1.1.45] [SP:TYSY_YEAST]YKL106WAAT1; aspartate aminotransferase [EC:2.6.1.1] [SP:AATM_YEAST]YOR374WALD4; aldehyde dehydrogenase EC:1.2.1.3] [SP:DHA4_YEAST]YOR374WALD4; aldehyde dehydrogenase [EC:2.6.1.1] [SP:AATM_YEAST]YDR148CKGD2; 2-oxoglutarate dehydrogenase [EC:1.2.1.3] [SP:DHA4_YEAST]YFR055Wcystathionine beta-lyase [EC:4.4.1.8] [SP:METC_YEAST]YFR055Wcystathionine beta-lyase [EC:4.4.1.8] [SP:METC_YEAST]YGR124WASN2; asparagine synthase (glutamine-hydrolysing) [EC:6.3.5.4] [SP:ASN2_YEAST]YGR070CRPB9; DNA-directed RNA polymerase II 14.2, kD polypeptide [EC:2.7.7.6] [SP:RPB9_YEAST]YGL070CRPB9; DNA-directed RNA polymerase
YBR145W       ADH5; alcohol dehydrogenase [EC:1.1.1.1] [SP:ADH5_YEAST]         YER073W       ALD3; aldehyde dehydrogenase [EC:1.2.1.3] [SP:DHA5_YEAST]         YER043C       SAH1; adenosylhomocysteinase [EC:3.3.1.1] [SP:SAHH_YEAST]         YFR055W       cystathionine beta-lyase [EC:4.4.1.8] [SP:METC_YEAST]         YFL022C       FRS2; phenylalanyl-tRNA synthetase alpha chain [EC:6.1.1.20] [SP:SYFB_YEAST]         YKL06W       AAT1; aspartate aminotransferase [EC:2.6.1.1] [SP:AATM_YEAST]         YKR047C       nicotinate-nucleotide pyrophosphorylase (carboxylating) [EC:2.4.2.19] [SP:NADC_YEAST]         YLR209C       YLR209C; probable purine nucleoside phosphorylase [EC:2.4.2.1] [SP:PNPH_YEAST]         YNR003C       RPC34; DNA-directed RNA polymerase III, 34 KD subunit [EC:1.17.4.1] [SP:RIR3_YEAST]         YOR074C       CDC21; thymidylate synthase (TS) [EC:2.1.1.45] [SP:TYSY_YEAST]         YOR074C       CDC21; thymidylate synthase (TS) [EC:2.6.1.1] [SP:RTM_YEAST]         YOR074W       AAT1; aspartate aminotransferase [EC:2.6.1.1] [SP:AM_YEAST]         YOR148C       KGD2; 2-coxoglutarate dehydrogenase E2 component (dihydrolipoamide succinyltransferase)         [EC:2.3.1.61] [SP:OD02_YEAST]       YFL018C         LPD1, DHLP1; dihydrolipoamide dehydrogenase [EC:1.8.1.4] [SP:DLDH_YEAST]         YGR055W       cystathionine beta-lyase [EC:4.4.1.8] [SP:METC_YEAST]         YFL018C       LPD1, DHLP1; dihydrolipoamide dehydrogenase [EC:1.8.1.4] [SP
YER073WALD3; aldehyde dehydrogenase[EC:1.2.1.3][SP:DHA5_YEAST]YER043CSAH1; adenosylhomocysteinase[EC:3.3.1.1][SP:SAHH.YEAST]YFR055Wcystathionine beta-lyase[EC:4.4.1.8][SP:METC.YEAST]YFL022CFRS2; phenylalanyl-tRNA synthetase alpha chain[EC:6.1.1.20][SP:SYFB_YEAST]YKL06WAAT1; aspartate aminotransferase[EC:2.6.1.1][SP:AATM_YEAST]YFR047Cnicotinate-nucleotide pyrophosphorylase (carboxylating)[EC:2.4.2.19][SP:NADC_YEAST]YLR209CYLR209C; probable purine nucleoside hosphorylase[EC:2.4.2.1][SP:PNPH_YEAST]YIL066CRNR3; ribonucleoside-diphosphate reductase alpha chain[EC:1.17.4.1][SP:RIR3_YEAST]YNR003CRPC34; DNA-directed RNA polymerase III, 34 KD subunit[EC:2.1.7.6][SP:RPC6_YEAST]YOR074CCDC21; thymidylate synthase (TS)[EC:2.1.1.45][SP:TYSY_YEAST]YOR374WALD4; aldehyde dehydrogenase[EC:1.2.1.3][SP:DHA4_YEAST]YOR374WALD4; aldehyde dehydrogenase [EC:1.2.1.3][SP:DHA4_YEAST]YF108CLPD1, DHLP1; dihydrolipoamide dehydrogenase [EC:1.8.1.4][SP:DDLP_YEAST]YFR055Wcystathionine beta-lyase [EC:4.4.1.8][SP:METC_YEAST]YFR055Wcystathionine beta-lyase [EC:4.4.1.8][SP:METC_YEAST]YFL18CLPD1, DHLP1; dihydrolipoamide dehydrogenase [EC:1.8.1.4][SP:DDLP_YEAST]YFR055Wcystathionine beta-lyase [EC:4.4.1.8][SP:METC_YEAST]YFR055Wcystathionine beta-lyase [EC:4.4.1.8][SP:METC_YEAST]YFR055Wcystathio
YER043C       SAH1; adenosylhomocysteinase [EC:3.3.1.1] [SP:SAHH_YEAST]         YFR055W       cystathionine beta-lyase [EC:4.4.1.8] [SP:METC_YEAST]         YFL02C       FRS2; phenylalanyl-tRNA synthetase alpha chain [EC:6.1.1.20] [SP:SYFB_YEAST]         YKL106W       AAT1; aspartate aminotransferase [EC:2.6.1.1] [SP:AATM_YEAST]         YFR047C       nicotinate-nucleotide pyrophosphorylase (carboxylating) [EC:2.4.2.19] [SP:NADC_YEAST]         YLR209C       YLR209C; probable purine nucleoside phosphorylase [EC:2.4.2.1] [SP:PNPH_YEAST]         YNR03C       RPC34; DNA-directed RNA polymerase III, 34 KD subunit [EC:1.17.4.1] [SP:RIR3_YEAST]         YNR03C       RPC34; DNA-directed RNA polymerase III, 34 KD subunit [EC:1.17.4.1] [SP:RIR3_YEAST]         YOR074C       CDC21; thymidylate synthase (TS) [EC:2.1.1.45] [SP:TYSY_YEAST]         YKL106W       AAT1; aspartate aminotransferase [EC:2.6.1.1] [SP:AATM_YEAST]         YOR374W       ALD4; aldehyde dehydrogenase [EC:1.1.1.4] [SP:DHA4_YEAST]         YDR148C       KGD2; 2-oxoglutarate dehydrogenase [EC:1.2.1] [SP:DHA4_YEAST]         YFR045W       cystathionine beta-lyse [EC:4.4.1.8] [SP:METC_YEAST]         YFR047C       RPC34; aldehyde dehydrogenase [EC:1.8.1.4] [SP:DLDH_YEAST]         YOR374W       ALD4; aldehyde dehydrogenase [EC:1.8.1.4] [SP:DLDH_YEAST]         YFR045W       cystathionine beta-lyse [EC:4.4.1.8] [SP:METC_YEAST]         YFR045W       cystathioninine beta-lyse [EC:4
YFR055W       cystathionine beta-lyase [EC:4.4.1.8] [SP:METC_YEAST]         YFL022C       FRS2; phenylalanyl-tRNA synthetase alpha chain [EC:6.1.1.20] [SP:SYFB_YEAST]         YKL106W       AAT1; aspartate aminotransferase [EC:2.6.1.1] [SP:AATM_YEAST]         YFR047C       nicotinate-nucleotide pyrophosphorylase (carboxylating) [EC:2.4.2.19] [SP:NADC_YEAST]         YLR209C       YLR209C; probable purine nucleoside phosphorylase [EC:2.4.2.1] [SP:PNPH_YEAST]         YLR06C       RNR3; ribonucleoside-diphosphate reductase alpha chain [EC:1.17.4.1] [SP:RIR3_YEAST]         YNR06C       RNR3; ribonucleoside-diphosphate reductase alpha chain [EC:1.17.4.1] [SP:RIR3_YEAST]         YUL066C       RNR3; ribonucleoside-diphosphate reductase alpha chain [EC:1.17.4.1] [SP:RIR3_YEAST]         YOR074C       CDC21; thymidylate synthase (TS) [EC:2.1.1.45] [SP:TYSY_YEAST]         YOR374W       AAT1; aspartate aminotransferase [EC:1.2.1] [SP:ATM_YEAST]         YOR374W       ALD4; aldehyde dehydrogenase [EC:1.1.3] [SP:DHA4_YEAST]         YDR148C       KGD2; 2-oxoglutarate dehydrogenase [EC:1.2.1.3] [SP:DLDH_YEAST]         YFL018C       LPD1, DHLP1; dihydrolipoamide dehydrogenase [EC:1.8.1.4] [SP:DLDH_YEAST]         YGR724W       ASN2; asparagine synthase (glutamine-hydrolysing) [EC:6.3.5.4] [SP:ASN2_YEAST]         YGR124W       ASN2; asparagine synthase (glutamine-hydrolysing) [EC:6.3.5.4] [SP:ASN2_YEAST]         YGR070C       RPB9; DNA-directed RNA polymerase II 14.2 kD polypept
YFL022C       FRS2; phenylalanyl-tRNA synthetase alpha chain [EC:6.1.1.20] [SP:SYFB_YEAST]         YKL106W       AAT1; aspartate aminotransferase [EC:2.6.1.1] [SP:AATM_YEAST]         YFR047C       nicotinate-nucleotide pyrophosphorylase (carboxylating) [EC:2.4.2.19] [SP:NADC_YEAST]         YLR209C       YLR209C; probable purine nucleoside phosphorylase [EC:2.4.2.1] [SP:PNPH_YEAST]         YL066C       RNR3; ribonucleoside-diphosphate reductase alpha chain [EC:1.17.4.1] [SP:RIR3_YEAST]         YNR003C       RPC34; DNA-directed RNA polymerase III, 34 KD subunit [EC:1.77.4] [SP:RIR3_YEAST]         YOR074C       CDC21; thymidylate synthase (TS) [EC:2.1.1.45] [SP:TYSY_YEAST]         YOR074C       CDC21; thymidylate synthase (ES:2.6.1.1] [SP:ATM_YEAST]         YOR374W       ALD4; aldehyde dehydrogenase [EC:1.1.3] [SP:TYSY_YEAST]         YDR148C       KGD2; 2-coxoglutarate dehydrogenase [EC:1.1.3] [SP:DLATM_YEAST]         YFL018C       LPD1, DHLP1; dihydrolipoamide dehydrogenase [EC:1.8.1.4] [SP:DLDH_YEAST]         YFR055W       cystathionine beta-1yase [EC:4.4.1.8] [SP:METC_YEAST]         YGR070C       RPB9; DNA-directed RNA polymerase II 14.2 kD polypeptide [EC:2.7.7.6] [SP:RPB9_YEAST]         YGL070C       RPB9; DNA-directed RNA polymerase [EC:2.7.4.6] [SP:NDK_YEAST]         YGL070C       RPB9; DNA-directed RNA polymerase [EC:2.7.4.6] [SP:NDK_YEAST]         YGL070C       RPB9; DNA-directed RNA polymerase [EC:2.7.7.6] [SP:RPB9_YEAST]
YKL106WAAT1; aspartate aminotransferase [EC:2.6.1.1] [SP:AATM_YEAST]YFR047Cnicotinate-nucleotide pyrophosphorylase (carboxylating) [EC:2.4.2.19] [SP:NADC_YEAST]YLR209CYLR209C; probable purine nucleoside phosphorylase [EC:2.4.2.1] [SP:PNPH_YEAST]YIL066CRNR3; ribonucleoside-diphosphate reductase alpha chain [EC:1.17.4.1] [SP:RIR3_YEAST]YNR003CRPC34; DNA-directed RNA polymerase III, 34 KD subunit [EC:2.7.7.6] [SP:RPC6_YEAST]YIL066CRNR3; ribonucleoside-diphosphate reductase alpha chain [EC:1.17.4.1] [SP:RIR3_YEAST]YOR074CCDC21; thymidylate synthase (TS) [EC:2.1.1.45] [SP:TYSY_YEAST]YKL106WAAT1; aspartate aminotransferase [EC:2.6.1.1] [SP:AATM_YEAST]YOR374WALD4; aldehyde dehydrogenase [EC:1.2.1.3] [SP:DHA4_YEAST]YDR148CKGD2; 2-coxoglutarate dehydrogenase [EC:1.2.1.3] [SP:DDH_YEAST]YFL018CLPD1, DHLP1; dihydrolipoamide dehydrogenase [EC:1.8.1.4] [SP:DDLP_YEAST]YFR055Wcystathionine beta-lyase [CS:4.4.1.8] [SP:METC_YEAST]YGR124WASN2; asparagine synthase (glutamine-hydrolysing) [EC:6.3.5.4] [SP:ASN2_YEAST]YGL070CRPB9; DNA-directed RNA polymerase III 14.2 kD polypeptide [EC:2.7.7.6] [SP:RPB9_YEAST]YKL06WYNK1; nucleoside-diphosphate kinase [EC:1.1.1.205] [SP:NDK_YEAST]YHR26WPUR5; IMP dehydrogenase [EC:1.1.1.205] [SP:IMH1_YEAST]
YFR047C       nicotinate-nucleotide pyrophosphorylase (carboxylating) [EC:2.4.2.19] [SP:NADC_YEAST]         YLR209C       YLR209C; probable purine nucleoside phosphorylase [EC:2.4.2.1] [SP:PNPH_YEAST]         YIL066C       RNR3; ribonucleoside-diphosphate reductase alpha chain [EC:1.17.4.1] [SP:RIR3_YEAST]         YIN003C       RPC34; DNA-directed RNA polymerase III, 34 KD subunit [EC:2.17.4.1] [SP:RIR3_YEAST]         YIL066C       RNR3; ribonucleoside-diphosphate reductase alpha chain [EC:1.17.4.1] [SP:RIR3_YEAST]         YOR074C       CDC21; thymidylate synthase (TS) [EC:2.1.1.45] [SP:TYSY_YEAST]         YOR374W       ALD4; aldehyde dehydrogenase [EC:2.6.1.1] [SP:ATM_YEAST]         YOR374W       ALD4; aldehyde dehydrogenase [EC:1.2.1.3] [SP:DLA4_YEAST]         YDR148C       KGD2; 2-oxoglutarate dehydrogenase [EC:1.8.1.4] [SP:DLDH_YEAST]         YFL018C       LPD1, DHLP1; dihydrolipoamide dehydrogenase [EC:1.8.1.4] [SP:DLDH_YEAST]         YGR124W       ASN2; asparagine synthase (glutamine-hydrolysing) [EC:6.3.5.4] [SP:ASN2_YEAST]         YGL070C       RPB9; DNA-directed RNA polymerase II 14.2 kD polypeptide [EC:2.7.7.6] [SP:RPB9_YEAST]         YKL067W       YNR1; nucleoside-diphosphate kinase [EC:2.1.1.1.205] [SP:NDK_YEAST]         YHR216W       PUR5; IMP dehydrogenase [EC:1.1.1.205] [SP:NDK_YEAST]
YLR209C       YLR209C; probable purine nucleoside phosphorylase [EC:2.4.2.1] [SP:PNPH_YEAST]         YIL066C       RNR3; ribonucleoside-diphosphate reductase alpha chain [EC:1.17.4.1] [SP:RIR3_YEAST]         YNR003C       RPC34; DNA-directed RNA polymerase III, 34 KD subunit [EC:2.7.7.6] [SP:RPC6-YEAST]         YIL066C       RNR3; ribonucleoside-diphosphate reductase alpha chain [EC:1.17.4.1] [SP:RIR3_YEAST]         YOR074C       CDC21; thymidylate synthase (TS) [EC:2.1.1.45] [SP:TYSY_YEAST]         YOR074W       AAT1; aspartate aminotransferase [EC:2.6.1.1] [SP:ATM_YEAST]         YOR374W       ALD4; aldehyde dehydrogenase [EC:1.2.1.3] [SP:DHA4_YEAST]         YDR148C       KGD2; 2-coxoglutarate dehydrogenase [EC:1.2.1.3] [SP:DLDH_YEAST]         YFL018C       LPD1, DHLP1; dihydrolipoamide dehydrogenase [EC:1.8.1.4] [SP:DLDH_YEAST]         YFR055W       cystathionine beta-lyase [C:4.4.1.8] [SP:METC_YEAST]         YGR124W       ASN2; asparagine synthase (glutamine-hydrolysing) [EC:6.3.5.4] [SP:ASN2_YEAST]         YGL070C       RPB9; DNA-directed RNA polymerase II 14.2 kD polypeptide [EC:2.7.7.6] [SP:RPB9_YEAST]         YKL067W       YNK1; nucleoside-diphosphate kinase [EC:2.7.4.6] [SP:NDK_YEAST]         YKL067W       YNK1; nucleoside-diphosphate kinase [EC:2.7.4.6] [SP:NDK_YEAST]         YKL067W       YNK1; nucleoside-diphosphate kinase [EC:2.7.4.6] [SP:NDK_YEAST]         YHR216W       PUR5; IMP dehydrogenase [EC:1.1.1.205] [SP:IMH1_YEAST]
YIL066C       RNR3; ribonucleoside-diphosphate reductase alpha chain [EC:1.17.4.1] [SP:RIR3_YEAST]         YNR003C       RPC34; DNA-directed RNA polymerase III, 34 KD subunit [EC:2.7.7.6] [SP:RPC6_YEAST]         YIL066C       RNR3; ribonucleoside-diphosphate reductase alpha chain [EC:1.17.4.1] [SP:RIR3_YEAST]         YOR074C       CDC21; thymidylate synthase (TS) [EC:2.11.45] [SP:TYSY_YEAST]         YOR074C       CDC21; thymidylate synthase (TS) [EC:2.1.1.45] [SP:TYSY_YEAST]         YOR374W       AAT1; aspartate aminotransferase [EC:2.6.1.1] [SP:AATM_YEAST]         YOR374W       ALD4; aldehyde dehydrogenase [EC:1.2.1.3] [SP:DHA4_YEAST]         YDR148C       KGD2; 2-coxoglutarate dehydrogenase E2 component (dihydrolipoamide succinyltransferase)         [EC:2.3.1.61] [SP:OD02_YEAST]       [SP:DDD4_YEAST]         YFR055W       cystathionine beta-lyase [EC:4.4.1.8] [SP:METC_YEAST]         YGR124W       ASN2; asparagine synthase (glutamine-hydrolysing) [EC:6.3.5.4] [SP:ASN2_YEAST]         YGL070C       RPB9; DNA-directed RNA polymerase II 14.2 kD polypeptide [EC:2.7.7.6] [SP:RPB9_YEAST]         YKL067W       YNK1; nucleoside-diphosphate kinase [EC:2.7.4.6] [SP:NDK_YEAST]         YHR216W       PUR5; IMP dehydrogenase [EC:1.1.1.205] [SP:IM11_YEAST]
YNR003C         RPC34; DNA-directed RNA polymerase III, 34 KD subunit [EC:2.7.7.6] [SP:RPC6-YEAST]           YIL066C         RNR3; ribonucleoside-diphosphate reductase alpha chain [EC:1.17.4.1] [SP:RIR3_YEAST]           YOR074C         CDC21; thymidylate synthase (TS) [EC:2.1.1.45] [SP:TYSY_YEAST]           YKL106W         AAT1; aspartate aminotransferase [EC:2.6.1.1] [SP:AATM_YEAST]           YOR374W         ALD4; aldehyde dehydrogenase [EC:1.2.1.3] [SP:DHA4_YEAST]           YDR148C         KGD2; 2-coxoglutarate dehydrogenase [EC:1.2.1.3] [SP:DHA4_YEAST]           YDR148C         LFD1; OHD02_YEAST]           YFL018C         LPD1, DHLP1; dihydrolipoamide dehydrogenase [EC:1.8.1.4] [SP:DLDH_YEAST]           YFR058V         cystathionine beta-lyase [EC:4.4.1.8] [SP:METC_YEAST]           YGR124W         ASN2; asparagine synthase (glutamine-hydrolysing) [EC:6.3.5.4] [SP:ASN2_YEAST]           YGL070C         RPB9; DNA-directed RNA polymerase II 14.2 kD polypeptide [EC:2.7.7.6] [SP:RPB9_YEAST]           YKL067W         YNK1; nucleoside-diphosphate [EC:1.1.1.205] [SP:NDK_YEAST]           YHR216W         PUR5; IMP dehydrogenase [EC:1.1.1.205] [SP:MI1_YEAST]
YNR003C         RPC34; DNA-directed RNA polymerase III, 34 KD subunit [EC:2.7.7.6] [SP:RPC6-YEAST]           YIL066C         RNR3; ribonucleoside-diphosphate reductase alpha chain [EC:1.17.4.1] [SP:RIR3_YEAST]           YOR074C         CDC21; thymidylate synthase (TS) [EC:2.1.1.45] [SP:TYSY_YEAST]           YKL106W         AAT1; aspartate aminotransferase [EC:2.6.1.1] [SP:AATM_YEAST]           YOR374W         ALD4; aldehyde dehydrogenase [EC:1.2.1.3] [SP:DHA4_YEAST]           YDR148C         KGD2; 2-coxoglutarate dehydrogenase [EC:1.2.1.3] [SP:DHA4_YEAST]           YDR148C         LFD1; OHD02_YEAST]           YFL018C         LPD1, DHLP1; dihydrolipoamide dehydrogenase [EC:1.8.1.4] [SP:DLDH_YEAST]           YFR058V         cystathionine beta-lyase [EC:4.4.1.8] [SP:METC_YEAST]           YGR124W         ASN2; asparagine synthase (glutamine-hydrolysing) [EC:6.3.5.4] [SP:ASN2_YEAST]           YGL070C         RPB9; DNA-directed RNA polymerase II 14.2 kD polypeptide [EC:2.7.7.6] [SP:RPB9_YEAST]           YKL067W         YNK1; nucleoside-diphosphate [EC:1.1.1.205] [SP:NDK_YEAST]           YHR216W         PUR5; IMP dehydrogenase [EC:1.1.1.205] [SP:MI1_YEAST]
YIL066C       RNR3; ribonucleoside-diphosphate reductase alpha chain [EC:1.17.4.1] [SP:RIR3_YEAST]         YOR074C       CDC21; thymidylate synthase (TS) [EC:2.1.1.45] [SP:TYSY_YEAST]         YKL106W       AAT1; aspartate aminotransferase [EC:2.6.1.1] [SP:ATM_YEAST]         YOR374W       ALD4; aldehyde dehydrogenase [EC:1.2.1.3] [SP:DHA4_YEAST]         YDR148C       KGD2; 2-oxoglutarate dehydrogenase E2 component (dihydrolipoamide succinyltransferase) [EC:2.3.1.61] [SP:ODO2_YEAST]         YFL018C       LPD1, DHLP1; dihydrolipoamide dehydrogenase [EC:1.8.1.4] [SP:DLDH_YEAST]         YFR055W       cystathionine beta-lyase [EC:4.4.1.8] [SP:METC_YEAST]         YGR124W       ASN2; asparagine synthase (glutamine-hydrolysing) [EC:6.3.5.4] [SP:ASN2_YEAST]         YGL070C       RPB9; DNA-directed RNA polymerase II 14.2 kD polypeptide [EC:2.7.7.6] [SP:RPB9_YEAST]         YKL067W       YNK1; nucleoside-diphosphate kinase [EC:2.7.4.6] [SP:NDK_YEAST]         YHR216W       PUR5; IMP dehydrogenase [EC:1.1.1.205] [SP:IMH1_YEAST]
YOR074C       CDC21; thymidylate synthase (TS) [EC:2.1.1.45] [SP:TYSY_YEAST]         YKL106W       AAT1; aspartate aminotransferase [EC:2.6.1.1] [SP:AATM_YEAST]         YOR374W       ALD4; aldehyde dehydrogenase [EC:1.2.1.3] [SP:DHA4_YEAST]         YDR148C       KGD2; 2-oxoglutarate dehydrogenase E2 component (dihydrolipoamide succinyltransferase) [EC:2.3.1.61] [SP:ODO2_YEAST]         YFL018C       LPD1, DHLP1; dihydrolipoamide dehydrogenase [EC:1.8.1.4] [SP:DLDH_YEAST]         YFR055W       cystathionine beta-lyase [EC:4.4.1.8] [SP:METC_YEAST]         YGR124W       ASN2; asparagine synthase (glutamine-hydrolysing) [EC:6.3.5.4] [SP:ASN2_YEAST]         YGL070C       RPB9; DNA-directed RNA polymerase II 14.2 kD polypeptide [EC:2.7.7.6] [SP:RPB9_YEAST]         YKL067W       YNK1; nucleoside-diphosphate kinase [EC:2.7.4.6] [SP:NDK_YEAST]         YHR216W       PUR5; IMP dehydrogenase [EC:1.1.1.205] [SP:IMH1_YEAST]
YKL106W       AAT1; aspartate aminotransferase [EC:2.6.1.1] [SP:AATM_YEAST]         YOR374W       ALD4; aldehyde dehydrogenase [EC:1.2.13] [SP:DHA4_YEAST]         YDR148C       KGD2; 2-oxoglutarate dehydrogenase E2 component (dihydrolipoamide succinyltransferase) [EC:2.3.1.61] [SP:ODO2_YEAST]         YFL018C       LPD1, DHLP1; dihydrolipoamide dehydrogenase [EC:1.8.1.4] [SP:DLDH_YEAST]         YFR055W       cystathionine beta-lyase [EC:4.4.1.8] [SP:METC_YEAST]         YGR124W       ASN2; asparagine synthase (glutamine-hydrolysing) [EC:6.3.5.4] [SP:ASN2_YEAST]         YGL070C       RPB9; DNA-directed RNA polymerase II 14.2 kD polypeptide [EC:2.7.7.6] [SP:RPB9_YEAST]         YKL067W       YNK1; nucleoside-diphosphate kinase [EC:1.1.1.205] [SP:IMH1_YEAST]         YH216W       PUR5; IMP dehydrogenase [EC:1.1.1.205] [SP:IMH1_YEAST]
YOR374W       ALD4; aldehyde dehydrogenase [EC:1.2.1.3] [SP:DHA4_YEAST]         YDR148C       KGD2; 2-oxoglutarate dehydrogenase E2 component (dihydrolipoamide succinyltransferase) [EC:2.3.1.61] [SP:ODO2_YEAST]         YFL018C       LPD1, DHLP1; dihydrolipoamide dehydrogenase [EC:1.8.1.4] [SP:DLDH_YEAST]         YFR055W       cystathionine beta-lyase [EC:4.4.1.8] [SP:METC_YEAST]         YGR124W       ASN2; asparagine synthase (glutamine-hydrolysing) [EC:6.3.5.4] [SP:ASN2_YEAST]         YGL070C       RPB9; DNA-directed RNA polymerase II 14.2 kD polypeptide [EC:2.7.7.6] [SP:RPB9_YEAST]         YKL067W       YNK1; nucleoside-diphosphate kinase [EC:2.7.4.6] [SP:NDK_YEAST]         YHR216W       PUR5; IMP dehydrogenase [EC:1.1.1.205] [SP:IMH1_YEAST]
YDR148C       KGD2; 2-oxoglutarate dehydrogenase E2 component (dihydrolipoamide succinyltransferase) [EC:2.3.1.61] [SP:ODO2 YEAST]         YFL018C       LPD1, DHLP1; dihydrolipoamide dehydrogenase [EC:1.8.1.4] [SP:DLDH_YEAST]         YFR055W       cystathionine beta-lyase [EC:4.4.1.8] [SP:METC_YEAST]         YGR124W       ASN2; asparagine synthase (glutamine-hydrolysing) [EC:6.3.5.4] [SP:ASN2_YEAST]         YGL070C       RPB9; DNA-directed RNA polymerase II 14.2 kD polypeptide [EC:2.7.7.6] [SP:RPB9_YEAST]         YKL067W       YNK1; nucleoside-diphosphate kinase [EC:2.7.4.6] [SP:NDK_YEAST]         YHR216W       PUR5; IMP dehydrogenase [EC:1.1.1.205] [SP:IMH1_YEAST]
[EC:2.3.1.61] [SP:ODO2_YEAST]         YFL018C       LPD1, DHLP1; dihydrolipoamide dehydrogenase [EC:1.8.1.4] [SP:DLDH_YEAST]         YFR055W       cystathionine beta-lyase [EC:4.4.1.8] [SP:METC_YEAST]         YGR124W       ASN2; asparagine synthase (glutamine-hydrolysing) [EC:6.3.5.4] [SP:ASN2_YEAST]         YGL070C       RPB9; DNA-directed RNA polymerase II 14.2 kD polypeptide [EC:2.7.7.6] [SP:RPB9_YEAST]         YKL067W       YNK1; nucleoside-diphosphate kinase [EC:2.7.4.6] [SP:NDK_YEAST]         YHR216W       PUR5; IMP dehydrogenase [EC:1.1.1.205] [SP:IMH1_YEAST]
YFL018C         LPD1, DHLP1; dihydrolipoamide dehydrogenase [EC:1.8.1.4] [SP:DLDH_YEAST]           YFR055W         cystathionine beta-lyase [EC:4.4.1.8] [SP:METC_YEAST]           YGR124W         ASN2; asparagine synthase (glutamine-hydrolysing) [EC:6.3.5.4] [SP:ASN2_YEAST]           YGL070C         RPB9; DNA-directed RNA polymerase II 14.2 kD polypeptide [EC:2.7.7.6] [SP:RPB9_YEAST]           YKL067W         YNK1; nucleoside-diphosphate kinase [EC:2.7.4.6] [SP:NDK_YEAST]           YHR216W         PUR5; IMP dehydrogenase [EC:1.1.1.205] [SP:IMH1_YEAST]
YFR055W       cystathionine beta-lyase [EC:4.4.1.8] [SP:METC_YEAST]         YGR124W       ASN2; asparagine synthase (glutamine-hydrolysing) [EC:6.3.5.4] [SP:ASN2_YEAST]         YGL070C       RPB9; DNA-directed RNA polymerase II 14.2 kD polypeptide [EC:2.7.7.6] [SP:RPB9_YEAST]         YKL067W       YNK1; nucleoside-diphosphate kinase [EC:2.7.4.6] [SP:NDK_YEAST]         YHR216W       PUR5; IMP dehydrogenase [EC:1.1.1.205] [SP:IMH1_YEAST]
YGR124W       ASN2; asparagine synthase (glutamine-hydrolysing) [EC:6.3.5.4] [SP:ASN2_YEAST]         YGL070C       RPB9; DNA-directed RNA polymerase II 14.2 kD polypeptide [EC:2.7.7.6] [SP:RPB9_YEAST]         YKL067W       YNK1; nucleoside-diphosphate kinase [EC:2.7.4.6] [SP:NDK_YEAST]         YHR216W       PUR5; IMP dehydrogenase [EC:1.1.1.205] [SP:IMH1_YEAST]
YGL070C       RPB9; DNA-directed RNA polymerase II 14.2 kD polypeptide [EC:2.7.7.6] [SP:RPB9_YEAST]         YKL067W       YNK1; nucleoside-diphosphate kinase [EC:2.7.4.6] [SP:NDK_YEAST]         YHR216W       PUR5; IMP dehydrogenase [EC:1.1.1.205] [SP:IMH1_YEAST]
YKL067W         YNK1; nucleoside-diphosphate kinase [EC:2.7.4.6] [SP:NDK_YEAST]           YHR216W         PUR5; IMP dehydrogenase [EC:1.1.1205] [SP:IMH1_YEAST]
YHR216W PUR5; IMP dehydrogenase [EC:1.1.1.205] [SP:IMH1_YEAST]
YLR209C YLR209C; probable purine nucleoside phosphorylase [EC:2.4.2.1] [SP:PNPH_YEAST]
YBR035C PDX3; pyridoxamine 5'-phosphate oxidase [EC:1.4.3.5] [SP:PDX3_YEAST]
YLR058C SHM2; serine hydroxymethyltransferase, cytosolic (glycine hydroxymethyltransferase) [EC:2.1.2.1] [SP:GLYC_YEAST]
YGR204W ADE3; methylenetetrahydrofolate dehydrogenase (NADP+) / methenyltetrahydrofolate cyclohydrolase / formate-
tetrahydrofolate ligase [EC:1.5.1.5 3.5.4.9 6.3.4.3] [SP:C1TC_YEAST]

#### (A) Correlated gene clusters with single EC number <u>YJL140W</u> RPB4: DNA-directed RNA polymerase II 32 kD polypepti

Table 4: Correlated gene clusters found in two-hybrid and pathway datasets.

sce:YBR020W	GAL1; galactokinase [EC:2.7.1.6] [SP:GAL1_YEAST]
eco:b0757	galK, galA; galactokinase [EC:2.7.1.6] [SP:GAL1_ECOLI]
sce:YBR018C	GAL7; galactose-1-phosphate uridylyltransferase [EC:2.7.7.10] [SP:GAL7_YEAST]
eco:b0758	galT, galB; galactose-1-phosphate uridylyltransferase [EC:2.7.7.10] [SP:GAL7_ECOLI]
sce:YCR021C	HSP30; heat shock protein [SP:HS30_YEAST]
eco:b2611	hypothetical protein
sce:YOR232W	MGE1; GRPE protein homolog precursor [SP:GRPE_YEAST]
eco:b2614	grpE; heat shock protein grpE (heat shock protein b25.3) (HSP24) [SP:GRPE_ECOLI]
sce:YMR058W	FET3; iron transport multicopper oxidase precursor [EC:1] [SP:FET3_YEAST]
eco:b0123	yacK; probable 53.4 kD blue-copper protein yacq precursor [SP:YACK_ECOLI]
sce:YNL036W	NCE103; involved in non-classical protein export pathway [SP:NCE3_YEAST]
eco:b0126	yadF; hypothetical 25.1 kD protein in hpt-panD intergenic region [SP:YADF_ECOLI]
sce:YDR226W	ADK1; adenylate kinase [EC:2.7.4.3] [SP:KAD1_YEAST]
eco:b0474	adk, plsA, dnaW; adenylate kinase [EC:2.7.4.3] [SP:KAD_ECOLI]
sce:YOR176W	
eco:b0475	hemH, popA, visA; ferrochelatase (protoheme ferro-lyase) (hemE synthetase) [EC:4.99.1.1] [SP:HEMZ_ECOLI]
sce:YGR263C	unknown [SP:YG5J_YEAST]
eco:b0476	aes; acetyl esterase [EC:3.1.1] [SP:AES_ECOLI]
sce:YPR125W	MRS7; suppressor of mrs2-1 mutation
eco:b1384	feaR, maoR, maoB; transcriptional activator feaR [SP:FEAR_ECOLI]
sce:YOR374W	ALD4; aldehyde dehydrogenase [EC:1.2.1.3] [SP:DHA4_YEAST]
eco:b1385	feaB, padA, maoB; phenylacetaldehyde dehydrogenase (PAD) [EC:1.2.1.39] [SP:FEAB_ECOLI]
sce:YPL005W	YPL005W; Lpa12p
eco:b1696	putative ARAC-type regulatory protein
sce:YGR207C	ETF-BETA; electron transfer flavoprotein beta-subunit [SP:ETFB_YEAST]
eco:b1697	ydiQ; putative electron transfer flavoprotein subunit ydiq [SP:YDIQ_ECOLI]
sce:YPL252C	YAH1; similar to adrenodoxin and ferrodoxin
eco:b2525	fdx; ferredoxin, 2fe-2s [SP:FER_ECOLI]
sce:YGL018C	JAC1; molecular chaperone [SP:YGB8_YEAST]
eco:b2527	hscB; chaperone protein hscB (hsc20) [SP:HSCB_ECOLI]
sce:YMR253C	unknown [SP:YM87_YEAST]
eco:b3184	yhbE; hypothetical 35.0 kD protein in dacB-rpmA intergenic region (F321) [SP:YHBE_ECOLI]
sce:YNL005C	MRPL2; mitochondrial ribosomal protein L2 precursor [SP:RM02_YEAST]
eco:b3185	rpmA; 50S ribosomal protein L27 [SP:RL27_ECOLI]
sce:YBR034C	HMT1, ODP1, RMT1; hnRNP arginine N-methyltransferase [EC:2.1.1] [SP:HMT1_YEAST] prmA; ribosomal protein l11 methyltransferase [EC:2.1.1] [SP:PRMA_ECOLI]
eco:b3259 sce:YLR401C	prmA; ribosomal protein III methyltransferase [EC:2.1.1] [SP:PRMA_ECOLI] unknown [SP:YL01_YEAST]
eco:b3260	unknown [SP:YLDI_YEAS1] yhdG; hypothetical 35.9 kD protein in pmra-fis intergenic region (ORF1) [SP:YHDG_ECOLI]
	yndG; nypotheticar 55.9 kD protein in pinra-ns intergenc region (OKF1) [57:1 HDG_ECOLI] MSW1; mitochondrial tryptophanyl-tRNA synthetase [EC:6.1.1.2] [SP:SYWM_YEAST]
sce:YDR268W	
eco:b3384 sce:YOR131C	trpS; tryptophanyl-tRNA synthetase [EC:6.1.1.2] [SP:SYW_ECOLI] unknown
eco:b3385	gph; phosphoglycolate phosphatase [EC:3.1.3.18] [SP:GPH_ECOLI] CRM1; chromosome region maintenance protein [SP:CRM1_YEAST]
sce:YGR218W	CRM1; chromosome region maintenance protein [SP:CRM12 FEAST] gntR; gluconate utilization system gnt-1 transcriptional repressor [SP:GNTR_ECOLI]
eco:b3438 sce:YMR315W	
eco:b3440	unknown [SP:YM94_YEAST] yhhX; hypothetical 38.8 kD protein in gntR-ggt intergenic region (F345) [SP:YHHX_ECOLI]
ec0:D3440	ynna, nypotnetical 30.0 kD protein in gnta-ggt intergenic region (F343) [SF: I HHA_ECOLI]

Table 5: Correlated gene clusters obtained by multiple organism comparison.

the positions in the *S.cerevisiae* genome sequence and the protein-protein interactions by two-hybrid analysis, and  $G_2$  is the binary relationships among *E.coli* genes with respect to the positions in the *E.coli* genome sequence. To extract correlated gene clusters in the *S.cerevisiae* two-hybrid dataset  $G_3$ by using the *E.coli* genome dataset  $G_2$ , *S.cerevisiae* genes in  $G_1$  are mapped to *E.coli* genes in  $G_2$ (dashed arrows). Then, the nodes in  $G_2$  and those in  $G_3$  are connected by hyperedges (dashed lines), and by clustering those hyperedges as explained in the previous sections we obtain correlated gene clusters like  $C_1$  and  $C_2$  that contain sets of genes reserving their mutual relationships in  $G_2$  and  $G_3$ .

Actually, we connected the *S.cerevisiae* two-hybrid dataset and the *E.coli* dataset via 934 homologous relationships between two genes of these organisms.<sup>8</sup> By clustering the hyperedges we found eleven correlated gene clusters as shown in Table 5 (execution time was 14 seconds). Each *S.cerevisiae* gene is attached by its *E.coli* homologue. Here, genes that interact through at most one intermediate gene were included in the same cluster (i.e., for the *i*th graph, setting  $p_i = 2$ ). The result includes, for example, correlated gene clusters related to the galactose metabolism (sce:YBR020W (GAL1) and sce:YBR018C (GAL7)) and heat shock proteins (sce:YCR021C (HSP30) and sce:YOR232W (MGE1)).

### 4 Discussions

One crucial point of the current method is whether the graphs being compared really can provide biological information to classify genes. Even if the dataset is based on biological facts, we must con-

See http://ssdb.genome.ad.jp/ for details.

<sup>&</sup>lt;sup>8</sup>We used "best-best" entries of the KEGG/SSDB database.

sider its appropriateness for this purpose. For example, when we compared the *S.cerevisiae* genome dataset and the *S.cerevisiae* two-hybrid dataset, we actually found a total 106 "correlated gene clusters". However, considering the characteristics of the eukaryote genome sequences, it may not be easy to interpret the result. For example, YOL147C and YOL148C are next to each other on the *S.cerevisiae* genome sequence, and they are also connected through one intermediate gene YPR086W in the two-hybrid dataset. The annotations of these genes are as follows:

- sce:YOL147C PEX11; peroxisomal membrane protein [SP:PEXB\_YEAST]
- sce:YOL148C SPT20, ADA5; transcription factor [SP:SP20\_YEAST]
- sce:YPR086W SUA7; transcription initiation factor IIB [SP:TF2B\_YEAST]

But, different from prokaryote genomes that contain functional links as represented by operons, it is not clear whether the inclusion of the *S.cerevisiae* genome dataset can improve the confidence of screening the two-hybrid dataset. It is biologically true that the two genes above are next to each other in the *S.cerevisiae* genome sequence, but it cannot support that the interaction detected by two-hybrid analysis is biologically meaningful.

Currently, the output of the method is just a list of correlated gene clusters. Deriving sub-networks that indicate how genes are connected in a correlated gene cluster is a next subject of our analysis. They may be found by gathering the shortest paths between the genes in a correlated gene clusters. Those sub-networks may reveal intermediate members which are not contained in the list of genes in the correlated gene clusters, but which may still be of interest.

Finally, in this paper, we have focused on whether or not two genes are connected by means of binary relationships. Now, we can extend the framework so that it can cope with graphs whose edges have weights according to similarity scores, binding constants, and other quantitative relationships. Our algorithm works for this purpose too, but we must consider normalization of edge weights among different kinds of graphs (e.g., corresponding to a genome and a pathway) since comparison between their absolute values do not always make sense.

### Acknowledgements

Part of this work done by A.N. and S.G. was supported by Grant-in-Aid for Scientific Research on Priority Areas (C) "Genome Information Science" from the Ministry of Education, Culture, Sports, Science and Technology of Japan. The work was also supported by the Research for the Future Program of the Japan Society for the Promotion of Science. The computing resource was provided by the Supercomputer Laboratory, Bioinformatics Center, Institute for Chemical Research, Kyoto University.

### References

- DeRisi, J.L., Iyer, V.R., and Brown, P.O., Exploring the metabolic and genetic control of gene expression on a genome scale, *Science*, 278(5338):680–686, 1997.
- [2] Erlandsen, H., Abola, E.E., and Stevens, R.C., Combining structural genomics and enzymology: completing the picture in metabolic pathways and enzyme active sites, *Curr. Opin. Struct. Biol.*, 10(6):719–730, 2000.
- [3] Ito, T., Chiba, T., Ozawa, R., Yoshida, M., Hattori, M., and Sakaki, Y., A comprehensive twohybrid analysis to explore the yeast protein interactome, *Proc. Natl. Acad. Sci. USA*, 98(8):4569– 4574, 2001.
- [4] Murzin, A.G., Brenner, S.E., Hubbard, T., and Chothia, C., SCOP: A structural classification of proteins database for the investigation of sequences and structures, J. Mol. Biol., 247:536–540, 1995.
- [5] Ogata, H., Fujibuchi, W., Goto, S., and Kanehisa, M., A heuristic graph comparison algorithm and its application to detect functionally related enzyme clusters, *Nucleic Acids Res.*, 28:4021– 4028, 2000.