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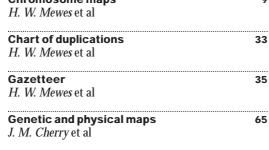
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Residents of a particular city notoriously have never visited most sights shown to tourists. In the same way, the complete genomic sequence of the brewer's yeast, *Saccharomyces cerevisiae*, has now been available for over a year, proving its usefulness to molecular biologists in a hundred quiet ways, without attracting the concerted attention that is its due. This *Directory* is intended to remedy that situation, by presenting papers on all the hitherto undescribed chromosomal sequences alongside an overview of the entire genomic sequence.

Like many a monument ignored by locals, familiarity has obscured what an achievement it represents. For one thing, it is still almost three times as large as any other genome sequenced so far. Then, too, this size necessitated a unique international collaboration which will surely inspire related projects in the future. Most importantly, it represents the first complete sequence of a eukaryotic genome, the last of the three superkingdoms of life to have a fully sequenced representative.

As such, it will be a rich mine of information for everyone concerned with all kinds of eukaryotic genomes, up to and including those of human beings. The opportunity this represents is equalled only by the challenge: dauntingly, of the 5,800 open reading frames in the sequence, the function of 45% cannot even be guessed. For now, we can only be grateful to the European Commission (DG XII – Life Sciences) for initiating and supporting, since 1989, the international project whose success has allowed *Nature* to present a unified account of this vital resource, and look forward to the flood of information that its study will surely release.

Nicholas Short

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# **The Yeast Genome Directory**

This directory was made possible by a unique international collaboration between the 633 scientists whose names appear below. It represents both the first published description of the complete sequence of most chromsomes from Saccharomyces cerevisiae, and the first published overview of the entire sequence. As such, the authors would like future papers referring to the entire sequence and/or its contents to cite this directory; future papers referring to the sequence of individual chromosomes should refer to the papers listed at the head of page 9. The authors' affiliations appear in the papers describing the individual chromosomes.

A. Goffeau, R. Aert, M. L. Agostini-Carbone, A. Ahmed, M. Aigle, L. Alberghina, K. Albermann, M. Albers, M. Aldea, D. Alexandraki, G. Aljinovic, E. Allen, J. Alt-Mörbe, B. André, S. Andrews, W. Ansorge, G. Antoine, R. Anwar, A. Aparicio, R. Araujo, J. Arino, F. Arnold, J. Arroyo, E. Aviles, U. Backes, M. C. Baclet, K. Badcock, A. Bahr, V. Baladron, J. P. G. Ballesta, A. T. Bankier, A. Banrevi, M. Bargues, L. Baron, T. Barreiros, B. G. Barrell, C. Barthe, A. B. Barton, A. Baur, A.-M. Bécam, A. Becker, I. Becker, J. Beinhauer, V. Benes, P. Benit, G. Berben, E. Bergantino, P. Bergez, A. Berno, I. Bertani, N. Biteau, A. J. Bjourson, H. Blöcker, C. Blugeon, C. Bohn, E. Boles, P. A. Bolle, M. Bolotin-Fukuhara, R. Bordonné, J. Boskovic, P. Bossier, D. Botstein, G. Bou, S. Bowman, J. Boyer, P. Brandt, T. Brandt, M. Brendel, T. Brennan, R. Brinkman, A. Brown, A. J. P. Brown, D. Brown, M. Brückner, C. V. Bruschi, J. M. Buhler, M. J. Buitrago, F. Bussereau, H. Bussey, A. Camasses, C. Carcano, G. Carignani, J. Carpenter, A. Casamayor, C. Casas, L. Castagnoli, H. Cederberg, E. Cerdan, N. Chalwatzis, R. Chanet, E. Chen, G. Chéret, J. M. Cherry, T. Chillingworth, C. Christiansen, J.-C. Chuat, E. Chung, C. Churcher, C. M. Churcher, M. W. Clark, M. L. Clemente, A. Coblenz, M. Coglievina, E. Coissac, L. Colleaux, R. Connor, R. Contreras, J. Cooper, T. Copsey, F. Coster, R. Coster, J. Couch, M. Crouzet, C. Cziepluch, B. Daignan-Fornier, F. Dal Paro, D. V. Dang, M. D'Angelo, C. J. Davies, K. Davis, R. W. Davis, A. De Antoni, S. Dear, K. Dedman, E. Defoor, M. De Haan, Th. Delaveau, S. Del Bino, M. Delgado, H. Delius, D. Delneri, F. Del Rey, J. Demolder, N. Démolis, K. Devlin, P. de Wergifosse, F. S. Dietrich, H. Ding, C. Dion, T. Dipaolo, F. Doignon, C. Doira, H. Domdey, J. Dover, Z. Du, E. Dubois, B. Dujon, M. Duncan, P. Durand, A. Düsterhöft, S. Düsterhus, T. Eki, M. El Bakkoury, L. G. Eide, K.-D. Entian, P. Eraso, D. Erdmann, H. Erfle, V. Escribano, M. Esteban, L. Fabiani, F. Fabre, C. Fairhead, B. Fartmann, A. Favello, G. Faye, H. Feldmann, L. Fernandes, F. Feroli, M. Feuermann, T. Fiedler, W. Fiers, U. N. Fleig, M. Flöth, G. M. Fobo, N. Fortin, F. Foury, M. C. Francingues-Gaillard, L. Franco, A. Fraser, J.D. Friesen, C. Fritz, L. Frontali, H. Fukuhara, L. Fulton, L. J. Fuller, C. Gabel, C. Gaillardin, L. Gaillon, F. Galibert, F. Galisson, P. Galland, F.-J. Gamo, C. Gancedo, J. M. Garcia-Cantalejo, M. I. García-Gonzalez, J. J. Garcia-Ramirez, M. García-Saéz, H. Gassenhuber, M. Gatius, S. Gattung, C. Geisel, M. E. Gent, S. Gentles, M. Ghazvini, D. Gigot, V. Gilliquet, N. Glansdorff, A. Gómez-Peris, A. Gonzaléz, S. E. Goulding, C. Granotier, T. Greco, M. Grenson, P. Grisanti, L. A. Grivell, D. Grothues, U. Gueldener, P. Guerreiro, E. Guzman, M. Haasemann, B. Habbig, H. Hagiwara, J. Hall, K. Hallsworth, N. Hamlin, N. J. Hand, V. Hanemann, J. Hani, T. Hankeln, M. Hansen, D. Harris, D. E. Harris, G. Hartzell, D. Hatat, U. Hattenhorst, J. Hawkins, U. Hebling, J. Hegemann, C. Hein, A. Hennemann, K. Hennessy, C. J. Herbert, K. Hernandez, Y. Hernando, E. Herrero, K. Heumann, D. Heuss-Neitzel, N. Hewitt, R. Hiesel, H. Hilbert, F. Hilger, L. Hillier, C. Ho, J. Hoenicka, B. Hofmann, J. Hoheisel, S. Hohmann, C. P. Hollenberg, K. Holmstrøm, O. Horaitis, T. S. Horsnell, M.-E. Huang, B. Hughes, S. Hunicke-Smith, S. Hunt, S. E. Hunt, K. Huse, R. W. Hyman, F. Iborra, K. J. Indge, I. Iraqui Houssaini, K. Isono, C. Jacq, M. Jacquet, A. Jacquier, K. Jagels, W. Jäger, C. M. James, J. C. Jauniaux, Y. Jia, M. Jier, A. Jimenez, D. Johnson, L. Johnston, M. Johnston, M. Jones, J.-L. Jonniaux, D. B. Kaback, T. Kallesøe, S. Kalman, A. Kalogeropoulos, L. Karpfinger-Hartl, D. Kashkari, C. Katsoulou, A. Kayser, A. Kelly, T. Keng, H. Keuchel, P. Kiesau, L. Kirchrath, J. Kirsten, K. Kleine, U. Kleinhans, R. Klima, C. Komp, E. Kordes, S. Korol, P. Kötter, C. Krämer, B. Kramer, P. Kreisl, T. Kucaba, H. Kuester, O. Kurdi, P. Laamanen, M. J. Lafuente,

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# Overview of the yeast genome

H. W. Mewes, K. Albermann, M. Bähr, D. Frishman, A. Gleissner, J. Hani, K. Heumann, K. Kleine, A. Maierl, S. G. Oliver<sup>1</sup>, F. Pfeiffer & A. Zollner

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The collaboration of more than 600 scientists from over 100 laboratories to sequence the *Saccharomyces cerevisiae* genome was the largest decentralised experiment in modern molecular biology and resulted in a unique data resource representing the first complete set of genes from a eukaryotic organism. 12 million bases were sequenced in a truly international effort involving European, US, Canadian and Japanese laboratories. While the yeast genome represents only a small fraction of the information in today's public sequence databases, the complete, ordered and non-redundant sequence provides an invaluable resource for the detailed analysis of cellular gene function and genome architecture. In terms of throughput, completeness and information content, yeast has always been the lead eukaryotic organism in genomics; it is still the largest genome to be completely sequenced.

The Yeast Genome Directory presents the basic features of this sequence: the arrangement of the 6,000 genes on 16 chromosomes; a summary of the function of the encoded proteins; and a view of the genome's architecture, based on an exhaustive intra-genomic sequence comparison¹. The complete yeast sequence can be retrieved from a number of public databases, as well as from specialized World-Wide Web sites, which provide sophisticated query interfaces (see Box). These data are maintained and updated continuously. Although the form of the genome directory shown in this printed volume must present static information, its intention is to document the interpretation of the yeast genome shortly after its completion. To present the genome in a printable form, we have had to include a very limited selection of fact-oriented data. The Yeast Genome Directory cannot answer the question "What's in the yeast genome?" exhaustively, but summarizes what is known to be in it.

The sequence The final sequence was assembled from roughly 300,000 independent sequence reads, with error rates from 0.5 to 1%, resulting in an estimated error rate of the final sequence of less than 3 errors in 10,000 bases (0.03%). For the European Union part of the sequencing effort, a central database and informatics used to assemble, verify and analyse contiguous sequences submitted by the participating laboratories was provided by the Martinsrieder Institut für Protein Sequenzen (MIPS). The complete sequence was made available to the public on 24 April 1996. The first map represents the open reading frames (ORFs) of each of the successive chromosomes, at a uniform scale of 5 mm per kilobase. ORFs are named according to the location of the gene, using the convention Y (for yeast) followed by a letter denoting the chromosome (A for I, B for II, and so forth), a letter denoting the arm (R or L), a three-digit code ordering the ORFs from the centromere, and a letter denoting the coding strand (w or c).

**Duplications** The availability of the complete sequence of yeast allows us for the first time to examine the evolution of a eukaryotic species in a truly comprehensive manner. The footprints that indicate the evolutionary path taken by the yeast genome may be recognized by internal similarities between distinct regions of the present-day genome. Our approach to the inspection of these relationships is based on an all-against-all comparison of the genomic sequence data, applying local sequence alignments. Investigation of the yeast genome involved more than 24,000 blocks of 500 nucleotides. For each block, the six-frame translation into protein sequences was also generated, to allow for the concurrent comparison of DNA and amino-acid sequences<sup>2</sup>.

Once an all-against-all matching of the yeast genome had been accomplished, duplication patterns within the genome could be investigated in a systematic way. The frequent, collinear block duplications found by our method seem to be an important consequence of the evolutionary development of *S. cerevisiae*. We have systematically inspected the genome for clusters of genes that have been produced by local duplication events. This involved evaluating the parameters that describe a cluster: it's size; the degree of similarity of the duplicated ORFs; and the compactness of the cluster. Scanning this parameter-space at a sensitivity just above noise level (50% identity on the DNA level), we found that a window size of 25

kb and an enforced compactness of 10% of the coding region in that window generated an optimal representation of gene clusters. These criteria allowed us to identify 53 regions of clustered gene duplications, not including the well-known high level of similarity in the telomeric and subtelomeric regions. The second map shows the set of all collinear clusters of genes in the genome as a two-page fold-out. The significant number of gene duplications in yeast must reflect an evolutionarily successful strategy: gene duplications allow for evolutionary modifications in one of the copies without disturbing possibly vital functions of the other.

Gene function The computational analysis of the yeast genome is a challenging task<sup>3</sup>. The scientific assessment of raw sequence data aims to connect genetic entities to biological knowledge, either by computational analysis or by linking sequence-deduced information to other experimental evidence (such as a genetic locus). Sophisticated data modelling is required to reflect the correct relationship between the sequence and any associated information and to allow for the consistent integration of complex, heterogeneous biological data. For example, the precursor of the ADP/ATP carrier protein AAC2p is represented five times in the EMBL Nucleic Acid Data Library, although four of the coding sequences reported are identical. The current nucleic acid databases (EBI/NCBI/DDBJ) contain 2,678 entries covering the yeast genome with a high degree of redundancy and inconsistency. Thus the traditional model of collecting

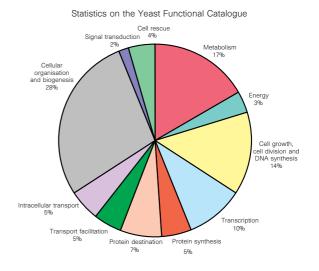


Figure 1 This shows the relative number of ORFs assigned to individual categories in the Gazetteer. There are eleven functional categories. Only proteins with a known function, or similarity or strong similarity to known proteins were assigned to one of the categories (similarities were measured by FASTA scores). In total, 3167 ORFs were assigned to at least one category. A single ORF can be assigned to more than one category.

### introduction

database entries and presenting them as individual reports does not seem to be suitable for coping with the data analysis of complete genomes. Like the printed page, the traditional layout of the sequence databases is static, incorporating information from scientific annotation at the time of publication. Additional information extracted from the literature must be translated manually into the formal framework of a database entry. The knowledge of the functional properties of an uncharacterized gene may be published independently, and family members found in other organisms may allow for characterization by homology. Suitable models must thus be developed to cope with the data analysis of a complete genome, and to enable integrated views of the genomic sequence and associated information.

Only 43.3 % of the yeast genes are currently classified as 'functionally characterized', having experimentally well-investigated properties, being members of well-defined protein families, or displaying strong homology to proteins with known biochemical functions. The systematic functional analysis of these genes, currently in progress<sup>4</sup>, will identify the functions of many of the uncharacterized 'orphans'. Various experimental methods, including improved 'in silico' analysis, will also increase dramatically the information content of the biological databases. Previously, individual attempts have been made to analyse specific chromosomes systematically by sequence analysis<sup>5,6</sup>, and the results of an automated software system, 'Genecrunch', to 'crunch' the complete yeast genome have been offered as an Internet service (http://genecrunch.sgi.com).

To provide information on the biochemical and physiological context of protein function, we have compiled a gazetteer listing all the ORFs that can be related to well-understood functions. Similarities between biological sequences were measured by FASTA scores<sup>7</sup>: a FASTA score between 100 and 200 was defined as a 'weak similarity'; between 200 and a third of the self-score (the score of the protein when aligned with itself) for the protein was defined as a 'similarity'; and higher than a third of the self-score was defined as a 'strong similarity'. Weak similarities were not considered. In addition to the similarity scores, we have used pattern data<sup>8</sup>, including experimental data from the literature combined with genetic data, to characterize ORFs.

Each entry in the gazetteer lists the ORF name (defined as above), the gene name (if any), and the name or a short description of the protein. Entries are divided into 11 categories representing the cellular function of the individual ORFs (such as metabolism, energy or transcription), and each category is divided into sub-categories<sup>9</sup>. The yeast genome encodes about 5,800 proteins, less than half of which are 'known' in the sense that they have been genetically and biochemically well characterized. For about 20% of the remaining proteins, the experimental data are heterogeneous and provide only some indication of their functions *in vivo*. The remaining 38% either show similarities to other uncharacterized proteins or show no similarities at all. Defined categories provoke redundant entries, such as the classification of multifunctional enzymes. As gene names are used elsewhere in a very inconsistent way, we have used the name from the *Saccharomyces* genome database (see Box) register whenever possible. Gene names that are used twice for different ORF names are written in brackets.

Sequences of common evolutionary origin (homologous *sensu stricto*) reflect their relatedness by sequence similarities, and the organization of related primary, secondary and tertiary structures into groups ('families') remains the most powerful principle in sequence data analysis. We have used this principle to cluster proteins into families and superfamilies, following a previous scheme<sup>10</sup>, allowing us to cope with the many taxonomic complications inherent in protein evolution.

The World-Wide Web site of the Martinsrieder Institut für Protein Sequenzen yeast resource combines information generated by automated procedures with the results of systematic analysis by yeast researchers. Users can: (1) visualize chromosomes and selected regions to inspect genetic elements, such as ORFs, Ty's, tRNAs etc.; (2) receive detailed information on a yeast gene by searching with accession numbers, systematic codes, or gene names; (3) browse yeast genes according to their functional classification; (4) search for human homologues; (5) obtain information on functional properties; (6) download nucleic-acid or protein sequence data; (7) inspect up-to-date sequence homologies and alignments (FASTA database); (8) browse the family and superfamily classification of yeast proteins; (9) search

the yeast genome interactively for sequence patterns and sequence similarities; and (10) inspect the yeast genome for gene redundancy.

As a complement to the printed information in the *Yeast Genome Directory*, a CD-ROM compiled by Martinsrieder Institut für Protein Sequenzen, is available on request to subscribers of *Nature* and *Science* for the exploration of the yeast genome on a local, network-independent installation. The basic functionality of the retrieval software and the databases incorporated is equivalent to our World-Wide Web resource. The CD-ROM can be installed on Windows95, WindowsNT and Power-Macintosh operating systems, and is accompanied by a detailed description of its functionality, installation procedures and system requirements.

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### **BOX** Useful World-Wide Web addresses

### Yeast databases

Munich Information Centre for Protein Sequences (MIPS) http://www.mips.biochem.mpg.de/mips/yeast/

Yeast Protein Database (YPD)

http://quest7.proteome.com/YPDhome.html

Saccharomyces Genome Database (SGD)

http://genome-www.stanford.edu/Saccharomyces/

### **Specialized Yeast Databases**

Sacch3D - Structural information for yeast proteins http://genome-www.stanford.edu/Sacch3D/

Yeast Gene Duplications

http://acer.gen.tcd.ie/~khwolfe/yeast/topmenu.html

Related human disease genes (NIH XREFdb) http://www.ncbi.nlm.nih.gov/XREFdb/

Genetic and physical maps (hyperlinked to biological information) http://genome-www.stanford.edu/cgi-bin/SGD/pgMAP/pgMap

NIH yeast information page

http://www.ncbi.nlm.nih.gov/Yeast/budding.html

Schizosaccharomyces pombe http://www2.bio.uva.nl/pombe/

Candida albicans information

http://alces.med.umn.edu/Candida.html

### Common DNA and protein databases

European Bioinformatics Institute (EBI)

http://www.ebi.ac.uk/services/services.html

National Center for Biotechnology Information (NCBI) http://www.ncbi.nlm.nih.gov/

DNA Data Bank of Japan (DDBJ) http://www.ddbj.nig.ac.jp/

PIR-International

http://www.mips.biochem.mpg.de

SwissProt

http://expasy.hcuge.ch/sprot/sprot-top.html

### References to be cited for the complete sequence and individual chromosomes

**Complete sequence**, The Yeast Genome Directory Goffeau, A. *et al. Nature* **387** (suppl.), 1–105 (1997)

**Chromosome 1**, The nucleotide sequence of chromosome 1 from *Saccharomyces cerevisiae* Bussey, H. *et al. Proc. Natl Acad. Sci. USA* **92**, 3809–3813 (1995)

EMBL accession numbers: U12980, L20125, L05146, L22015, L28920

**Chromosome 2**, Complete DNA sequence of yeast chromosome II

Feldmann, H. et al. EMBOJ. 13, 5795–5809 (1994) EMBL accession numbers: Y08934, Z35762-Z35869, Z35870-Z36171

**Chromosome 3**, The complete DNA sequence of yeast chromosome III Oliver, S. et al. Nature 357, 38–46 (1992) EMBL accession number: X59720

**Chromosome 4**, The nucleotide sequence of *Saccharomyces cerevisiae* chromosome IV Jacq, C. *et al. Nature* **387** (suppl.), 75–78 (1997) **EMBL accession numbers**: Z74051-Z74296, Z48008, Z74305-Z74385, Z49770, Z47814, Z68196, Z54075, Z49812, Z49209, Z46796, Z50111, Z47746, Z48758, Z48179, Z54139, Z50046, Z47813, Z46727, Z48784, Z68194, Z68195, Z48612, Z49701, Z68329, Z70202, Z68290, U51030, U51031, U28374, U32517, U51032, U28372, U28373, U32274, U33050, U33057, Z74389

**Chromosome 5**, The nucleotide sequence of *Saccharomyces cerevisiae* chromosome V Dietrich, F. S. *et al. Nature* **387** (suppl.), 78–81 (1997) **EMBL accession numbers**: U73806, U18795, L10830, U18779, U18530, U18778, U18796, U18813, U18814,

U18839, U18916, U18917, L10718, U18922

Chromosome 6, Analysis of the nucleotide sequence of chromosome VI from Saccharomyces cerevisiae Murakami, Y. et al. Nature Genet. 10, 261–268 (1995) EMBL accession number: D50617

Chromosome 7, The nucleotide sequence of Saccharomyces cerevisiae chromosome VII Tettelin, H. et al. Nature 387 (suppl.), 81–84 (1997) EMBL accession numbers: X94357, Z72785–Z73081

**Chromosome 8**, Complete nucleotide sequence of Saccharomyces cerevisiae Chromosome VIII Johnston, M. *et al. Science* **265**, 2077–2082 (1994) **EMBL accession numbers:** U11583, U11582, U11581, U10555, U10400, U10399, U00062, U00061, U10556, U00060, U00059, U10398, U10397, U00027, U00028, U100030, U00029

**Chromosome 9.** The nucleotide sequence of *Saccharomyces cerevisiae* chromosome IX Barrell, B. G. et al. *Nature* 387 (suppl.), 84–87 (1997) EMBL accession number: Z47047

**Chromosome 10**, Complete nucleotide sequence of *Saccharomyces cerevisiae* Chromosome X Galibert, F. *et al. EMBO J.* 15, 2031–2049 (1996) *EMBL* accession numbers: Z34098, Z49276–Z49662

**Chromosome 11**, Complete DNA sequence of yeast chromosome XI Dujon, B. *et al. Nature* **369**, 371–378 (1994)

EMBL accession numbers: Z28001-Z28330

**Chromosome 12**, The nucleotide sequence of *Saccharomyces cerevisiae* chromosome XII

Johnston, M. et al. Nature 387 (suppl.), 87–90 (1997) EMBL accession numbers: Z73106-Z73327, U53879, U51921, U17246, U14913, U19027, U20865, U17244, U17245, U17243, U17247, U20618, U19028, U19102, U19103, U19104, U19729, U20162, U20939, U21094, U22382, U22383

Chromosome 13, The nucleotide sequence of Saccharomyces cerevisiae chromosome XIII
Barrell, B. et al. Nature 387 (suppl.), 90–93 (1997)
EMBL accession numbers: Z50178, Z49218, Z49210,
X80835, Z46660, Z46373, Z38114, Z46729, Z47816,
Z48430, Z46659, Z49810, Z48613, Z49211, Z49213,
Z48502, Z49703, Z48952, Z49259, Z49807, Z50179,
Z49702, Z49273, Z4862, Z47071, Z49700, Z49808,
Z47815, Z48755, Z49809, Z49939, Z48756, Z48639,
Z49260, Z49704, X80836, Z49212, Z54141

**Chromosome 14**, The nucleotide sequence of *Saccharomyces cerevisiae* chromosome XIV and its evolutionary implications Philippsen, P. *et al. Nature* **387** (suppl.), 93–98 (1997) EMBL accession numbers: Z71277–Z71692

**Chromosome 15**, The nucleotide sequence of *Saccharomyces cerevisiae* chromosome XV Dujon, B. *et al. Nature* **387** (suppl.), 98–102 (1997) EMBL accession numbers: Z74743-Z75302

**Chromosome 16**, The nucleotide sequence of *Saccharomyces cerevisiae* chromosome XVI Bussey, H. *et al. Nature* 387 (suppl.), 103–105 (1997) EMBL accession numbers: Z73521, Z73499-Z73638, U43703, U43503, U43281, U41849, U39205, U44030, U36624, U33335, Z48951, Z49919, Z49274, Z68111, Z49219, U51033, U32445, U40828, U40829, U28371, U25840, U25842, U25841, Z73537, Z73541

### Legend of the chromosome displays

ORF (Open Reading Frame)

proteins of known function

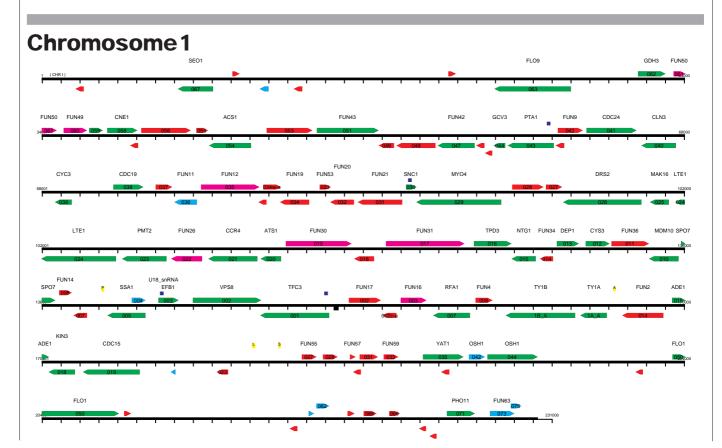
similarity to proteins of known function (more than one third of self-score)

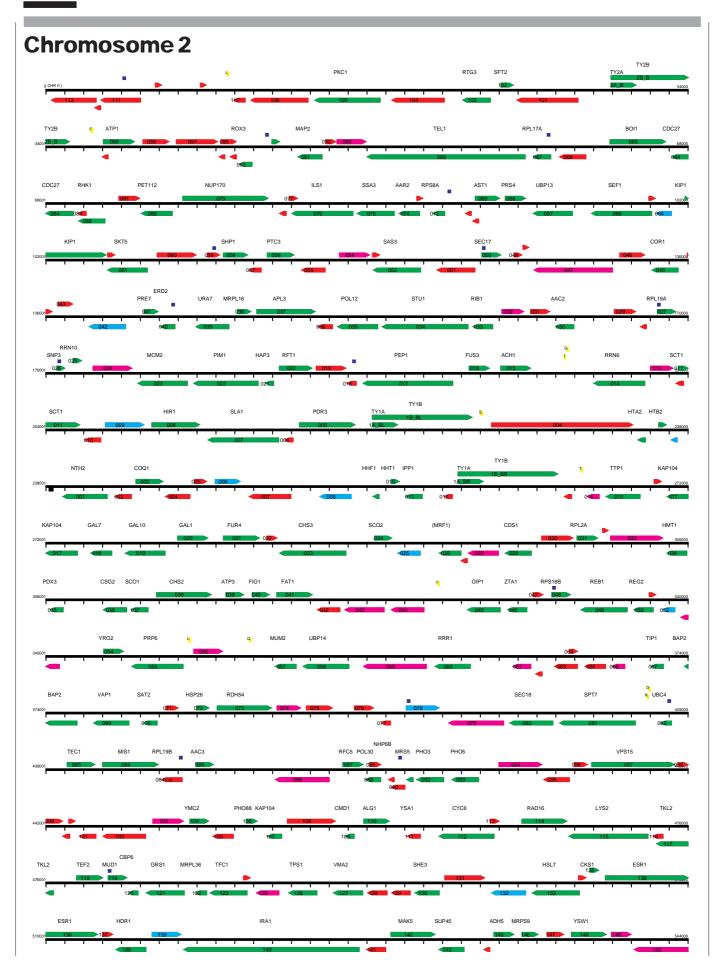
weak similarity to proteins of known function (lower than one third of self-score)

Intron

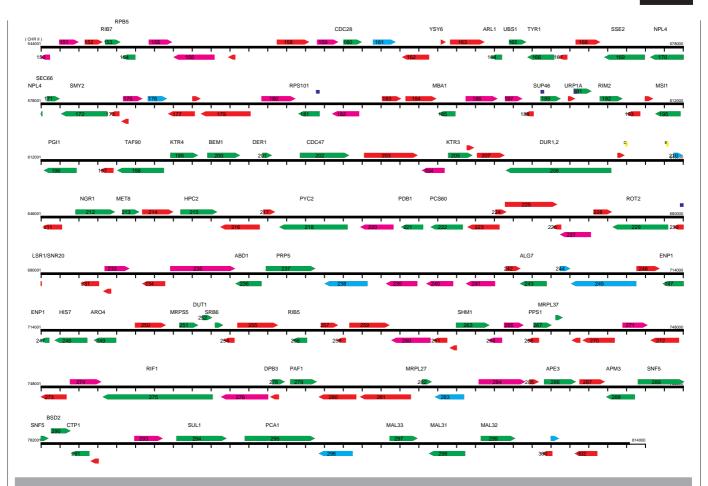
tRNA

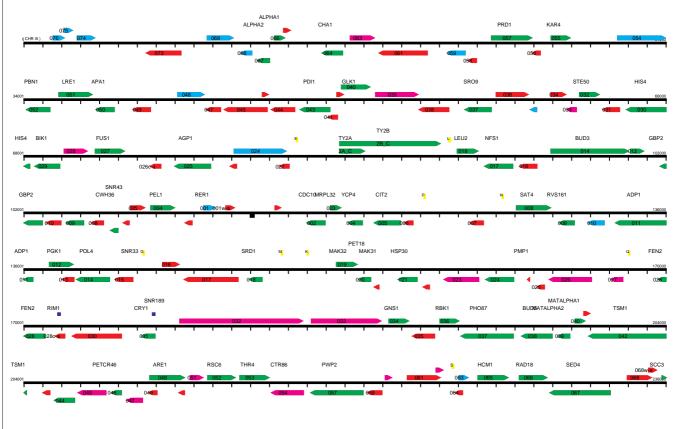
Centromer



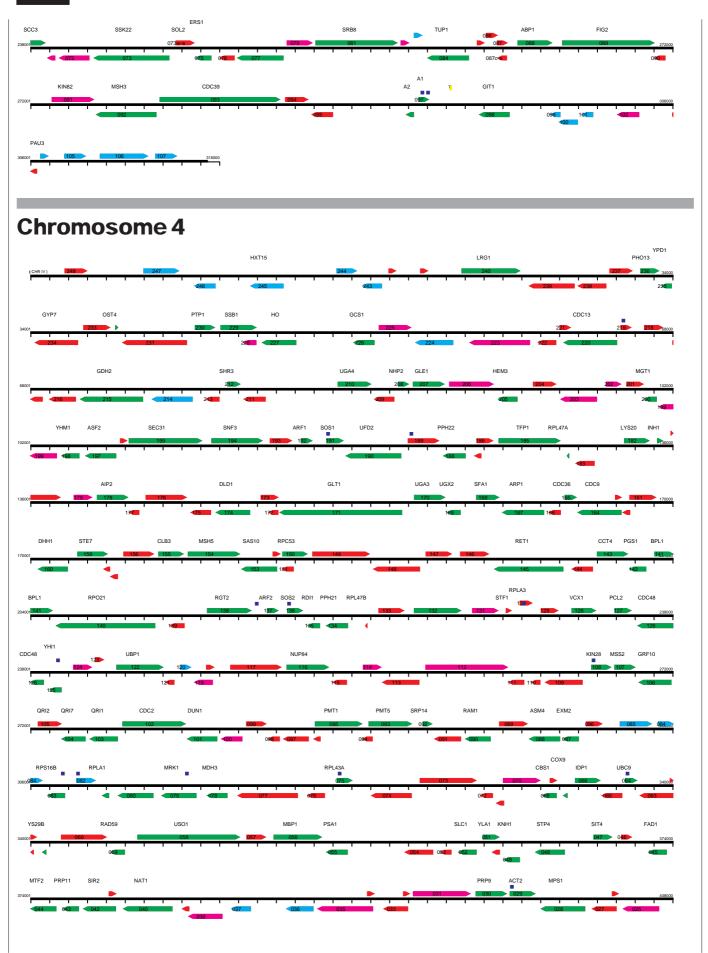




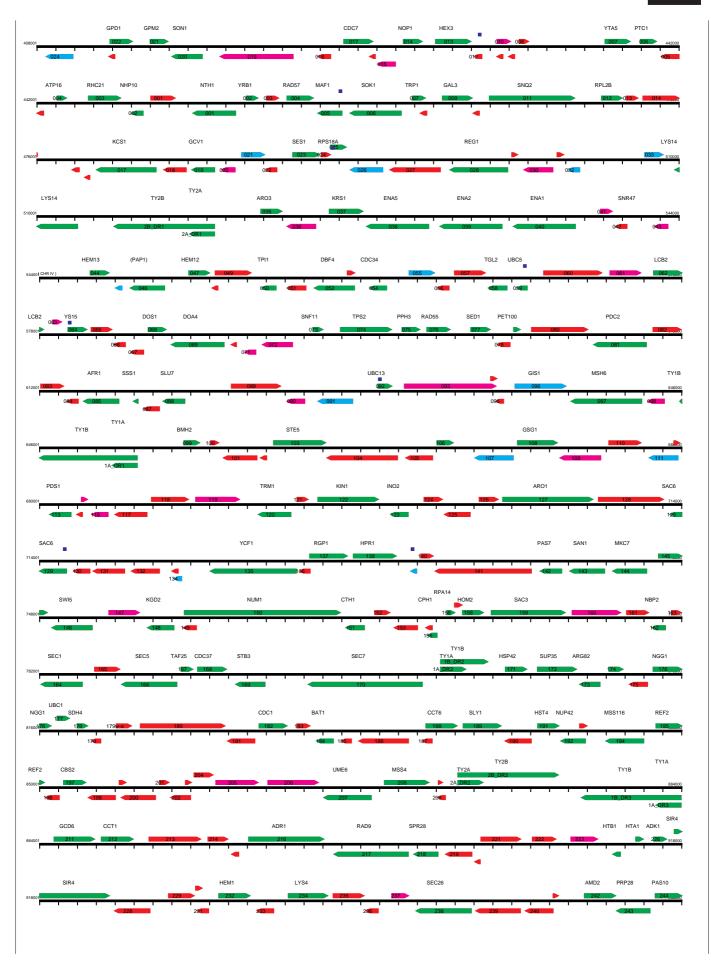


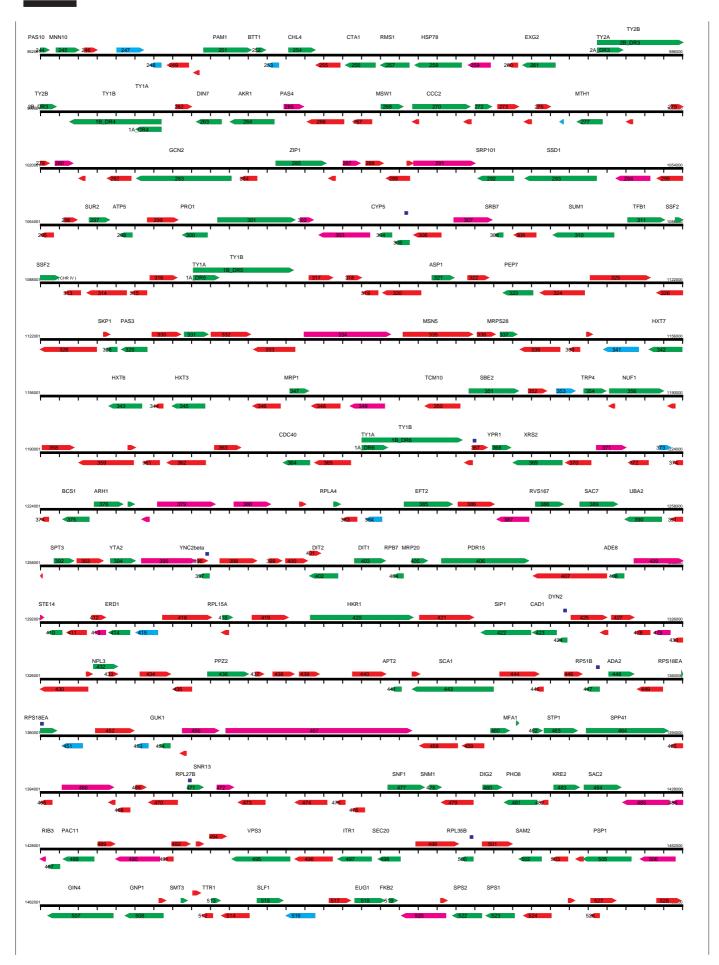




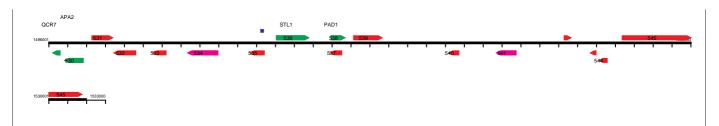


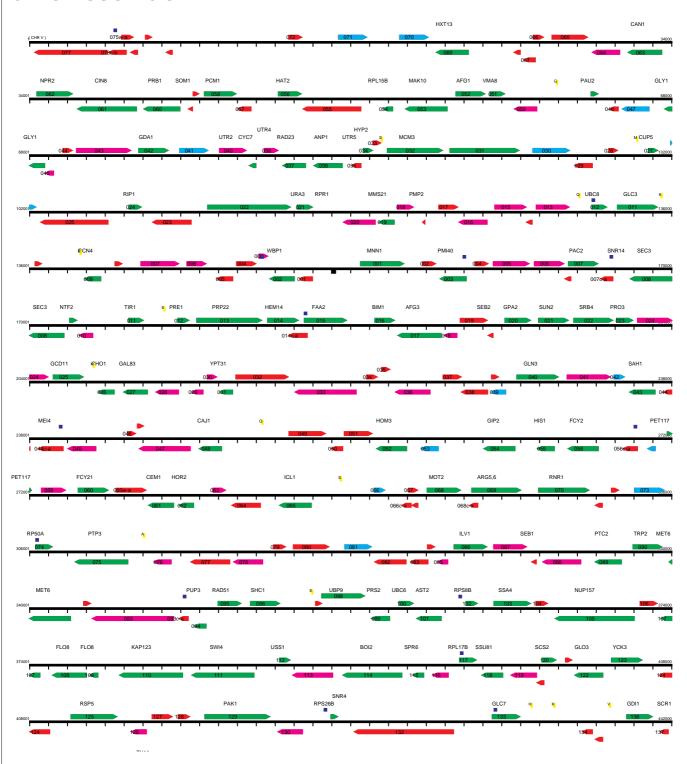


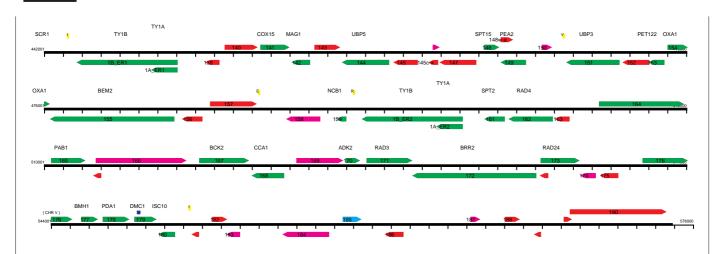




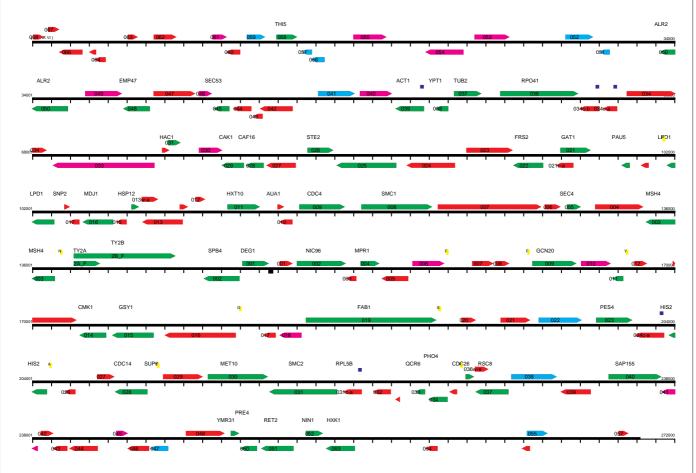


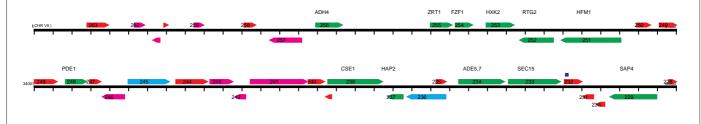




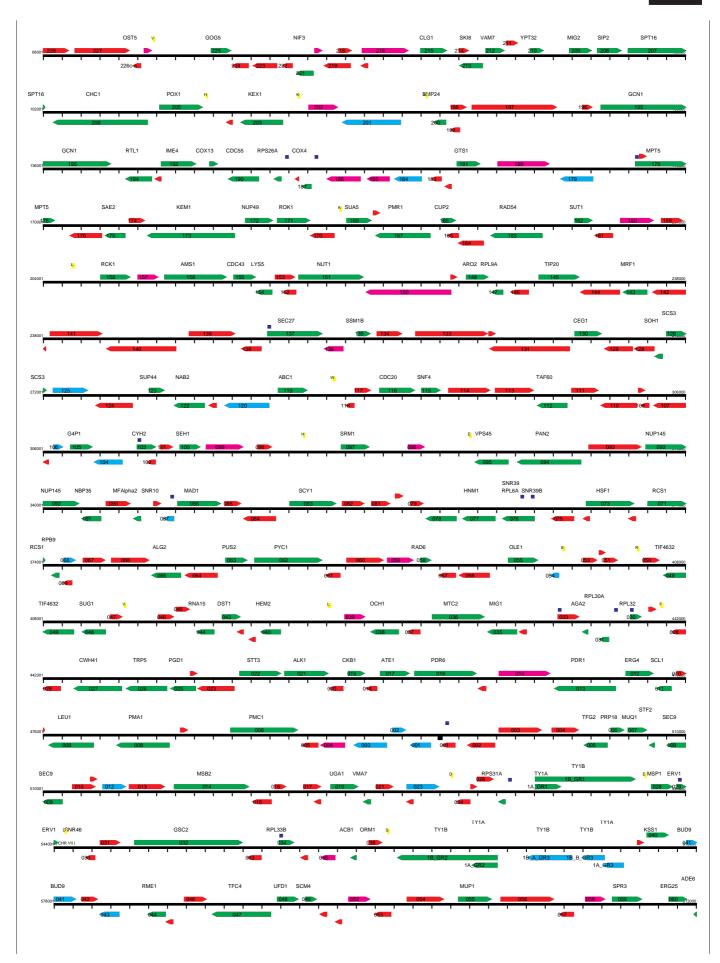


### Chromosome 6

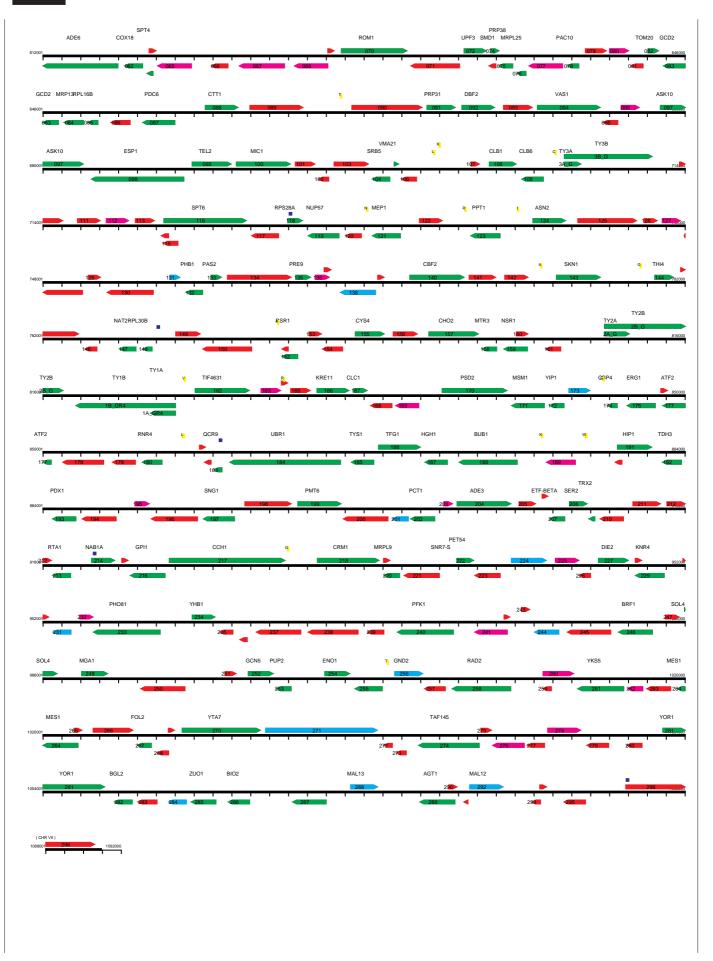




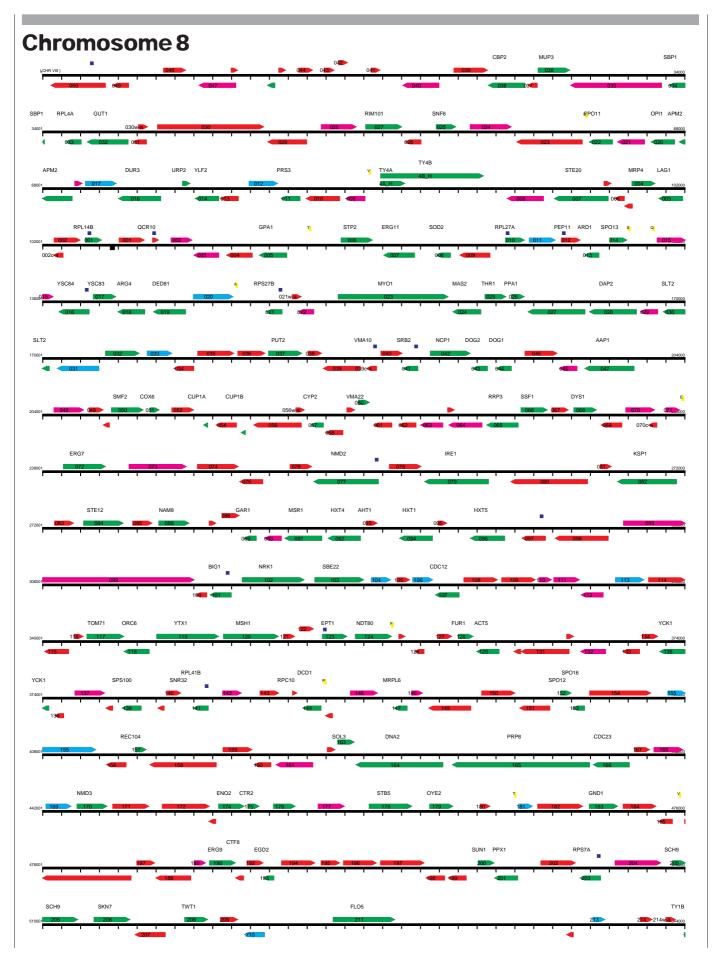




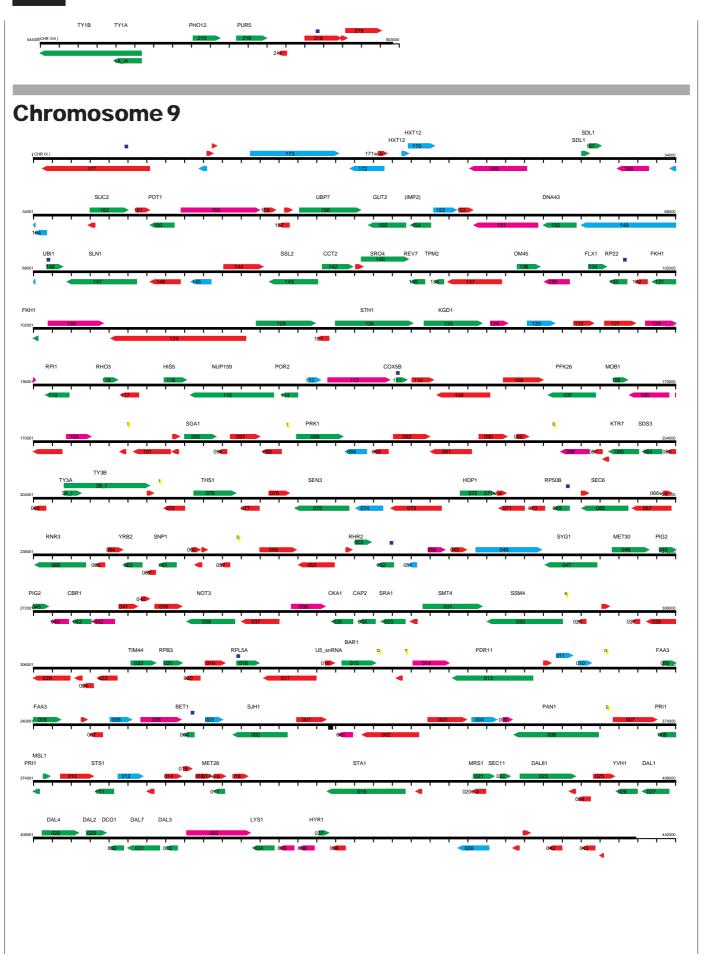






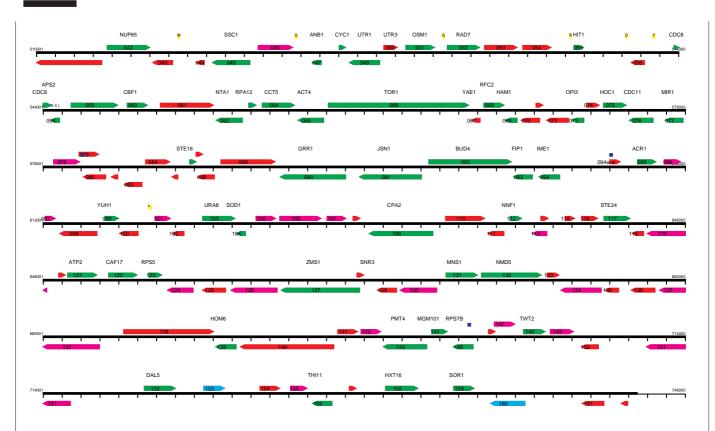


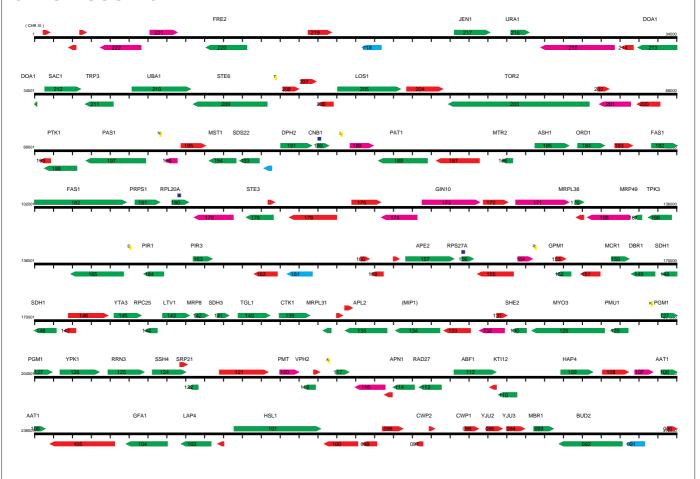






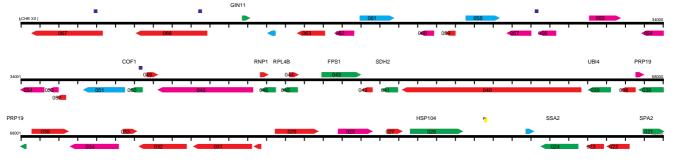




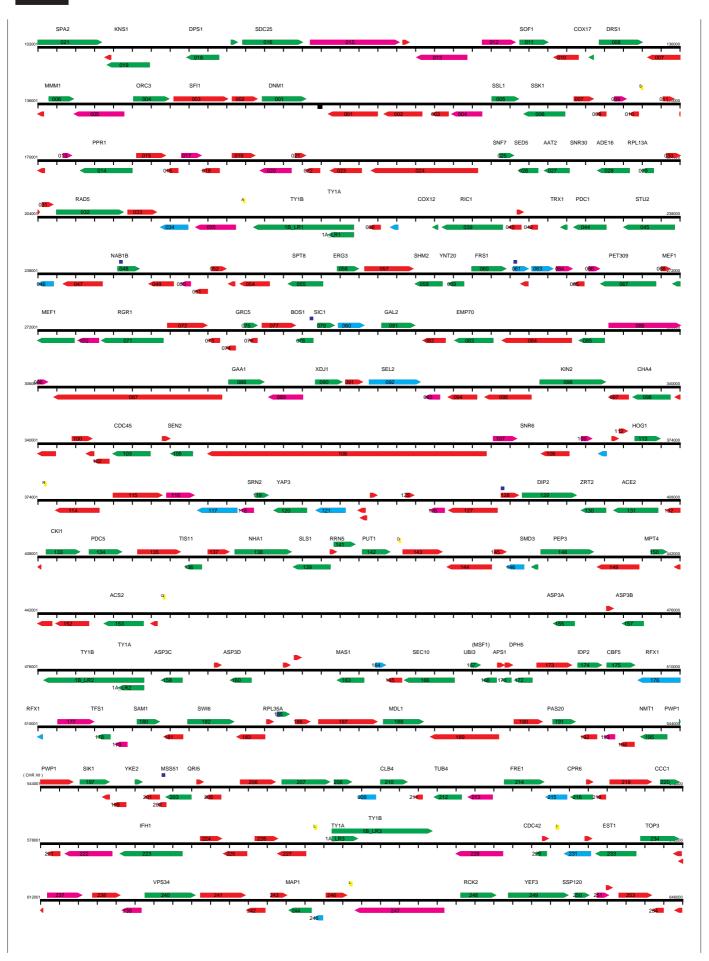




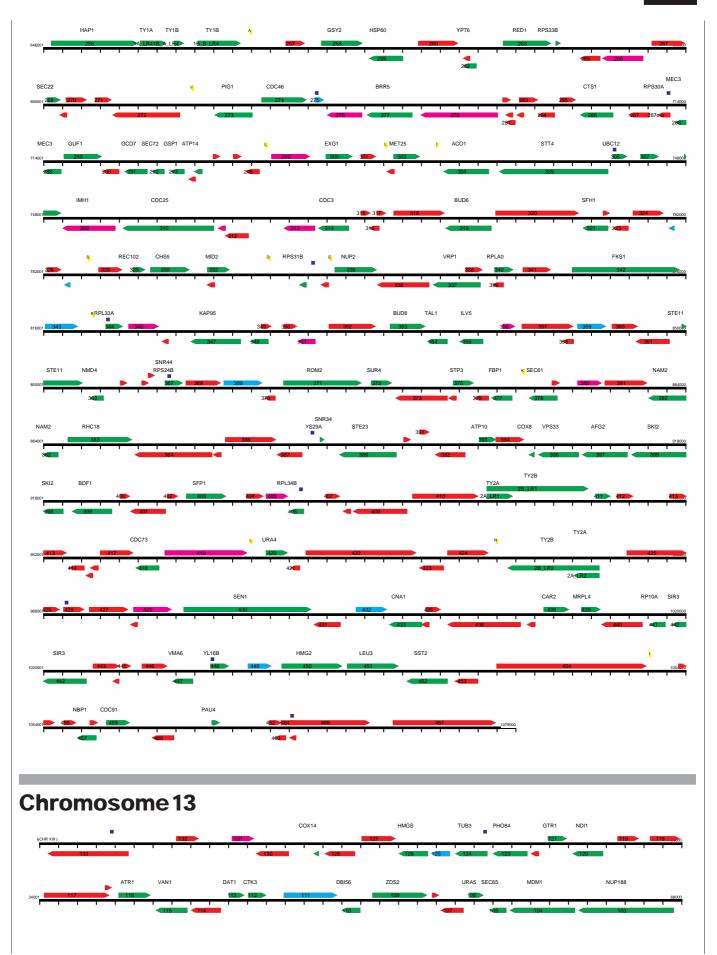




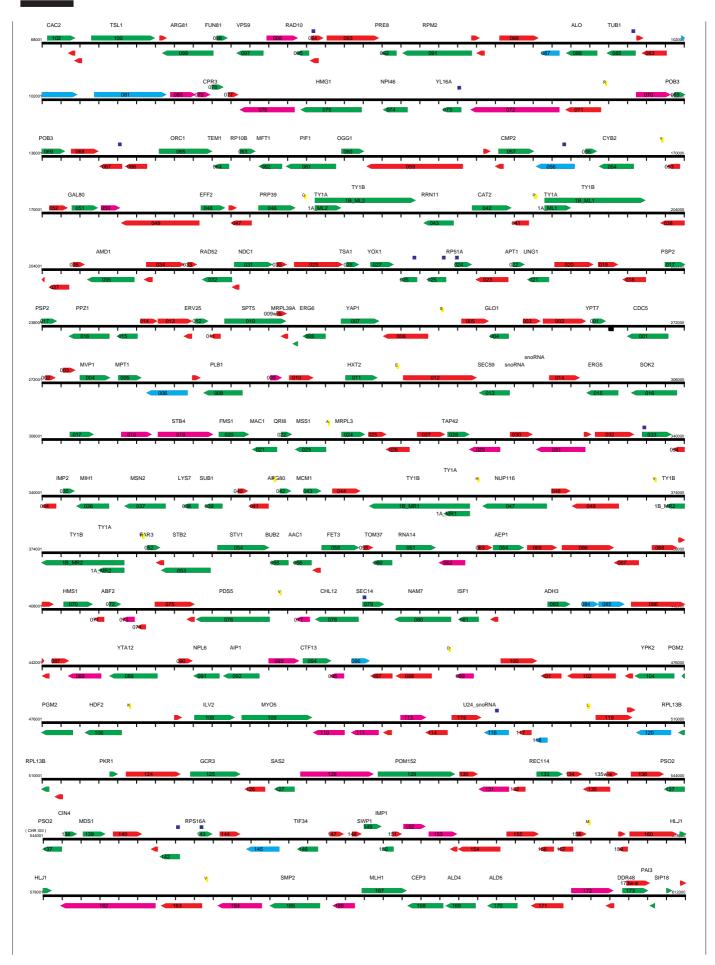






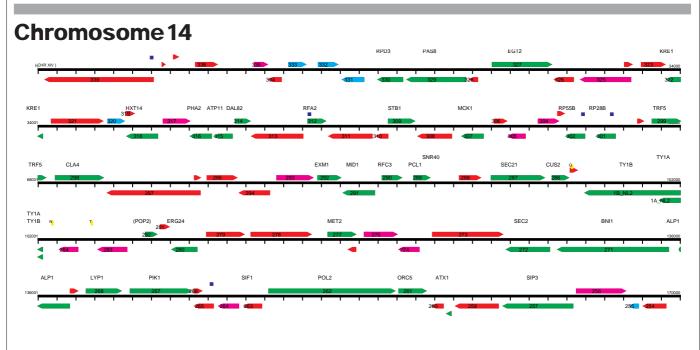






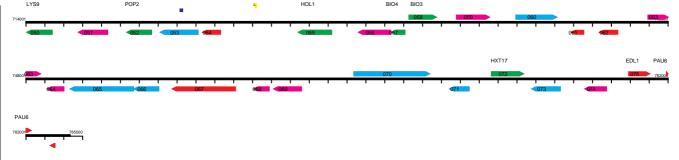










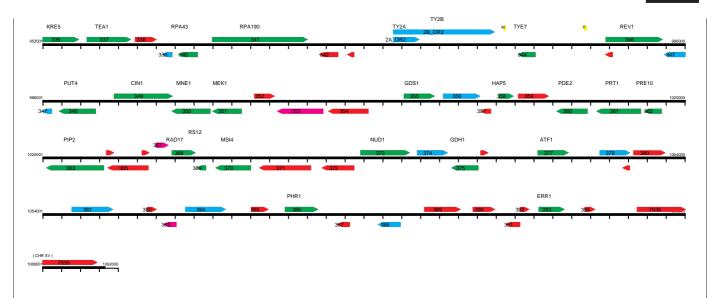


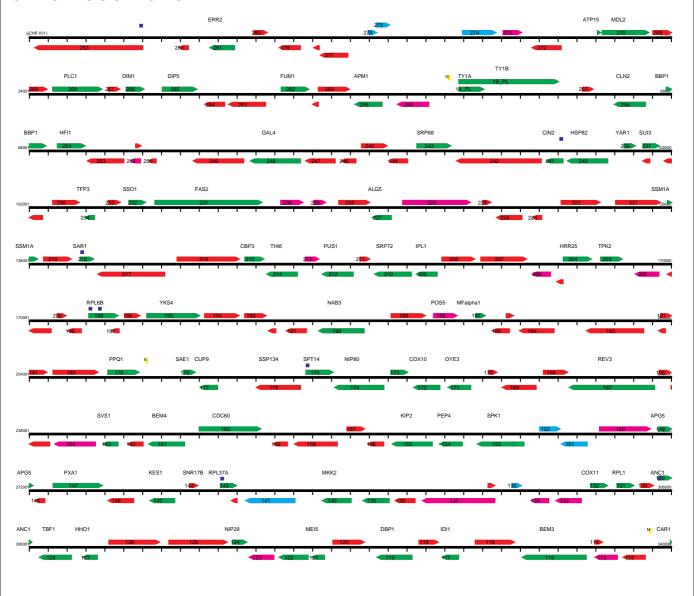
# **Chromosome 15** PEP12 CYC2





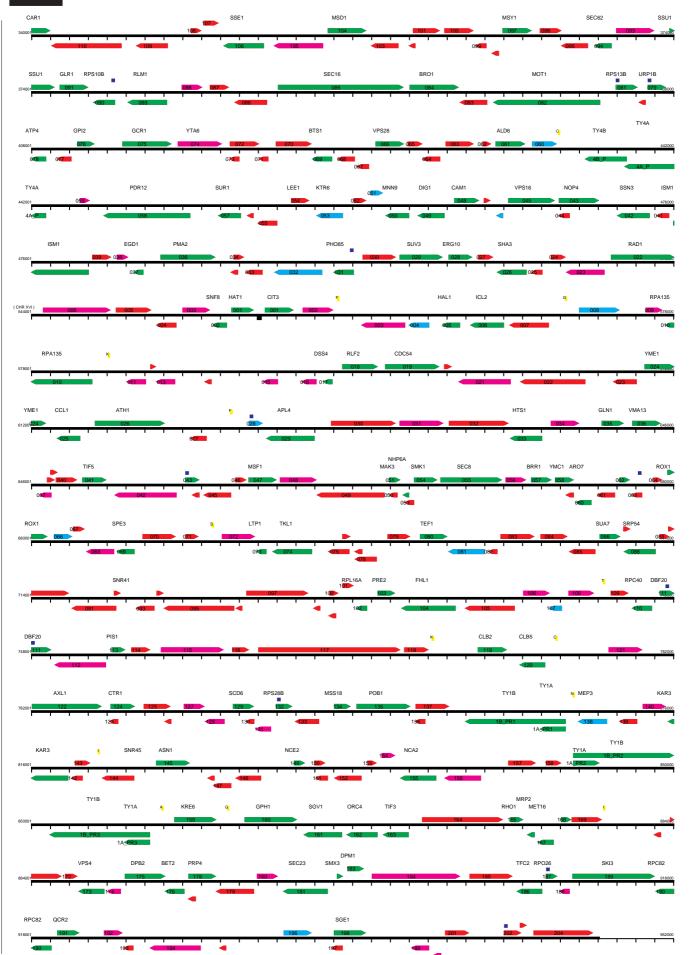


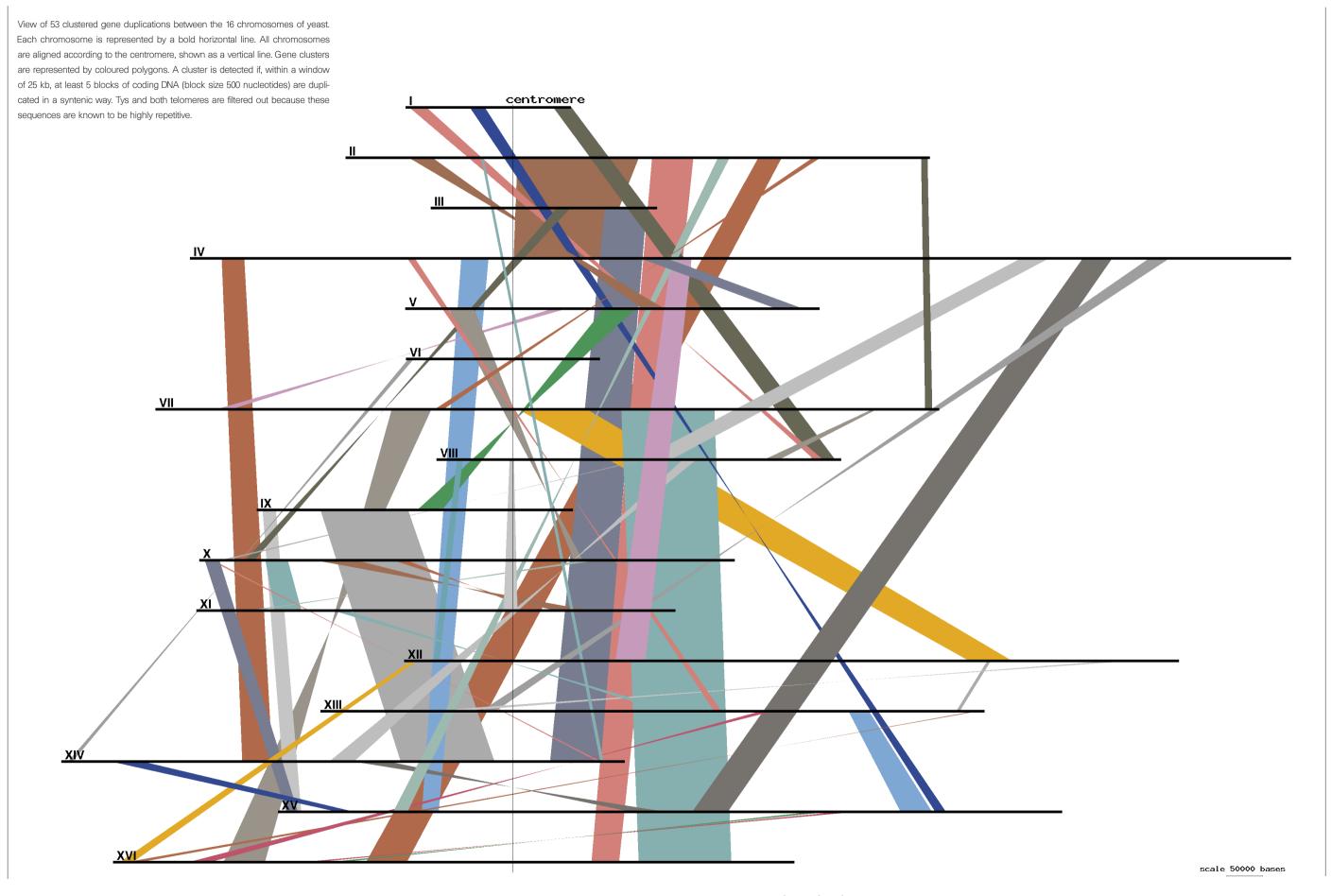






32





### mitochondrial transport vesicular transport (Golgi network, etc.) tRNA modification other tRNA-transcription activities Metabolism 35 amino-acid metabolism nitrogen and sulphur metabolism mRNA synthesis peroxisomal transport mRNA processing (splicing) mRNA processing (5'-end, 3'-end processing and mRNA degradation) nucleotide metabolism vacuolar transport extracellular transport phosphate metabolism carbohydrate metabolism cellular import other mRNA-transcription activities RNA transport lipid, fatty-acid and sterol metabolism other intracellular-transport activities biosynthesis of vitamins, cofactors and prosthetic groups other transcription activities Cellular organization and biogenesis organization and biogenesis of cell wall and plasma membrane organization and biogenesis of ionic homeostasis 48 Protein synthesis **Energy** glycolysis 40 ribosomal proteins translation (initiation, elongation and cytoskeleton termination) translational control organization and biogenesis of endoplasmic reticulum and Golgi gluconeogenesis pentose-phosphate pathway tricarboxylic-acid pathway tRNA synthetases organization and biogenesis of chromosome structure mitochondrial organization and biogenesis peroxisomal organization and biogenesis respiration other protein-synthesis activities fermentation metabolism of energy reserves (glycogen **Protein destination** 49 protein folding and stabilization protein targeting, sorting and translocation protein modification (glycosylation, acylation, endosomal organization and biogenesis vacuolar and lysosomal organization and and trehalose) other energy-generation activities other cellular organization and biogenesis Cell growth, cell division and DNA myristylation, palmitylation, farnesylation synthesis cell growth budding, cell polarity and filament formation 41 and processing) assembly of protein complexes activities proteolysis Signal transduction 58 pheromone response and mating-type determination other protein-destination activities pheromone response generation morphogenesis sporulation and germination Transport facilitation 51 osmosensing ion channels ion transporters meiosis nutritional response DNA synthesis and replication other signal-transduction activities recombination and DNA repair sugar and carbohydrate transporters 59 cell-cycle control and mitosis amino-acid transporters Cell rescue stress response generation lipid transporters cvtokinesis other cell-growth, cell-division and DNApurine and pyrimidine transporters DNA repair (direct repair, base excision synthesis activities allantoin and allantoate transporters transport ATPases repair and nucleotide excision repair) detoxificaton ABC transporters cell death and ageing Transcription 45 rRNA synthesis rRNA processing other rRNA-transcription activities drug transporters other transport-facilitators degradation of exogenous polynucleotides other cell-rescue activities tRNA synthesis Intracellular transport 53 **Unclassified proteins** 60 tRNA processing nuclear transport YBR084w MIS1 C1-tetrahydrofolate synthase. mitochondria Matahalism amino-acid metabolism

ı	V	Ц	e	ι	a	U	U	Ш	5	I	I	l	

amino-acid biosynthesis								
[ORF]	[Gene]	[Encoded or related protein]						
YHR037w	PUT2	1-pyrroline-5-carboxylate dehydrogenase						
YDR035w	ARO3	2-dehydro-3-deoxyphosphoheptonate						
		aldolase, phenylalanine-inhibited						
YBR249c	ARO4	2-dehydro-3-deoxyphosphoheptonate						
		aldolase, tyrosine-inhibited						
YNL104c	LEU4	2-isopropylmalalate synthase						
YGL009c	LEU1	3-isopropylmalate dehydratase						
YPR167c	MET16	3'-phosphoadenylylsulphate reductase						
YGR019w	UGA1	4-aminobutyrate aminotransferase (GABA						
		transaminase)						
YER091c	MET6	5-methyltetrahydropteroyltriglutamate-						
		homocysteine methyltransferase						
YMR108w	ILV2	acetolactate synthase						
YCL009c	ILV6	acetolactate synthase, regulatory subunit						
YER069w	ARG5,6	acetylglutamate kinase and						
:		acetylglutamyl-phosphate reductase						
YJL071w	ARG2	acetylglutamate synthase						
YOL140w YDR234w	ARG8 I YS4	acetylornithine aminotransferase						
YER086w	LYS4 ILV1	aconitate hydratase anabolic serine and threonine						
YERU86W	ILVI	dehydratase						
YDR354w	TRP4	anthranilate phosphoribosyltransferase						
YER090w	TRP2	anthranilate synthase component I						
YKL211c	TRP3	anthranilate synthase component II						
YJR109c	CPA2	arginine-specific carbamoylphosphate						
		synthase, large subunit						
YOR303w	CPA1	arginine-specific carbamoylphosphate						
		synthase, small subunit						
YOL058w	ARG1	argininosuccinate synthetase						
YHR018c	ARG4	arginosuccinate lyase						
YDR127w	ARO1	arom pentafunctional enzyme						
YPR145w	ASN1	asparagine synthetase						
YGR124w	ASN2	asparagine synthetase						
YLR027c	AAT2	aspartate aminotransferase, cytosolic						
YKL106w	AAT1	aspartate transaminase, mitochondrial						
YDR158w	HOM2	aspartate-semialdehyde dehydrogenase						
YFR030w	MET10	assimilatory sulphite reductase flavin- binding subunit						
YER055c	HIS1	ATP phosphoribosyltransferase						
YCL018w	LEU2	β-isopropyl-malate dehydrogenase						
YIR148w	TWT2	branched-chain amino acid						
		aminotransferase, cytosolic						
YHR208w	TWT1	branched-chain amino acid						
		aminotransferase, mitochondrial						
YGR204w	ADE3	C1-tetrahydrofolate synthase, cytoplasmic						

YPR060c	ARO7	chorismate mutase
YGL148w	ARO2	chorismate synthase
YGR155w	CYS4	cystathionine β-synthase
YAL012w	CYS3	cystathionine γ-lyase
YER023w	PRO3	δ 1-pyrroline-5-carboxylate reductase
YHR068w	DYS1	deoxyhypusine synthase
YOR236w	DFR1	dihydrofolate reductase
YFL018c	LPD1	dihydrolipoamide dehydrogenase
YJR016c	ILV3	dihydroxy-acid dehydratase
YLR172c	DPH5	diphthamide methyltransferase
YKL191w	DPH2	diphtheria toxin resistance protein
YOR323c	PRO2	γ-glutamyl phosphate reductase
YDR300c	PRO1	glutamate 5-kinase
YDL171c	GLT1	glutamate synthase (NAPDPH) (GOGAT)
YPR035w	GLN1	glutamate-ammonia ligase
YBR248c	HIS7	glutamine amidotransferase/cyclase
YFR025c	HIS2	histidinol phosphatase
YIL116w	HIS5	histidinol-phosphate aminotransferase
YMR038c	LYS7	homocitrate dehydrogenase
YDL182w	LYS20	homocitrate synthase
YJR139c	НОМ6	homoserine dehydrogenase
YHR025w	THR1	homoserine kinase
YNL277w	MET2	homoserine O-acetyltransferase
YOR202w	HIS3	imidazoleglycerol-phosphate dehydratase
YLR355c	ILV5	ketol-acid reducto-isomerase
YBR115c	LYS2	L-aminoadipate-semialdehyde
	2,02	dehydrogenase, large subunit
YGL154c	LYS5	L-aminoadipate-semialdehyde
101010	2100	dehydrogenase, small subunit
YER052c	НОМ3	L-aspartate 4-P-transferase
YLR303w	MET25	O-acetylhomoserine sulphydrylase
YLR438w	CAR2	ornithine aminotransferase
YJL088w	ARG3	ornithine carbamoyltransferase
YCL030c	HIS4	phosphoribosyl-AMP
1020000	11101	cyclohydrolase/phosphoribosyl-ATP
		pyrophosphatase/histidinol
		dehydrogenase
YDR007w	TRP1	phosphoribosylanthranilate isomerase
YGR208w	SER2	phosphoserine phosphatase
YOR184w	SER1	phosphoserine transaminase
YNL316c	PHA2	prephenate dehydratase
YBR166c	TYR1	prephenate dehydrogenase (NADP+)
YLR142w	PUT1	proline oxidase
YOL064c	MET22	protein ser/thr phosphatase
YCR054c	CTR86	putative threonine biosynthesis pathway
10110040	CITIOU	potein
YEL046c	GI Y1	required for glycine prototrophy in SHMT1
I L'LU40C	ULII	and SHMT2 double mutant
YIR034c	LYS1	saccharopine dehydrogenase
YNR050c	LYS9	
DOCOUNT	L109	saccharopine dehydrogenase (NADP*, L- glutamate forming)
		giulainale ioiniing)

YCL009c		similarity to acetolactate synthase III small
YLR089c YGL184c YHR112c YIL074c		subunit similarity to alanine transaminases similarity to cystathionine β-lyase similarity to cystathionine γ-synthases similarity to <i>E. coli</i> phosphoglycerate dehydrogenase
YGR012w YMR250w YMR062c YDL131w		similarity to <i>E. nidulans</i> cysteine synthase similarity to glutamate decarboxylases similarity to glutamate N-acetyltransferase similarity to homocitrate synthases and isopropylmalate synthases
YIL094c		similarity to isopropyl malate and tartrate
YEL038w	UTR4	dehydrogenases similarity to <i>K. oxytoca</i> enolase- phosphatase E-1
YML082w		similarity to <i>N. crassa</i> O-succinylhomoserine (thiol)-lyase
YJR130c		similarity to O-succinylhomoserine (thiol)-lyase (thiol)-lyase
YKL215c YOR280c		similarity to <i>P. aeruginosa</i> hyuA and hyuB similarity to <i>S. pombe</i> dihydrofolate reductase
YFL030w YOR108w		similarity to several transaminases strong similarity to 2-isopropylmalate synthase
YAL004w		strong similarity to <i>A. klebsiana</i> glutamate dehydrogenase
YDR111c YFR055w YHR033w YHR070w		strong similarity to alanine transaminase strong similarity to β-cystathionases strong similarity to glutamate 5-kinase strong similarity to <i>N. crassa</i> met-10+
YLL058w		protein strong similarity to <i>N. crassa</i> O-succinvlhomoserine (thiol)-lyase
YER081w		strong similarity to phosphoglycerate dehydrogenases
YJR010w YCR053w	MET3 THR4	sulphate adenylyltransferase threonine synthase (o-p-homoserine p-lyase)
YPR074c YBR117c YGL026c YML096w	TKL1 TKL2 TRP5	p-lyase) transketolase 1 transketolase 2 tryptophan synthase weak similarity to asparagine synthases
regulation	of amino	-acid metabolism

arginine metabolism transcription factor

ATP phosphoribosyltransferase

DNA-directed RNA polymerase II suppressor protein

ARS-binding factor

global regulator protein

YDR173c

YKI 112w

YER055c

YBR253w

YNL236w SIN4

ARG82

ARF1

HIS1

SRRA

## gazetteer

YFL010w-a	ALIA1	involved in ammonia regulation of amino-	other ami	no-acid m	netabolism activities	nucleot	ide met	tabolism
		acid transport	YKL157w	APE2	aminopeptidase yscll			
YIL046w YJR060w	MET30 CBF1	involved in regulation of sulphur assimilation genes kinetochore protein	YGL017w YPR069c	ATE1 SPE3	arginyl tRNA transferase putrescine aminopropyltransferase (spermidine synthase)		ADE16	de metabolism 5-aminoimidazole-4-carboxamide ribotide transformylase
YDR159w	SAC3	leucine permease transcriptional regulator	YFR018c		similarity to human glutaminyl-peptide	YGR061c	ADE6	5'-phosphoribosylformyl glycinamidine
YDR207c YKL015w	UME6 PUT3	negative transcriptional regulator positive activator of the proline utilisation			cyclotransferase	YML022w	ADT1	synthetase adenine phosphoribosyltransferase
TKLUIOW	FU13	pathway	nitroge	n and su	ılphur metabolism	YDR441c		adenine phosphoribosyltransferase
YCR028c	FEN2	similarity to allantoate permease	nitrogen	and eulnh	ur utilization	YNL220w		adenylosuccinate synthetase
YMR116c		transporter strong similarity to <i>N. crassa</i> CPC2		MET16	3'-phosphoadenylylsulphate reductase	YIR027c YIR029w	DAL1 DAL2	allantoinase allantoinase
\//\/D000	D404	protein	YIR027c	DAL1	allantoinase	YMR300c		amidophosphoribosyltransferase
YKR099w YLR098c	BAS1 CHA4	transcription factor transcription factor	YIR029w YDR242w	DAL2 AMD2	allantoinase amidase	YML035c YGR204w	ADE3	AMP deaminase C1-tetrahydrofolate synthase, cytoplasmic
YLR451w	LEU3	transcription factor	YOL058w		argininosuccinate synthetase	YBR084w	MIS1	C1-tetrahydrofolate synthase,
YMR042w	AKG8U	transcription factor involved in arginine metabolism	YLR027c YFR030w	AAT2 MET10	aspartate aminotransferase, cytosolic assimilatory sulphite reductase flavin-	YOR236w	DFR1	mitochondrial dihydrofolate reductase
YML099c	ARG81	transcription factor involved in arginine	V/// 004 -	META	binding subunit	YMR217w		GMP synthase (glutamine-hydrolyzing)
YMR043w	MCM1	metabolism transcription factor of the MADS box	YKL001c	MET14	ATP adenosine-5'-phosphosulphate 3'-phosphotransferase	YHR216w YIR031c	PUR5 DAL7	IMP dehydrogenase malate synthase 2
VIDOOO	DALOS	family	YHR176w YOR375c	FMO GDH1	flavin-containing monooxygenase	YKR080w	MTD1	methylenetetrahydrofolate dehydrogenase (NAD <sup>+</sup> )
YIR023w	DAL81	transcriptional activator for allantoin and GABA catabolic genes	YDL171c	GLT1	glutamate dehydrogenase (NADP*) glutamate synthase (NAPDPH) (GOGAT)	YAR015w	ADE1	phosphoribosylamidoimidazole-
YEL009c	GCN4	transcriptional activator of amino acid biosynthetic genes	YPR035w YJL172w	GLN1 CPS1	glutamate-ammonia ligase Gly-X carboxypeptidase YSCS	YGL234w	ADE5.7	succinocarboxamide synthase phosphoribosylamine-glycine ligase and
YDR034c	LYS14	transcriptional activator of lysine pathway	YAL062w	GDH3	NADP-glutamate dehydrogenase	TOLLOW	71020,7	phosphoribosylformylglycinamidine
YIR017c	MET28	genes transcriptional activator of sulphur amino	YDL215c	GDH2	NAD-specific glutamate dehydrogenase (NAD)	YOR128c	ADE2	cyclo-ligase phosphoribosylaminoimidazole
		acid metabolism	YLR438w	CAR2	ornithine aminotransferase			carboxylase
YNL103w	IVIĖ I 4	transcriptional activator of sulphur metabolism	YJR149w YLR089c		similarity to 2-nitropropane dioxygenase similarity to alanine transaminases	YDR408c	ADE8	phosphoribosylglycinamide formyltransferase (GART)
amino-aci	d transco		YMR293c		similarity to amidases	YKL181w	PRPS1	ribose-phosphate pyrophosphokinase
YBR068c	BAP2	amino-acid permease	YFL061w		similarity to <i>M. verrucaria</i> cyanamide hydratase	YER099c YHL011c	PRS2 PRS3	ribose-phosphate pyrophosphokinase ribose-phosphate pyrophosphokinase
YEL063c	CAN1	amino-acid permease	YFL030w		similarity to several transaminases similarity to thiosulphate	YBL068w	PRS4 SHM2	ribose-phosphate pyrophosphokinase
YBR069c YCL025c	VAP1 AGP1	amino-acid permease asparagine and glutamine permease	YOR251c		similarity to thiosulphate sulphurtransferases	YLR058c	SHIVI2	serine hydroxymethyltransferase, cytoplasmic
YPL265w		dicarboxylic amino-acid permease general amino-acid permease	YDR111c		strong similarity to alanine transaminase	YBR263w	SHM1	serine hydroxymethyltransferase,
YKR039w YDR508c	GAP1 GNP1	high-affinity glutamine permease	YER057c		strong similarity to Azotobacter nitrogen fixation vnfA protein	YNL141w		mitochondrial similarity to adenosine deaminase
YGR055w	MUP1 ALP1	high-affinity methionine permease high-affinity permease for basic amino	YIL051c		strong similarity to Azotobacter nitrogen	YBR284w		similarity to AMP deaminase
YNL270c	ALFI	acids	YJL060w		fixation vnfA protein strong similarity to kynurenine	YJL070c YLR017w		similarity to AMP deaminases similarity to human 5'-
YOL020w YGR191w	HIP1	high-affinity tryptophan transport protein histidine permease	YPL135w		aminotransferase strong similarity to nitrogen fixation	YOL061w		methylthioadenosine phosphorylase similarity to ribose-phosphate
YLR375w	STP3	involved in pre-tRNA splicing and in uptake of branched-chain amino acids	YOR226c		protein (nifU) strong similarity to nitrogen fixation	YOR280c		pyrophosphokinases similarity to <i>S. pombe</i> dihydrofolate
YDL048c	STP4	involved in pre-tRNA splicing and in uptake of branched-chain amino acids	YJR010w	MET3	proteins sulphate adenylyltransferase	YDR020c		reductase similarity to uridine kinases and
YNL268w YOR130c		lysine-specific high affinity permease member of the mitochondrial carrier family (MCF)	YJR137c YBR208c YIR032c	DUR1,2 DAL3	sulphite reductase urea amidolyase ureidoglycolate hydrolase	YLR359w		phosphoribulokinases strong similarity to adenylosuccinate lyase
YHL036w YOR348c	MUP3 PUT4	methionine permease proline and γaminobutyrate permease	YJL035c		weak similarity to <i>B. japonicum</i> nitrogen fixation protein	YMR120c		strong similarity to chicken purH bifunctional enzyme
YFL055w		similarity to Gap1p and other amino-acid permeases	YKL040c		weak similarity to nitrogen fixation protein nifU	YJR105w		strong similarity to human adenosine kinase
YDR160w YLL061w		similarity to lysine transport protein LYP1 strong similarity to amino-acid transport	regulation	of nitrog	en and sulphur utilization	YAR075w YML056c		strong similarity to IMP dehydrogenases strong similarity to IMP dehydrogenases
YPL274w		protein Gap1p strong similarity to amino-acid transport	YGR019w	UGA1	4-aminobutyrate aminotransferase (GABA transaminase)	YAR073w YLR432w	FUN63	strong similarity to IMP dehydrogenases strong similarity to IMP dehydrogenases,
YDR046c	(PAP1)	proteins	YPL111w YKL112w	CAR1 ABF1	arginase ARS-binding factor	YLR209c		Pur5p and YML056c
	(FAFI)	strong similarity to amino-acid transport proteins	YNL216w	RAP1	DNA-binding protein with repressor and			strong similarity to purine-nucleoside phosphorylases
YBR132c		strong similarity to amino-acid permeases	YFL010w-a	AUA1	activator activity involved in ammonia regulation of amino	YBR208c YIR032c	DUR1,2 DAL3	urea amidolyase ureidoglycolate hydrolase
amino-aci					acid transport			leotide metabolism
YPL111w YDR321w	CAR1 ASP1	argınase asparaginase	YIR030c YBR213w	DCG1 MET8	involved in nitrogen-catabolite metabolism involved in the expression of PAPS	YBL039c		CTP synthase 1
YOR375c	GDH1	glutamate dehydrogenase (NADP+)			reductase and sulphite reductase	YJR103w	URA8 DCD1	CTP synthase 2 deoxycytidylate deaminase
YMR189w YDR019c	GCV1	glycine decarboxylase subunit glycine decarboxylase T subunit	YDR207c YNL229c	UME6 URE2	negative transcriptional regulator nitrogen catabolite repression regulator	YHR144c YLR420w	URA4	dihydroorotase
YDR272w YOR040w		glyoxalase II glyoxalase II	YEL062w YNL183c	NPR2 NPR1	nitrogen permease regulator ser/thr protein kinase	YKL216w YJR057w	URA1 CDC8	dihydroorotate dehydrogenase dTMP kinase
YLR155c	ASP3A	L-asparaginase II	YCR028c	FEN2	similarity to allantoate permease	YBR252w	DUT1	dUTP pyrophosphatase, mitochondrial
YLR157c YLR158c	ASP3B ASP3C	L-asparaginase II L-asparaginase II	YLR013w		transporter similarity to nitrogen regulatory proteins	YJL130c	URA2	multifunctional pyrimidine biosynthesis protein
YLR160c	ASP3D	L-asparaginase II	YGL254w	FZF1	sulphite resistance protein	YML106w		orotate phosphoribosyltransferase 1
YCL064c YAL062w	CHA1 GDH3	L-serine/L-threonine deaminase NADP-glutamate dehydrogenase	YFL021w YER040w	GAT1 GLN3	transcription factor for nitrogen regulation transcription factor for positive nitrogen	YMR271c YEL021w	URA10 URA3	orotate phosphoribosyltransferase 2 orotidine-5'-phosphate decarboxylase
YDL215c	GDH2	NAD-specific glutamate dehydrogenase			regulation	YFL058w	THI5	pyrimidine biosynthesis protein
YKL184w		(NAD) ornithine decarboxylase	YMR042w		transcription factor involved in arginine metabolism	YKL181w YER099c	PRPS1 PRS2	ribose-phosphate pyrophosphokinase ribose-phosphate pyrophosphokinase
YLR142w YLR180w	PUT1 SAM1	proline oxidase S-adenosylmethionine synthetase 1	YML099c	ARG81	transcription factor involved in arginine metabolism	YHL011c YBL068w	PRS3 PRS4	ribose-phosphate pyrophosphokinase ribose-phosphate pyrophosphokinase
YDR502c	SAM2	S-adenosylmethionine synthetase 2	YMR043w	MCM1	transcription factor of the MADS box	YOL061w	rno4	similarity to ribose-phosphate
YIL167w YDR294c	SDL1	serine dehydratase similarity to glutamate decarboxylases	YIR023w	DAL81	family transcriptional activator for allantoin and	YOR280c		pyrophosphokinases similarity to <i>S. pombe</i> dihydrofolate
YJR078w		similarity to indoleamine 2,3-dioxygenase			GABA catabolic genes			reductase
YIL042c		similarity to rat branched-chain α-ketoacid dehydrogenase kinase	YDL170w	UGA3	transcriptional activator for GABA catabolic genes	YLR245c		strong similarity to <i>B. subtilis</i> cytidine deaminase
YGL202w		similarity to rat kynurenine/	YNL103w	MET4	transcriptional activator of sulphur	YNL332w		strong similarity to Thi5p, YJR156c,
YHR137w		α-aminoadipate aminotransferase similarity to rat kynurenine/	YKR034w	DAL80	metabolism transcriptional repressor for allantoin and			YDL244w and <i>A. parasiticus</i> , <i>S. pombe</i> Nmt1p
		α-aminoadipate aminotransferase			GABA catabolic genes	YDL244w		strong similarity to Thi5p, YJR156c,
YFL030w YDR111c		similarity to several transaminases strong similarity to alanine transaminase			ur transport			YNL332w and <i>A. parasiticus</i> , <i>S. pombe</i> nmt1 protein
YBR006w		strong similarity to <i>E. coli</i> succinate semialdehyde dehydrogenase	YGR121c	MEP1	ammonia permease of high capacity and moderate affinity	YJR156c	THI11	thiamine regulated gene, homologous to nmt1a in S. pombe
YAL044c	GCV3	strong similarity to human glycine	YNL142w	MEP2	high-affinity low-capacity ammonia	YHR128W	FUR1	uracil phosphoribosyltransferase
YIL168w	SDL1	cleavage system protein H strong similarity to L-serine dehydratase	YBR294w	SUL1	permease high-affinity sulphate transport protein	YNR012w YKL024c	URK1 URA6	uridine kinase uridine-monophosphate kinase
YLR231c		Cha1p strong similarity to rat kynureninase	YPR003c YPR138c	MEP3	similarity to sulphate transporter proteins strong similarity to ammonium transport	deoxyribo	nucleotid	le metabolism
YKL218c YBR208c	DUR1,2	strong similarity to threonine dehydratase urea amidolyase	YLR092w	SEL2	proteins strong similarity to Sul1p	YDR513w YER070w	TTR1 RNR1	glutaredoxin ribonucleoside-diphosphate reductase,
וטוובטטט	۵,۱۱۱٫۷	a.ca armadiyado	YHL016c	DUR3	urea transport protein	1210/000	1114111	large subunit

YJL026w	RNR2	ribonucleoside-diphosphate reductase,	YHR043c	DOG2	2-deoxyglucose-6-phosphate	YPR001w		citrate (si)-synthase, mitochondrial
YGR180c	RNR4	small subunit ribonucleotide reductase small subunit	YMR282c	AFP2	phosphatase 2'-O-ribosyl phosphate transferase	YCR005c YML086c	CIT2 ALO	citrate (si)-synthase, peroxisomal D-arabinino-1,4-lactone oxidase
YIL066c	RNR3	ribonucleotide reductase, repair inducible	YBR092c	PHO3	constitutive acid phosphatase	YNL071w	LAT1	dihydrolipoamide S-acetyltransferase
YBR014c		large subunit similarity to glutaredoxin	YHR201c YBR011c	PPX1 IPP1	exopolyphosphatase inorganic pyrophosphatase, cytoplasmic	YDL174c	DLD1	D-lactate ferricytochrome c oxidoreductase (D-LCR)
YPL059w		similarity to glutaredoxins	YMR267w		inorganic pyrophosphatase, cytopiasmic inorganic pyrophosphatase, mitochondrial	YER062c	HOR2	DL-glycerol phosphatase
YOR269w	PAC1	similarity to human LIS-1 protein	YBR093c		repressible acid phosphatase	YIL053w	RHR2	DL-glycerol phosphatase
YDL010w		similarity to hypothetical protein YBR014c and glutaredoxins	YAR071w YHR215w		secreted acid phosphatase secreted acid phosphatase	YPL227c YPR183w	ALG5 DPM1	dolichol-P-glucose synthetase dolichyl-phosphate β-D-
YCL035c		strong similarity to glutaredoxin	YDL024c		strong similarity to acid phosphatase			mannosyltransferase
YDR353w		strong similarity to thioredoxin reductase (NADPH)	YNL330c YBR243c	RPD3 ALG7	transcription modifier protein UDP-N-acetylglucosamine-1-phosphate	YJR143c	PMT4	dolichyl-phosphate-mannose-protein O-mannosyl transferase
YHR106w		strong similarity to thioredoxin reductases	TBILLIOO	/ ILC/	transferase	YOR095c	RKI1	D-ribose-5-phosphate ketol-isomerase
YOR074c	CDC21	thymidylate synthase	regulation	of phosi	phate utilization	YJL121c YGR282c	POS18 BGL2	D-ribulose-5-phosphate 3-epimerase endo-1,3glucanase of the cell wall
		ic and unusual nucleotides	YOL001w	PHO80	cyclin	YLR286c	CTS1	endochitinase
YJL005w YCL050c	CYR1 APA1	adenylate cyclase ATP adenylyltransferase I	YGR233c YPL031c	PHO81 PHO85	cyclin-dependent kinase inhibitor cyclin-dependent protein kinase	YGR254w	ENO1	enolase I (2-phosphoglycerate dehydratase)
	APA2	ATP adenylyltransferase II	YML121w		GTP-binding protein	YHR174w	ENO2	enolase II (2-phosphoglycerate
YOL081w	IRA2	GTPase-activating protein for RAS	YDL106c	GRF10	homeodomain protein	VODOOO.	E004	dehydratase)
YOR360c	PDE2	proteins high affinity 3',5'-cyclic-nucleotide	YBR106w YFR034c	PHO88 PHO4	involved in phosphate transport transcription factor	YOR393w YPL281c	ERR1 ERR2	enolase-related protein enolase-related protein
\/DI 010	51101	phosphodiesterase	phoophot	e transpo		YOR190w	SPR1	exo-1,3glucanase
YPL212c YGL063w	PUS1 PUS2	pseudouridine synthase 1 pseudouridine synthase 2	YLR348c	e transpo	dicarboxylate carrier protein	YDR261c YLR300w	EXG2 EXG1	exo-1,3-glucanase minor isoform exo-1,3-glucanase(I/II), major isoform
			YML123c	PHO84	high-affinity inorganic phosphate/H*	YIR019c	STA1	extracellular α-1,4-glucan glucosidase
YOL081w		otide metabolism GTPase-activating protein for RAS	YJL117w	PHO86	symporter inorganic phospate transporter	YLR377c YJL155c	FBP1 FBP26	fructose-1,6-bisphosphatase fructose-2,6-bisphosphatase
		proteins	YBR106w	PH088	involved in phosphate transport	YKL060c	FBA1	fructose-bisphosphate aldolase
YOR101w YNL098c	RAS1 RAS2	GTP-binding protein GTP-binding protein	YCR037c	PH087	member of the phosphate permease family	YDL049c YBR020w	KNH1 GAL1	functional homologue of Kre9p galactokinase
YDL106c	GRF10	homeodomain protein	YJR077c	MIR1	phosphate transport protein,	YDR009w	GAL3	galactokinase
YGL248w	PDE1	low-affinity 3',5'-cyclic-nucleotide phosphodiesterase	YNR013c		mitochondrial (MCF) similarity to membrane protein Pho87p	YOR120w	GCY1	galactose-induced protein of aldo/keto reductase family
YNL076w	MKS1	negative regulator of RAS-cAMP pathway			and hypothetical protein YJL198w	YPR159w	KRE6	glucan synthase subunit
YJL096w		putative regulator of purine and/or pyrimidine biosynthesis	YCR098c	GIT1	similarity to phosphate transporter proteins	YGR143w YKL104c	SKN1 GFA1	glucan synthase subunit glucosamine-fructose-6-phosphate
YOL110w	SHR5	RAS suppressor	YER053c		strong similarity to mitochondrial			transaminase
YKR099w	BAS1 PPR1	transcription factor	YJL198w		phosphate carrier protein	YNL241c YBR196c	ZWF1 PGI1	glucose-6-phosphate dehydrogenase
YLR014c	rrni	transcription factor regulating pyrimidine pathway	YBR296c		strong similarity to Pho87p strong similarity to phosphate-repressible	YBR229c	ROT2	glucose-6-phosphate isomerase glucosidase II, catalytic subunit
YIR023w	DAL81	transcriptional activator for allantoin and			phosphate permease	YOR002w	ALG6	glucosyltransferase
YNL314w	DAL82	GABA catabolic genes transcriptional activator for allantoin	other pho	sphate-m	etabolism activities	YOR067c YJL052w	ALG8 TDH1	glucosyltransferase glyceraldehyde-3-phosphate
		catabolic genes	YDL236w		4-nitrophenylphosphatase			dehydrogenase 1
polynucle	otide deg	radation	YOR008c	SLGT	weak similarity to <i>L. mexicana</i> Imsap2 gene	YJR009c	TDH2	glyceraldehyde-3-phosphate dehydrogenase 2
YMR287c	MSU1	3'-5' exonuclease for RNA 3' ss-tail,				YGR192c	TDH3	glyceraldehyde-3-phosphate
YPL029w	SUV3	mitochondrial ATP-dependent RNA helicase,	carbon	yarater	metabolism	YHL032c	GUT1	dehydrogenase 3 glycerol kinase
		mitochondrial		rate utiliza		YDL022w	GPD1	glycerol-3-phosphate dehydrogenase
YOR033c YKL149c	DHS1 DBR1	exonuclease, interacting with Msh2p lariat-debranching enzyme	YLR342w YGR032w		1,3—D-glucan synthase, catalytic subunit 1,3—D-glucan synthase, subunit	YOL059w	GPD3	(NAD*), cytoplasmic glycerol-3-phosphate dehydrogenase
YGL173c	KEM1	multifunctional nuclease	YEL011w	GLC3	1,4-glucan branching enzyme (glycogen			(NAD <sup>+</sup> ), mitochondrial
YLR363c YJR132w	NMD4 NMD5	Nam7p/Upf1p-interacting protein Nam7p/Upf1p-interacting protein	YHR044c	DOG1	branching enzyme) 2-deoxyglucose-6-phosphate	YIL155c	GUT2	glycerol-3-phosphate dehydrogenase, mitochondrial
YMR080c	NAM7	nonsense-mediated mRNA decay protein			phosphatase	YPR160w	GPH1	glycogen phosphorylase
YGR072w YHR077c	UPF3 NMD2	nonsense-mediated mRNA decay protein nonsense-mediated mRNA decay protein	YHR043c	DOG2	2-deoxyglucose-6-phosphate phosphatase	YFL014w YFR053c	HSP12 HXK1	heat-shock protein hexokinase I
		2	YIL125w	KGD1	2-oxoglutarate dehydrogenase complex	YGL253w	HXK2	hexokinase II
YJL208c YMR234w	NUC1	nuclease, mitochondrial ribonuclease H	YDR148c	KGD2	E1 component 2-oxoglutarate dehydrogenase complex	YDL013w YDL182w	HEX3 LYS20	hexose metabolism-related protein
YPL123c	וחווחו	similarity to ribonucleases	1 DN 1460		E2 component	YOR126c	EST2	homocitrate synthase isoamyl acetate hydrolytic enzyme
YGR195w		weak similarity to <i>P. aeruginosa</i> RNase PH	YGR240c	PFK1 PFK2	6-phosphofructokinase, α subunit	YNL037c	IDH1	isocitrate dehydrogenase (NAD*) subunit
		• • •	YMR205c YIL107c	PFK26	6-phosphofructokinase, β subunit 6-phosphofructose-2-kinase, isoenzyme 1	YOR136w	IDH2	<ol> <li>mitochondrial isocitrate dehydrogenase (NAD<sup>+</sup>) subunit</li> </ol>
nucleotide			YOL136c		6-phosphofructose-2-kinase, isoenzyme 2	V/DI 000	IDD4	2, mitochondrial
YMR056c YBL030c		ADP/ATP carrier protein (MCF) ADP/ATP carrier protein (MCF)	YHR183w YBR001c	NTH2	6-phosphogluconate dehydrogenase α,α-trehalase	YDL066w	IDP1	isocitrate dehydrogenase (NADP*), mitochondrial
YBR085w	AAC3	ADP/ATP carrier protein (MCF)	YDR074w		α,α-trehalose-phosphate synthase, 105K	YLR174w	IDP2	isocitrate dehydrogenase, cytosolic
YER056c YER060w	FCY2 FCY21	purine-cytosine permease purine-cytosine permease	YMR261c	TPS3	subunit α,α-trehalose-phosphate synthase, 115K	YER065c YOR336w	ICL1 KRE5	isocitrate lyase killer toxin-resistance protein
YOR222w		similarity to ADP/ATP carrier proteins			subunit	YML054c	CYB2	lactate dehydrogenase cytochrome b2
YPR011c		similarity to ADP/ATP carrier proteins and Graves disease carrier protein	YML100w	TSL1	α,α-trehalose-phosphate synthase, 123K subunit	YDL168w YOL126c	SFA1 MDH2	long-chain alcohol dehydrogenase malate dehydrogenase, cytoplasmic
YOR071c		similarity to allantoin or uracil transport	YBR126c	TPS1	α,α-trehalose-phosphate synthase, 56K	YKL085w	MDH1	malate dehydrogenase, mitochondrial
YOR192c		proteins similarity to allantoin or uracil transport	YJR131w	MNS1	subunit α-1,2-mannosidase	YDL078c YNL117w	MDH3 MLS1	malate dehydrogenase, peroxisomal malate synthase 1
		proteins	YDR483w	KRE2	α-1,2-mannosyltransferase	YIR031c	DAL7	malate synthase 2
YLR237w YGR096w		similarity to allantoin transport protein similarity to bovine Graves disease carrier	YER001w YGL038c	MNN1 OCH1	α-1,3-mannosyltransferase α-1,6-mannosyltransferase	YDL055c YER003c	PSA1 PMI40	mannose-1-phosphate guanyltransferase mannose-6-phosphate isomerase
		protein	YAL054c	ACS1	acetyl-CoA synthetase	YGL065c	ALG2	mannosyltransferase
YHR002w		similarity to bovine mitochondrial carrier protein/Grave's disease carrier protein	YLR153c YPR026w	ACS2 ATH1	acetyl-CoA synthetase acid trehalase, vacuolar	YNL219c YKR061w	ALG9 KTR2	mannosyltransferase mannosyltransferase
YGL186c		similarity to hypothetical protein YER060w	YBR299w	MAL32	α-glucosidase	YDL095w	PMT1	mannosyltransferase
YBL042c		and weak similarity to Fcy2p strong similarity to allantoin and uracil	YGR292w YOR377w		α-glucosidase of the MAL1 locus alcohol acetyltransferase	YAL023c YOR321w	PMT2 PMT3	mannosyltransferase mannosyltransferase
		transport proteins	YOL086c	ADH1	alcohol dehydrogenase I	YBL082c	RHK1	mannosyltransferase
YER060w-a YBR021w		strong similarity to Fcy2p uracil permease	YMR303c YMR083w		alcohol dehydrogenase II alcohol dehydrogenase III	YJL139c YJL153c	YUR1 INO1	mannosyltransferase myo-inositol-1-phosphate synthase
			YGL256w		alcohol dehydrogenase IV	YPL175w	SPT14	N-acetylglucosaminyltransferase
other nuc YDR226w		etabolism activities adenylate kinase, cytosolic	YBR145w YGR177c		alcohol dehydrogenase V alcohol O-acetyltransferase	YDR001c YPR006c	NTH1 ICL2	neutral trehalase (α,α-trehalase) non-functional isocitrate lyase
YER170w	ADK2	adenylate kinase, mitochondrial	YCL040w	GLK1	aldohexose specific glucokinase	YJL002c	OST1	oligosaccharyltransferase α subunit
YDR454c YKL067w	GUK1 YNK1	guanylate kinase nucleoside diphosphate kinase	YGL156w YGL027c	AMS1 CWH41	α-mannosidase β-1,6-glucan assembly protein	YEL002c YMR149w	WBP1 SWP1	oligosaccharyltransferase β subunit oligosaccharyltransferase δ subunit
YDL125c	HNT1	similarity to protein kinase C inhibitor-I	YHR101c	BIG1	big cells phenotype	YOR103c	OST2	oligosaccharyltransferase ε subunit
YDR305c	HNT2	strong similarity to S. pombe diadenosine	YBR110w	ALG1 MIS1	β-mannosyltransferase	YOR085w	OST3	oligosaccharyltransferase γ subunit
		5',5"'-P1,P4-tetraphosphate asymmetrical hydrolase	YBR084w		C1-tetrahydrofolate synthase, mitochondrial	YDL232w YGL022w	OST4 STT3	oligosaccharyltransferase subunit oligosaccharyltransferase subunit
nhoonb	ato mo	,	YNL322c	KRE1	cell-wall protein	YEL058w	PCM1	phosphoacetylglucosamine mutase
		abolism	YJL174w YJL099w	KRE9 CHS6	cell-wall synthesis protein chitin biosynthesis protein	YKR097w YMR105c	PCK1 PGM2	phosphoenolpyruvate carboxykinase phosphoglucomutase, major isoform
phosphat			YNL192w	CHS1	chitin synthase I	YKL127w	PGM1	phosphoglucomutase, minor isoform
YHR044c	DUG1	2-deoxyglucose-6-phosphate phosphatase	YBR038w YBR023c	CHS2 CHS3	chitin synthase II chitin synthase III	YGR256w YCR012w	GND2 PGK1	phosphogluconate dehydrogenase phosphoglycerate kinase
		priospriatase	YNR001c	CIT1	citrate (si)-synthase, mitochondrial	YKL152c	GPM1	phosphoglycerate mutase

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YOL056w YFL045c	GPM3 SEC53	phosphoglycerate mutase phosphomannomutase	YJL218w		strong similarity to <i>E. coli</i> galactoside O-acetyltransferase	YCR081w	SRB8	DNA-directed RNA polymerase II holoenzyme and Kornberg's mediator
YCR034w	GNS1	probable 1,3glucan synthase subunit	YDR248c		strong similarity to E. coli thermoresistant			(SRB) subcomplex subunit
YIL045w YIL085c	PIG2 KTR7	Protein interacting with Gsy2p putative α-1,2-mannosyltransferase	YIL172c		gluconokinase strong similarity to Fsp2p	YNL025c	SSN8	DNA-directed RNA polymerase II holoenzyme and Kornberg's mediator
YNL029c	KTR5	putative mannosyltransferase	YDL037c		strong similarity to glucan			(SRB) subcomplex subunit, cyclin C
YGR199w YGL062w		putative mannosyltransferase pyruvate carboxylase, isozyme 1	YDR516c		1,4—glucosidase strong similarity to glucokinase	YLR071c	RGR1	homologue DNA-directed RNA polymerase II
YBR218c	PYC2	pyruvate carboxylase, isozyme 2	YOR299w		strong similarity to hypothetical protein			holoenzyme subunit
YDR081c YLR044c	PDC2 PDC1	pyruvate decarboxylase regulatory protein pyruvate decarboxylase, isozyme 1	YMR237w		YMR237w and similarity to Chs6p strong similarity to hypothetical protein	YBR253w	SRB6	DNA-directed RNA polymerase II suppressor protein
YLR134w	PDC5	pyruvate decarboxylase, isozyme 2			YOR299w and similarity to CHS6 protein	YOR047c	STD1	dosage-dependent modulator of glucose
YGR087c YER178w	PDC6 PDA1	pyruvate decarboxylase, isozyme 3 pyruvate dehydrogenase (lipoamide)	YNL009w		strong similarity to isocitrate dehydrogenase	YJL155c	FBP26	repression fructose-2,6-bisphosphatase
		α subunit	YJL216c		strong similarity to Mal62p	YPL037c	EGD1	GAL4 DNA-binding enhancer protein
YBR221c	PDB1	pyruvate dehydrogenase (lipoamide) β subunit	YGR287c YOR099w	KTR1	strong similarity to maltase strong similarity to mannosyltransferases	YDR009w YLL016w	GAL3 SDC25	galactokinase GDP/GTP exchange factor
YGR193c	PDX1	pyruvate dehydrogenase complex protein	YDR368w	YPR1	strong similarity to members of the	YLR310c	CDC25	GDP/GTP exchange factor for Ras1p and
YAL038w	CDC19	X pyruvate kinase	YDL021w	GPM2	aldo/keto reductase family strong similarity to phosphoglycerate	YGR070w	ROM1	Ras2p GDP/GTP exchange protein for Rho1p
YNL048w	ALG11	required for asparagine-linked	VA ADOOD		mutase Gpm1p	YLR371w	ROM2	GDP/GTP exchange protein for Rho1p
YCR036w	RBK1	glycosylation ribokinase	YMR323w		strong similarity to phosphopyruvate hydratases	YDR176w	NGG1	general transcriptional adaptor or co- activator
YJL137c	GLG2	self-glucosylating initiator of glycogen synthesis	YJR153w YDL080c		strong similarity to polygalacturonases strong similarity to pyruvate	YER054c YNL236w	GIP2 SIN4	Glc7p-interacting protein global regulator protein
YMR306w		similarity to 1,3glucan synthases			decarboxylases	YHL025w	SNF6	global transcription activator
YAL060w	FUN49	similarity to alcohol/sorbitol dehydrogenase	YOR347c YGR244c		strong similarity to pyruvate kinase strong similarity to rumen fungus	YER027c YNL199c	GAL83 GCR2	glucose repression protein glycolytic genes transcriptional activator
YAL061w	FUN50	similarity to alcohol/sorbitol			β-succinyl-CoA synthetase	YOR101w	RAS1	GTP-binding protein
YMR318c		dehydrogenase similarity to alcohol-dehydrogenase	YKL029c		strong similarity to <i>S. pombe</i> malate oxireductase	YNL098c YPR165w	RAS2 RHO1	GTP-binding protein GTP-binding protein of the RHO subfamily
YDL124w		similarity to aldose reductases	YBL001c		strong similarity to S. xylosus glucose			of RAS-like proteins
YHR204w YPL088w		similarity to α-mannosidases similarity to aryl-alcohol dehydrogenases	YLR164w		kinase strong similarity to Sdh4p	YNL090w	RHO2	GTP-binding protein of the RHO subfamily of RAS-like proteins
YML070w		similarity to C. feundii dihydroxyacetone	YDL246c		strong similarity to Sor1p	YDR420w	HKR1	Hansenula Mrakll k9 killer toxin-resistance
YIL124w		kinase similarity to <i>C. perfringens</i> nanH protein	YJL045w		strong similarity to succinate dehydrogenase flavoprotein	YGL253w	HXK2	protein hexokinase II
YDR371w		similarity to chitinases	YGR043c		strong similarity to transaldolase	YPL002c	SNF8	involved in glucose derepression
YIR036c		similarity to <i>E. coli</i> 3-ketoacyl-ACP reductase	YNR071c		strong similarity to UDP-glucose 4-epimerase Gal10p	YOR125c YML048w	CAT5 EFF2	involved in glucose repression involved in glucose repression
YBR149w		similarity to Gcy1p and aldose reductases	YDR384c		strong similarity to Y. lipolytica GPR1	YNL201c		involved in regulation of carbon
YBR056w YIL169c		similarity to glucan 1,3—glucosidase similarity to glucan 1,4—glucosidase	YHR210c		gene strong similarity UDP-glucose-4-epimerase	YGR227w	DIE2	metabolism ITR1 expression promoting protein
YOL155c		similarity to glucan 1,4glucosidase Mal5p	YKL148c YDR178w	SDH1 SDH4	succinate dehydrogenase flavoprotein succinate dehydrogenase membrane	YBR297w YGR288w	MAL33	maltose fermentation regulatory protein maltose pathway regulatory protein
YNL274c		similarity to glycerate- and formate-			anchor subunit for Sdh2p	YLR131c	ACE2	metallothionein expression activator
YPL113c		dehydrogenases similarity to glycerate dehydrogenases	YIL162w YJR075w	SUC2 HOC1	sucrose hydrolyzing enzyme suppressor of pkc1	YDR422c YML051w	SIP1 GAL 80	multicopy suppressor of <i>snf1</i> negative regulator for expression of
YPR184w		similarity to glycogen debranching	YLR354c	TAL1	transaldolase			galactose-induced genes
YDL131w		enzymes similarity to homocitrate synthases and	YPR074c YBR117c	TKL1 TKL2	transketolase 1 transketolase 2	YNL076w YIL119c	MKS1 RPI1	negative regulator of RAS-cAMP pathway negative regulator of RAS-cAMP pathway
		isopropylmalate synthases	YDR050c	TPI1	triose-phosphate isomerase	YLR025w	SNF7	nuclear protein
YJR096w YKR096w		similarity to <i>Leishmania</i> reductase similarity to mitochondrial aldehyde	YBR019c YBR018c	GAL10 GAL7	UDP-glucose 4-epimerase UDP-glucose-hexose-1-phosphate	YGL115w YLR273c	SNF4 PIG1	nuclear regulatory protein protein interacting with Gsy2p
		dehydrogenase Ald1p			uridylyltransferase	YIL045w	PIG2	protein Interacting with Gsy2p
YGL257c YIL014w		similarity to Mnn1p similarity to Mnn1p	YFR015c	GSY1	UDP-glucose-starch glucosyltransferase, isoform 1	YDL006w YDL134c	PTC1 PPH21	protein ser/thr phosphatase 2c protein ser/thr phosphatase PP2A-1
YEL020c		similarity to O. formigenes oxalyl-CoA	YLR258w	GSY2	UDP-glucose-starch glucosyltransferase,	YDL188c	PPH22	protein ser/thr phosphatase PP2A-2
YDL093w	PMT5	decarboxylase similarity to O-mannosyltransferases	YBR243c	ALG7	isoform 2 UDP-N-acetylglucosamine-1-phosphate	YBL061c	SKT5	protoplast regeneration and killer toxin resistance protein
		Pmt1p-Pmt4p			transferase	YOL110w	SHR5	RAS suppressor
YMR278w YDR307w		similarity to phosphomannomutases similarity to Pmt1p	YKL035w	UGP1	UTP-glucose-1-phosphate uridylyltransferase	YJR095w YKL038w	ACR1 RGT1	regulator of acetyl-CoA synthetase activity regulator of glucose induced genes
YDR380w YDR245w	A 40/0/14 O	similarity to pyruvate decarboxylases	YKR043c		weak similarity to phosphoglycerate	YDR028c	REG1	regulatory subunit for protein
YDR245W	IVIIVIVIO	similarity to S. pombe galactosyltransferase	YOR283w		mutase weak similarity to phosphoglycerate	YMR311c	GLC8	phosphatase Glc7p regulatory subunit for protein ser/thr
YLR070c YNR059w		similarity to sugar dehydrogenases			mutases	YBR050c	REG2	phosphatase Glc7p
YHL012w		similarity to to α-1,3-mannosyltransferase similarity to UDP glucose	regulation	of carbo	hydrate utilization	TENUOUC	nEG2	regulatory subunit of type I protein phosphatase
YJR159w	SOR1	pyrophosphorylase sorbitol dehydrogenase	YGR240c YMR205c		6-phosphofructokinase, α subunit 6-phosphofructokinase, β subunit	YDR277c YNR052c	MTH1 POP2	repressor of hexose transport genes required for glucose derepression
YIL099w	SGA1	sporulation specific glucan	YIL107c	PFK26	6-phosphofructose-2-kinase, isoenzyme 1	YJR090c	GRR1	required for glucose repression and for
YER096w	SHC1	1,4—glucosidase sporulation-specific protein	YOL136c YBR126c	PFK27 TPS1	6-phosphofructose-2-kinase, isoenzyme 2 α,α-trehalose-phosphate synthase, 56K	YGL252c	RTG2	glucose and cation transport retrograde regulation protein
YLR307w	CDA1	sporulation-specific chitin deacetylase			subunit	YJR076c	CDC11	septin
YLR308w YNL331c	CDA2	sporulation-specific chitin deacetylase strong similarity to aryl-alcohol reductase	YHR047c YGR229c	AAP1 KNR4	alanine/arginine aminopeptidase β-1,3-glucan synthesis protein	YHR107c YER133w	CDC12 GLC7	septin ser/thr phosphoprotein phosphatase 1,
YCR107w		strong similarity to aryl-alcohol reductases	YOL067c	RTG1	basic helix-loop-helix transcription factor			catalytic subunit
YPL017c		strong similarity to dihydrolipoamide dehydrogenases	YOR344c YGR166w	TYE7 KRE11	basic helix-loop-helix transcription factor β-glucan synthesis-associated protein	YOR178c	GAC1	ser/thr phosphoprotein phosphatase 1, regulatory subunit
YBR205w	KTR3	strong similarity to	YBL103c	RTG3	bHLH/zip transcription factor	YLR113w	HOG1	ser/thr protein kinase of MAP kinase
YBR199w	KTR4	α-1,2-mannosyltransferase strong similarity to	YPL161c YGL209w	BEM4 MIG2	bud emergence protein C2H2 zinc-finger protein	YLR345w		(MAPK) family similarity to 6-phosphofructo-2-kinase
		α-1,2-mannosyltransferase	YIL033c	SRA1	cAMP dependent protein kinase,	YCR028c	FEN2	similarity to allantoate permease
YPL053c	KTR6	strong similarity to α-1,2-mannosyltransferase Kre2p	YDR477w	SNF1	regulatory subunit carbon catabolite derepressing ser/thr	YFL053w		transporter similarity to <i>C. freundii</i> dihydroxyacetone
YJL221c YOL157c	FSP2	strong similarity to α-D-glucosidase strong similarity to α-glucosidases	YCR002c	CDC10	protein kinase cell division control protein	YDL225w		kinase similarity to Cdc11p, Cdc3p and human
YCR105w		strong similarity to alcohol	YLR330w	CHS5	chitin synthesis protein			CDC10 protein
YDL243c		dehydrogenases strong similarity to aryl-alcohol	YDR073w	SNF11	component of SWI/SNF transcription activator complex	YHR193c YDL203c	EGD2	similarity to human α-NAC similarity to Skt5p
		dehydrogenase	YOR290c	SNF2	component of SWI/SNF transcription	YNL257c	SIP3	Snf1p protein kinase interacting protein
YJR155w		strong similarity to aryl-alcohol dehydrogenase	YBR289w	SNF5	activator complex component of SWI/SNF transcription	YLR150w	MPT4	specific affinity for guanine-rich quadruplex nucleic acids
YFL056c		strong similarity to aryl-alcohol			activator complex	YFL052w		strong similarity to Mal63p, Mal23p and
YFL057c		dehydrogenases strong similarity to aryl-alcohol	YPL016w	SWI1	component of SWI/SNF transcription activator complex	YHR155w		Mal33p strong similarity to Snf1p-interacting
		dehydrogenases	YPL042c	SSN3	cyclin-dependent ser/thr protein kinase			protein Sip3p
YOL165c		strong similarity to aryl-alcohol dehydrogenases	YNL216w	RAP1	DNA-binding protein with repressor and activator activity	YNR002c	FUN34	strong similarity to <i>Y. lipolytica</i> glyoxylate pathway regulator GPR1
YKR027w		strong similarity to Chs6p	YOL051w	GAL11	DNA-directed RNA polymerase II	YCR010c		strong similarity to Y. lipolytica GPR1
YHR104w		strong similarity to D-xylose 1-dehydrogenase			holoenzyme and Kornberg's mediator (SRB) subcomplex subunit	YIL154c	(IMP2)	protein and Fun34p sugar utilization regulatory protein
YEL070w		strong similarity to E. coli D-mannonate	YDR443c	SCA1	DNA-directed RNA polymerase II	YPL026c	SKS1	suppressor kinase of snf3
YNR073c		oxidoreductase strong similarity to <i>E. coli</i> D-mannonate			holoenzyme and Kornberg's mediator (SRB) subcomplex subunit	YPL129w	ANC1	TFIIF subunit (transcription initiation factor), 30K
		oxidoreductase, identical to YEL070w				YPL248c YMR125w	GAL4 GCR3	transcription factor transcription factor for glycolytic genes
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YMR280c	CAT8	transcription factor involved in	YPL069c	BTS1	geranylgeranyl diphosphate synthase	YGL162w		hypoxic protein involved in sterol uptake
YMR043w	MCM1	gluconeogenesis transcription factor of the MADS box	YGL126w YOR237w	SCS3 HES1	inositol phospholipid synthesis protein involved in ergosterol biosynthesis	YMR208w YHL020c	ERG12 OPI1	mevalonate kinase negative regulator of phospholipid
TIVITIOTOVV	IVICIVII	family	YPL145c	KES1	involved in ergosterol biosynthesis	TTTLOZOC	OIII	biosynthesis pathway
YJL176c	SWI3	transcription regulatory protein	YPL117c	IDI1	isopentenyl-diphosphate δ-isomerase	YDR207c		negative transcriptional regulator
YPL075w	GCR1	transcriptional activator	YHR072w		lanosterol synthase	YAL051w	OAF1	peroxisome proliferating transcription
YOL116w YKL062w	MSN1 MSN4	transcriptional activator transcriptional activator	YMR246w YNL219c	ALG9	long-chain-fatty-acid-CoA ligase mannosyltransferase	YOR363c	PIP2	factor peroxisome proliferating transcription
YGL035c	MIG1	transcriptional repressor	YJR073c	OPI3	methylene-fatty-acyl-phospholipid	10110000	1112	factor
YIL147c	SLN1	two-component signal transducer			synthase	YNL169c	PSD1	phosphatidylserine decarboxylase 1
YLR006c	SSK1	two-component signal transducer	YNR043w	MVD1	mevalonate pyrophosphate	YAL013w	DEP1	regulator of phospholipid metabolism
YJL128c	PBS2	tyrosine protein kinase of the MAP kinase kinase family	YPL076w	GPI2	decarboxylase N-acetylglucosaminyl-phosphatidylinositol	YMR207c YCR028c	FEN2	similarity to acetyl-CoA carboxylase similarity to allantoate permease
YLR258w	GSY2	UDP-glucose-starch glucosyltransferase,	11 207000	GI IL	biosynthetic protein	10110200	1 2142	transporter
		isoform 2	YPL175w	SPT14	N-acetylglucosaminyltransferase	YMR043w	MCM1	transcription factor of the MADS box
YDR216w	ADR1	zinc-finger transcription factor	YGR157w	CHO2	phosphatidylethanolamine	YOL004w	CINIO	family transcription regulatory protein
carbohyd	Irate trans	sport	YDL142c	PGS1	N-methyltransferase phosphatidylglycerophosphate synthase	10L004W	SIIVS	transcription regulatory protein
YCL040w	GLK1	aldohexose specific glucokinase	YNL169c	PSD1	phosphatidylserine decarboxylase 1	lipid and		
YKL217w		carboxylic acid transporter protein	YGR170w	PSD2	phosphatidylserine decarboxylase 2	YGR037c	ACB1	acyl-CoA-binding protein (diazepam-
YBR291c	CTP1	citrate transport protein, mitochondrial (MCF)	YCL004w YMR220w	PEL1	phosphatidylserine synthase phosphomevalonate kinase	YNL130c	CPT1	binding inhibitor) diacylglycerol cholinephosphotransferase
YLR348c		dicarboxylate carrier protein	YCR034w		probable 1,3—glucan synthase subunit	YBR041w		fatty-acid transporter
YLR081w	GAL2	galactose (and glucose) permease	YGL001c		putative 3—hydroxysteroid dehydrogenase	YKL188c	PAT1	long-chain-fatty-acid transporter
YGR289c	AGT1 FPS1	general α-glucoside permease	YJL196c	ELO1 GPI1	required for elongation of fatty acids	YPL147w YOR317w	PXA1 FAA1	long-chain-fatty-acid transporter
YLL043w YNL318c	HXT14	glycerol channel protein hexose transport protein	YGR216c	GPII	required for N-acetylglucosaminyl phosphatidylinositol synthesis	YER015w	FAA1 FAA2	long-chain-fatty-acid-CoA ligase long-chain-fatty-acid-CoA ligase
YJL214w	HXT8	hexose transport protein	YML008c	ERG6	S-adenosyl-methionine δ-24-sterol-c-	YMR246w		long-chain-fatty-acid-CoA ligase
YJL219w	HXT9	hexose transport protein			methyltransferase	YAR035w	YAT1	outer carnitine acetyltransferase,
YFL011w YDL194w	HXT10 SNF3	hexose transporter high-affinity glucose transporter	YMR296c YDR062w	LCB1 LCB2	serine C-palmitoyltransferase subunit serine C-palmitoyltransferase subunit	YCL043c	PDI1	mitochondrial protein disulphide-isomerase
YEL069c	HXT13	high-affinity hexose transporter	YLR058c	SHM2	serine o-pairittoyttaristerase suburit serine hydroxymethyltransferase,	YER024w	, 511	similarity to carnitine O-acetyltransferase
YMR011w	HXT2	high-affinity hexose transporter			cytoplasmic			Yat1p
YDR343c YDR342c	HXT6 HXT7	high-affinity hexose transporter high-affinity hexose transporter	YBR263w	SHM1	serine hydroxymethyltransferase, mitochondrial	YKL174c		similarity to choline transport protein
	HXT11	low-affinity glucose transporter	YMR207c	HFA1	similarity to acetyl-CoA carboxylase	YNR056c		Ctr1p similarity to choline transport protein
YHR094c	HXT1	low-affinity hexose transporter	YDR147w		similarity to choline kinase			Ctr1p
YDR345c	HXT3	low-affinity hexose transporter	YBR159w		similarity to human 17—hydroxysteroid	YHR123w	EPT1	sn-1,2-diacylglycerol ethanolamine- and
YDR497c YBR298c	ITR1 MAL31	major myo-inositol permease maltose permease	YDR376w	ARH1	dehydrogenase similarity to human adrenodoxin			cholinephosphotransferase
YHR092c	HXT4	moderate- to low-affinity glucose	151107011	,	reductase	lipid and	fatty-acid	binding
VOI 400	ITDO	transporter	YML131w		similarity to human leukotriene b4	YHR001w	E1 404	similarity to Kes1p
YOL103w YIR035c	ITR2	myo-inositol transport protein similarity to <i>C. lanceolata</i> 3-oxoacyl-[acyl-	YAR042w	OSH1	12-hydroxydehydrogenase similarity to human oxysterol binding	YMR020w	FIVIS I	suppressor of fenpropimorph resistance mutation fen2
11110000		carrier-protein] reductase	.,	00///	protein			
YBR241c		similarity to glucose transport proteins	YDR208w	MSS4	similarity to human PI P 5-kinase			d and sterol metabolism activities
YGL104c YPR021c		similarity to glucose transport proteins similarity to human citrate transporter	YHR001w YKR003w		similarity to Kes1p similarity to Kes1p, Hes1p and Osh1p	YBR036c YMR079w		calcium dependent regulatory protein phosphatidylinositol/phosphatidylcholine
TTTTOLTO		protein	YDL019c		similarity to Osh1p	11011107000	02011	transfer protein
YDR387c		similarity to ltr1p and ltr2p	YHR073w		similarity to Osh1p, Hes1p, Kes1p	YNL264c		similarity to Sec14p
YDL199c YFL040w		similarity to sugar transporter proteins similarity to yeast glucose transport	YGR175c YGL055w	ERG1 OLE1	squalene monooxygenase stearoyl-CoA desaturase	YKL091c YIL002c	SJH1	strong similarity to Sec14p synaptojanin homologue 1
11 201000		proteins	YGL012w	ERG4	sterol C-24 reductase	YDR302w	Corri	weak similarity to human GPI-anchor
YHR096c	HXT5	strong similarity to hexose transporters	YLR372w	SUR4	sterol isomerase			biosynthesis protein
YDL245c YJR160c	HXT15	strong similarity to Hxt17p and Haxt7p strong similarity to Mal3Tp	YKL192c YNL045w		strong similarity to acyl-carrier proteins strong similarity to human leukotriene-A4	biosynt	hesis o	f vitamins, cofactors and
			==					
YDR536w	STL1	strong similarity to members of the sugar			hydrolase	prosthe	tuc grot	
	SIL1	permease family	hreakdow	n of linid		-	_	
YDR536W YDL247W	SIL1	permease family strong similarity to sugar transport			s and phospholipids	metabolis	m of vitar	mins, cofactors and prosthetic groups
	SIL1 HXT12	permease family	YPL268w	PLC1	s and phospholipids 1-phosphatidylinositol-4,5-bisphosphate phosphodiesterase	metabolis YOL096c	of vitar	mins, cofactors and prosthetic groups 3,4-dihydroxy-5-hexaprenylbenzoate methyltransferase
YDL247w YIL170w	HXT12	permease family strong similarity to sugar transport proteins strong similarity to sugar transport proteins	YPL268w YGL205w	PLC1 POX1	s and phospholipids 1-phosphatidylinositol-4,5-bisphosphate phosphodiesterase acyl-CoA oxidase	metabolis YOL096c YDR232w	coq3 HEM1	mins, cofactors and prosthetic groups 3,4-dihydroxy-5-hexaprenylbenzoate methyltransferase 5-aminolevulinate synthase
YDL247w		permease family strong similarity to sugar transport proteins strong similarity to sugar transport proteins strong similarity to sugar transport	YPL268w YGL205w YMR008c	PLC1 POX1 PLB1	s and phospholipids 1-phosphatidylinositol-4,5-bisphosphate phosphodiesterase acyl-CoA oxidase phospholipase B (lysophospholipase)	metabolis YOL096c YDR232w YOL143c	or of vitar COQ3 HEM1 RIB4	mins, cofactors and prosthetic groups 3,4-dihydroxy-5-hexaprenylbenzoate methyltransferase 5-aminolevulinate synthase 6,7-dimethyl-8-ribityllumazine synthase
YDL247w YIL170w	HXT12	permease family strong similarity to sugar transport proteins strong similarity to sugar transport proteins	YPL268w YGL205w	PLC1 POX1 PLB1	s and phospholipids 1-phosphatidylinositol-4,5-bisphosphate phosphodiesterase acyl-CoA oxidase	metabolis YOL096c YDR232w	om of vitar COQ3 HEM1 RIB4 BIO2	mins, cofactors and prosthetic groups 3,4-dihydroxy-5-hexaprenylbenzoate methyltransferase 5-aminolevulinate synthase
YDL247w YIL170w YIL171w YJR158w	HXT12 HXT12 HXT16	permease family strong similarity to sugar transport proteins	YPL268W YGL205W YMR008c YKR031c YLR020c YLL012W	PLC1 POX1 PLB1	s and phospholipids 1-phosphatidylinositol-4,5-bisphosphate phosphodiesterase acyl-CoA oxidase phospholipase B (lysophospholipase) phospholipase D similarity to triacylglycerol lipase similarity to triacylglycerol lipases	metabolis YOL096c YDR232w YOL143c YGR286c	om of vitar COQ3 HEM1 RIB4 BIO2 ADE3	mins, cofactors and prosthetic groups 3,4-dihydroxy-5-hexaprenylbenzoate methyltransferase 5-aminolevulinate synthase 6,7-dimethyl-8-ribityllumazine synthase biotin synthetase C1-tetrahydrofolate synthase, cytoplasmic C1-tetrahydrofolate synthase,
YDL247w YIL170w YIL171w YJR158w YNR072w	HXT12 HXT12 HXT16 HXT17	permease family strong similarity to sugar transport proteins sugar transport strong similarity to sugar transport proteins	YPL268W YGL205W YMR008c YKR031c YLR020c YLL012W YJL068c	PLC1 POX1 PLB1	s and phospholipids  1-phosphatidylinositol-4,5-bisphosphate phosphodiesterase acyl-CoA oxidase phospholipase B (lysophospholipase) phospholipase D similarity to triacylglycerol lipase similarity to triacylglycerol lipases strong similarity to human esterase D	metabolis YOL096c YDR232w YOL143c YGR286c YGR204w YBR084w	em of vitar COQ3 HEM1 RIB4 BIO2 ADE3 MIS1	mins, cofactors and prosthetic groups 3,4-dihydroxy-5-hexaprenylbenzoate methyltransferase 5-aminolevulinate synthase 6,7-dimethyl-8-ribityllumazine synthase biotin synthetase C1-tetrahydrofolate synthase, cytoplasmic C1-tetrahydrofolate synthase, mitochondrial
YDL247w YIL170w YIL171w YJR158w YNR072w YDL138w	HXT12 HXT12 HXT16 HXT17 RGT2	permease family strong similarity to sugar transport proteins sugar transport protein suppressor of sni3 mutant	YPL268W YGL205W YMR008c YKR031c YLR020c YLL012W	PLC1 POX1 PLB1	s and phospholipids 1-phosphatidylinositol-4,5-bisphosphate phosphodiesterase acyl-CoA oxidase phospholipase B (lysophospholipase) phospholipase D similarity to triacylglycerol lipase similarity to triacylglycerol lipases	metabolis YOL096c YDR232w YOL143c YGR286c YGR204w	em of vitar COQ3 HEM1 RIB4 BIO2 ADE3 MIS1 HEM13	mins, cofactors and prosthetic groups 3,4-dihydroxy-5-hexaprenylbenzoate methyltransferase 5-aminolevulinate synthase 6,7-dimethyl-8-ribityllumazine synthase biotin synthetase C1-tetrahydrofolate synthase, cytoplasmic C1-tetrahydrofolate synthase, mitochondrial coproporphyrinogen III oxidase
YDL247w YIL170w YIL171w YJR158w YNR072w YDL138w	HXT12 HXT12 HXT16 HXT17 RGT2	permease family strong similarity to sugar transport proteins sugar transport strong similarity to sugar transport proteins	YPL268W YGL205W YMR008c YKR031c YLR020c YLL012W YJL068c YOL011W YMR006c YKL140W	PLC1  POX1 PLB1 SPO14	s and phospholipids  1-phosphatidylinositol-4,5-bisphosphate phosphodiesterase acyl-CoA oxidase phospholipase B (lysophospholipase) phospholipase D similarity to triacylglycerol lipase similarity to triacylglycerol lipase strong similarity to phospholipases strong similarity to phospholipases strong similarity to phospholipases strong similarity to Plb1p triacylglycerol lipase	metabolis YOL096c YDR232w YOL143c YGR286c YGR204w YBR084w YDR044w YPL132w YNR058w	em of vitar COQ3 HEM1 RIB4 BIO2 ADE3 MIS1 HEM13 COX11 BIO3	mins, cofactors and prosthetic groups 3,4-dihydroxy-5-hexaprenylbenzoate methyltransferase 5-aminolevulinate synthase 6,7-dimethy8-ribityllumazine synthase biotin synthetase C1-tetrahydrofolate synthase, cytoplasmic C1-tetrahydrofolate synthase, mitochondrial coproporphyrinogen III oxidase cytochrome c oxidase assembly protein DAPA aminotransferase
YDL247w YIL170w YIL171w YJR158w YNR072w YDL138w <i>lipid, fat</i>	HXT12 HXT12 HXT16 HXT17 RGT2 tty-acid	permease family strong similarity to sugar transport proteins sugar transport protein suppressor of snf3 mutant al and sterol metabolism	YPL268w YGL205w YMR008c YKR031c YLR020c YLL012w YJL068c YOL011w YMR006c YKL140w YDR058c	PLC1 POX1 PLB1 SPO14	s and phospholipids  1-phosphatidylinositol-4,5-bisphosphate phosphodiesterase acyl-CoA oxidase phospholipase B (lysophospholipase) phospholipase D similarity to triacylglycerol lipase similarity to triacylglycerol lipases strong similarity to human esterase D strong similarity to phospholipases strong similarity to Pib1p triacylglycerol lipase triacylglycerol lipase	metabolis YOL096c YDR232w YOL143c YGR286c YGR204w YBR084w YDR044w YPL132w YNR058w YDR487c	m of vitar COQ3 HEM1 RIB4 BIO2 ADE3 MIS1 HEM13 COX11 BIO3 RIB3	mins, cofactors and prosthetic groups 3,4-dihydroxy-5-hexaprenylbenzoate methyltransferase 5-aminolevulinate synthase 6,7-dimethyl-8-ribityllumazine synthase biotin synthetase C1-tetrahydrofolate synthase, cytoplasmic C1-tetrahydrofolate synthase, mitochondrial coproporphyrinogen III oxidase cytochrome c oxidase assembly protein DAPA aminotransferase DBP synthase
YDL247w YIL170w YIL171w YJR158w YNR072w YDL138w <i>lipid, fat</i>	HXT12 HXT12 HXT16 HXT17 RGT2 tty-acid	permease family strong similarity to sugar transport proteins sugar transport protein suppressor of sni3 mutant	YPL268W YGL205W YMR008c YKR031c YLR020c YLL012W YJL068c YOL011W YMR006c YKL140W	PLC1  POX1 PLB1 SPO14	s and phospholipids  1-phosphatidylinositol-4,5-bisphosphate phosphodiesterase acyl-CoA oxidase phospholipase B (lysophospholipase) phospholipase D similarity to triacylglycerol lipase similarity to triacylglycerol lipase strong similarity to phospholipases strong similarity to phospholipases strong similarity to phospholipases strong similarity to Plb1p triacylglycerol lipase	metabolis YOL096c YDR232w YOL143c YGR286c YGR204w YBR084w YDR044w YPL132w YNR058w	em of vitar COQ3 HEM1 RIB4 BIO2 ADE3 MIS1 HEM13 COX11 BIO3	mins, cofactors and prosthetic groups 3,4-dihydroxy-5-hexaprenylbenzoate methyltransferase 5-aminolevulinate synthase 6,7-dimethyl-8-ribityllumazine synthase biotin synthetase C1-tetrahydrofolate synthase, cytoplasmic C1-tetrahydrofolate synthase, mitochondrial coproporphyrinogen III oxidase cytochrome c oxidase assembly protein DAPA aminotransferase DBP synthase DRAP deaminase farnesyl transferase
YDL247w YIL170w YIL171w YJR158w YNR072w YDL138w <i>lipid, fatty</i> YML075c	HXT12 HXT16 HXT17 RGT2 tty-acid	permease family strong similarity to sugar transport proteins sugar transport protein sugar transport protein suppressor of snf3 mutant suppressor of snf3 mutant sterol metabolism sterol metabolism sterol biosynthesis 3-hydroxy-3-methylglutaryl-CoA reductase 1	YPL268w  YGL205w  YMR008c  YKR031c  YLR020c  YLL012w  YJL068c  YOL011w  YMR006c  YKL140w  YDR058c  YJR107w	PLC1  POX1 PLB1 SPO14	s and phospholipids  1-phosphatidylinositol-4,5-bisphosphate phosphodiesterase acyl-CoA oxidase phospholipase B (lysophospholipase) phospholipase D similarity to triacylglycerol lipase similarity to triacylglycerol lipases strong similarity to human esterase D strong similarity to phospholipases strong similarity to phospholipases strong similarity to Plb1p triacylglycerol lipase triacylglycerol lipase triacylglycerol lipase weak similarity to acylglycerol lipase weak similarity to acylglycerol lipase	metabolis YOL096c YDR232w YOL143c YGR286c YGR204w YBR084w YDR044w YPL132w YNR058w YDR487c YOL066c YPL172c YOL176w	em of vital COQ3 HEM1 RIB4 BIO2 ADE3 MIS1 HEM13 COX11 BIO3 RIB3 RIB2 COX10 HEM15	mins, cofactors and prosthetic groups 3,4-dihydroxy-5-hexaprenylbenzoate methyltransferase 5-aminolevulinate synthase 6,7-dimethyl-8-ribityllumazine synthase biotin synthetase C1-tetrahydrofolate synthase, cytoplasmic C1-tetrahydrofolate synthase, mitochondrial coproporphyrinogen III oxidase cytochrome c oxidase assembly protein DAPA aminotransferase DBP synthase DRAP deaminase farnesyl transferase ferrochelatase
YDL247w YIL170w YIL171w YJR158w YNR072w YDL138w <i>lipid, fat</i> ty	HXT12 HXT12 HXT16 HXT17 RGT2 tty-acid	permease family strong similarity to sugar transport proteins sugar transport protein suppressor of sn/3 mutant suppressor of sn/3 mutant sterol biosynthesis 3-hydroxy-3-methylglutaryl-CoA reductase 1 3-hydroxy-3-methylglutaryl-CoA	YPL268w YGL205w YMR008c YKR031c YLR020c YLL012w YJL068c YOL011w YMR006c YKL140w YDR058c YJR107w YBR204c	PLC1 POX1 PLB1 SPO14  TGL1 TGL2	s and phospholipids  1-phosphatidylinositol-4,5-bisphosphate phosphodiesterase acyl-CoA oxidase phospholipase B (lysophospholipase) phospholipase D similarity to triacylglycerol lipase string similarity to phospholipases strong similarity to phospholipases strong similarity to phospholipases strong similarity to phospholipases strong similarity to plb1p triacylglycerol lipase triacylglycerol lipase weak similarity to acylglycerol lipase weak similarity to proxisomal serine-	metabolis YOL096c YDR232w YOL143c YGR286c YGR204w YBR084w YDR044w YPL132w YNR058w YDR487c YOL066c YPL172c	m of vitar COQ3 HEM1 RIB4 BIO2 ADE3 MIS1 HEM13 COX11 BIO3 RIB3 RIB3 RIB2 COX10	mins, cofactors and prosthetic groups 3,4-dihydroxy-5-hexaprenylbenzoate methyltransferase 5-aminolevulinate synthase 6,7-dimethyl-8-ribityllumazine synthase biotin synthetase C1-tetrahydrofolate synthase, cytoplasmic C1-tetrahydrofolate synthase, mitochondrial coproporphyrinogen III oxidase cytochrome c oxidase assembly protein DAPA aminotransferase DBP synthase DRAP deaminase farnesyl transferase ferrochelatase flavin adenine dinucleotide (FAD)
YDL247w YIL170w YIL171w YJR158w YNR072w YDL138w <b>lipid, fatt</b> YML075c YLR450w YML126c	HXT12 HXT16 HXT17 RGT2 tty-acid and HMG1 HMG2 HMGS	permease family strong similarity to sugar transport proteins sugar transport protein sugar transport protein suppressor of snf3 mutant snf3 mutant suppressor of snf3 mutant suppressor of snf3 mutant snf3 m	YPL268w YGL205w YMR008c YKR031c YLR020c YLL012w YJL068c YOL011w YMR006c YKL140w YDR058c YJR107w YBR204c  lipid, fatty YIL160c	PLC1  POX1 PLB1 SPO14  TGL1 TGL2  -acid and POT1	s and phospholipids  1-phosphatidylinositol-4,5-bisphosphate phosphodiesterase acyl-CoA oxidase phospholipase B (lysophospholipase) phospholipase D similarity to triacylglycerol lipase similarity to triacylglycerol lipases strong similarity to human esterase D strong similarity to phospholipases strong similarity to Plospholipases strong similarity to Plospholipases strong similarity to Plospholipases strong similarity to Plospholipases weak similarity to acylglycerol lipase weak similarity to acylglycerol lipase weak similarity to acylglycerol lipase weak similarity to peroxisomal serineactive lipase  sterol utilization acetyl-CoA C-acyltransferase, peroxisomal	metabolis YOL096c YDR232w YOL143c YGR286c YGR204w YBR084w YDR044w YPL132w YNR068w YDL066c YPL172c YOL166w YDL045c YGR267c	m of vital COQ3 HEM1 RIB4 BIO2 ADE3 MIS1 HEM13 COX11 BIO3 RIB3 RIB3 RIB3 RIB3 FAD1 FAD1	mins, cofactors and prosthetic groups 3,4-dihydroxy-5-hexaprenylbenzoate methyltransferase 5-aminolevulinate synthase 6,7-dimethyl-8-ribityllumazine synthase biotin synthetase C1-tetrahydrofolate synthase, cytoplasmic C1-tetrahydrofolate synthase, cytoplasmic C1-tetrahydrofolate synthase, mitochondrial coproporphyrinogen III oxidase cytochrome c oxidase assembly protein DAPA aminotransferase DBP synthase DRAP deaminase farnesyl transferase farerochelatase flavin adenine dinucleotide (FAD) synthetase GTP cyclohydrolase I
YDL247w YIL170w YIL171w YJR158w YNR072w YDL138w <b>lipid, fatty</b> YML075c YLR450w YML126c YPL028w	HXT12 HXT12 HXT16 HXT17 RGT2 tty-acid racid and HMG1 HMG2 HMG8 ERG10	permease family strong similarity to sugar transport proteins sugar transport protein suppressor of sn/3 mutant suppressor of sn/3 mutant sterol biosynthesis 3-hydroxy-3-methylglutaryl-CoA reductase 1 3-hydroxy-3-methylglutaryl-CoA reductase 2 3-hydroxy-3-methylglutaryl-CoA synthase acetyl-CoA C-acetyltransferase, cytosolic	YPL268w YGL205w YMR008c YKR031c YLR020c YLL012w YJL068c YOL011w YMR006c YKL140w YMR006c YKL140w YBR204c  lipid, fatty YlL160c YlL09w	PLC1  POX1 PLB1 SPO14  TGL1 TGL2  -acid and POT1 FAA3	s and phospholipids  1-phosphatidylinositol-4,5-bisphosphate phosphodiesterase acyl-CoA oxidase phospholipase B (lysophospholipase) phospholipase D similarity to triacylglycerol lipase similarity to triacylglycerol lipase strong similarity to human esterase D strong similarity to phospholipases strong similarity to phospholipases strong similarity to plotypholipases strong similarity to plotypholipases triacylglycerol lipase triacylglycerol lipase triacylglycerol lipase weak similarity to acylglycerol lipase weak similarity to peroxisomal serineactive lipase  sterol utilization acetyl-CoA C-acyltransferase, peroxisomal acyl-CoA synthase	metabolis YOL096c YDR232w YOL143c YGR286c YGR296c YGR204w YBR084w YDR044w YPL132w YNR058w YDH37c YOL066c YPL172c YOR176w YDL045c YGR267c YBL033c	m of vital COQ3 HEM1 RIB4 BIO2 ADE3 MIS1 HEM13 COX11 BIO3 RIB2 COX10 HEM15 FAD1	mins, cofactors and prosthetic groups 3,4-dihydroxy-5-hexaprenylbenzoate methyltransferase 5-aminolevulinate synthase 6,7-dimethyl-8-ribityllumazine synthase biotin synthetase C1-tetrahydrofolate synthase, cytoplasmic C1-tetrahydrofolate synthase, mitochondrial coproporphyrinogen III oxidase cytochrome c oxidase assembly protein DAPA aminotransferase DBP synthase DRAP deaminase farnesyl transferase farnesyl transferase flavin adenine dinucleotide (FAD) synthetase GTP cyclohydrolase I GTP cyclohydrolase II
YDL247w YIL170w YIL171w YJR158w YNR072w YDL138w Iipid, faty YML075c YLR450w YML126c YPL028w YNR016c	HXT12 HXT16 HXT17 RGT2  tty-acid and HMG1 HMG2 HMGS ERG10 ACC1	permease family strong similarity to sugar transport proteins sugar transport protein sugar transport protein suppressor of snf3 mutant snf3 mutant suppressor of snf3 mutant suppressor of snf3 mutant snf3 m	YPL268w YGL205w YMR008c YKR031c YLR020c YLL012w YJL068c YOL011w YMR006c YKL140w YDR058c YJR107w YBR204c  lipid, fatty YIL160c YIL09w YMR013c	PLC1  POX1 PLB1 SPO14  TGL1 TGL2  -acid and POT1 FAA3 SEC59	s and phospholipids  1-phosphatidylinositol-4,5-bisphosphate phosphodiesterase acyl-CoA oxidase phospholipase B (lysophospholipase) phospholipase D similarity to triacylglycerol lipase similarity to triacylglycerol lipase strong similarity to human esterase D strong similarity to phospholipases strong similarity to Pib1p triacylglycerol lipase strong similarity to Pib1p triacylglycerol lipase weak similarity to acylglycerol lipase weak similarity to peroxisomal serineactive lipase  sterol utilization acetyl-CoA C-acyltransferase, peroxisomal acyl-CoA synthase dolichol kinase	metabolis YOL096c YDR232w YOL143c YGR226c YGR204w YBR084w YDR044w YPL132w YNR058w YDR045c YOL066c YPL172c YOR176w YDL045c YGR267c YBL033c WBR0030w	Im of vital COQ3 HEM1 RIB4 BIO2 ADE3 MIS1 HEM13 COX11 BIO3 RIB3 RIB3 RIB3 FAD1 FAD1 FOL2 RIB1 COQ1	mins, cofactors and prosthetic groups 3,4-dihydroxy-5-hexaprenylbenzoate methyltransferase 5-aminolevulinate synthase 6,7-dimethyl-8-ribityllumazine synthase biotin synthetase C1-tetrahydrofolate synthase, cytoplasmic C1-tetrahydrofolate synthase, mitochondrial coproporphyrinogen III oxidase cytochrome c oxidase assembly protein DAPA aminotransferase DBP synthase DRAP deaminase farnesyl transferase flavia adenine dinucleotide (FAD) synthetase GTP cyclohydrolase I GTP cyclohydrolase II hexaprenyl pyrophosphate synthetase
YDL247w YIL170w YIL171w YJR158w YNR072w YDL138w <b>lipid, fatt</b> YML075c YLR450w YML126c YPL028w YNR016c YCR048w YNR016v	HXT12 HXT16 HXT17 RGT2  tty-acid and HMG1 HMG2 HMGS ERG10 ACC1 ARE1	permease family strong similarity to sugar transport proteins sugar transport protein supersesor of sn/3 mutant suppressor of sn/3 mutant sn/3 mutant suppressor of sn/3 mutant suppressor of sn/3 mutant sn	YPL268w YGL205w YMR008c YKR031c YLR020c YLL012w YJL068c YOL011w YMR006c YKL140w YMR006c YKL140w YBR204c  lipid, fatty YlL160c YlL09w	PLC1  POX1 PLB1 SPO14  TGL1 TGL2  -acid and POT1 FAA3 SEC59	s and phospholipids  1-phosphatidylinositol-4,5-bisphosphate phosphodiesterase acyl-CoA oxidase phospholipase B (lysophospholipase) phospholipase B imiliarity to triacylglycerol lipase similarity to triacylglycerol lipase similarity to triacylglycerol lipases strong similarity to phospholipases strong similarity to phospholipases strong similarity to Pib†p triacylglycerol lipase triacylglycerol lipase weak similarity to acylglycerol lipase weak similarity to proxisomal serineactive lipase  sterol utilization  acetyl-CoA C-acyltransferase, peroxisomal acyl-CoA C-acyltransferase, peroxisomal acyl-CoA carellarity for peroxisomal acyl-CoA carellarity for peroxisomal acyl-CoA carellarity for generation for GPI-anchor attachment farnesyl cysteine carboxyl-	metabolis YOL096c YDR232W YOL143c YGR2286c YGR204W YBR084W YDR044W YPL132W YNR058W YDR0487c YOL066c YPL172c YGR176W YDL045c YGR267c YGR267c YGR267c YGR267c YGR267c YGR267c YGR267c YGR267c YGR267c	m of vital COQ3 HEM1 RIB4 BIO2 ADE3 MIS1 HEM13 COX11 BIO3 RIB3 RIB3 RIB3 RIB3 RIB3 RIB3 RIB3 RIB1 COX10 HEM15 FAD1 FOL2 RIB1 COQ1 RIB7 LIP5	mins, cofactors and prosthetic groups 3,4-dihydroxy-5-hexaprenylbenzoate methyltransferase 5-aminolevulinate synthase 6,7-dimethyl-8-ribityllumazine synthase biotin synthetase C1-tetrahydrofolate synthase, cytoplasmic C1-tetrahydrofolate synthase, mitochondrial coproporphyrinogen III oxidase cytochrome c oxidase assembly protein DAPA aminotransferase DBP synthase DRAP deaminase farnesyl transferase ferrochelatase flavin adenine dinucleotide (FAD) synthetase GTP cyclohydrolase I TP cyclohydrolase II hexaprenyl pyrophosphate synthetase HTP reductase lipioic acid synthase
YDL247w YIL170w YIL171w YJR158w YJR158w Ilpid, fatt YML075c YLR450w YML126c YPL028w YNL026c YCR048w YNR019w YNL09w YNL09w YNL09w	HXT12 HXT16 HXT17 RGT2  tty-acid racid and HMG1 HMG2 HMG8 ERG10 ACC1 ARE1 ARE1 ARE2 FAA3	permease family strong similarity to sugar transport proteins sugar transport protein sugar transport protein suppressor of snf3 mutant suppressor snf3 mutant snf3 mutant suppressor snf3 mutant snf3 mutant suppressor snf3 mutant sn	YPL268w YGL205w YMR008c YKR031c YLR020c YLL012w YJL068c YOL011w YMR006c YKL140w YDR058c YJR107w YBR204c  Ipid, fatty YIL160c YIL009w YMR013c YDR331w YDR410c	PLC1 POX1 PLB1 SPO14  TGL1 TGL2  -acid and POT1 FAA3 SEC59 GP18 STE14	s and phospholipids  1-phosphatidylinositol-4,5-bisphosphate phosphodiesterase acyl-CoA oxidase phospholipase B (lysophospholipase) phospholipase D similarity to triacylglycerol lipase similarity to triacylglycerol lipases strong similarity to human esterase D strong similarity to phospholipases strong similarity to Pib1p triacylglycerol lipase strong similarity to Pib1p triacylglycerol lipase weak similarity to prospholipase weak similarity to proxisomal serineactive lipase  sterol utilization acetyl-CoA C-acyltransferase, peroxisomal acyl-CoA synthase dolichol kinase essential for GPI-anchor attachment farnesyl cysteine carboxyl-methyltransferase	metabolis YOL096c YDR232w YOL143c YGR204w YBR084w YDR044w YPL132w YNR058w YDR487c YOL066c YPL172c YGR176w YDL045c YGR267c YBL033c YBR003w YBR153w YOR196c YHR042w	IT Of vital COQ3 HEM1 RIB4 BIO2 ADE3 MIS1 HEM13 COX11 BIO3 RIB3 RIB2 COX10 HEM15 FAD1 FOL2 RIB1 RIB7 LIP5 FAD1	mins, cofactors and prosthetic groups 3,4-dihydroxy-5-hexaprenylbenzoate methyltransferase 5-aminolevulinate synthase 6,7-dimethyl-8-ribityllumazine synthase biotin synthetase C1-tetrahydrofolate synthase, cytoplasmic C1-tetrahydrofolate synthase, mitochondrial coproporphyrinogen III oxidase cytochrome c oxidase assembly protein DAPA aminotransferase DBP synthase DRAP deaminase farnesyl transferase ferrochelatase flavin adenine dinucleotide (FAD) synthetase GTP cyclohydrolase II GTP cyclohydrolase II GTP reductase III point acid synthase HTP reductase II poic acid synthase NADPH-cytochrome P450 reductase
YDL247w YIL170w YIL171w YJR158w YNR072w YDL138w <b>lipid, fatt</b> YML075c YLR450w YML126c YPL028w YNR016c YCR048w YNR016v	HXT12 HXT16 HXT17 RGT2  tty-acid and HMG1 HMG2 HMGS ERG10 ACC1 ARE1	permease family strong similarity to sugar transport proteins sugar transport protein suppressor of snf3 mutant snf3 mutant suppressor of snf3 mutant snf3 m	YPL268w YGL205w YMR008c YKR031c YLR020c YLL012w YJL068c YOL011w YMR006c YKL140w YDR058c YJR107w YBR204c  Ipid, fatty YIL160c YIL09sw YMR013c YDR313c YDR3110c YPL172c	PLC1 POX1 PLB1 SPO14  TGL1 TGL2  -acid and POT1 FAA3 SEC59 GP18 STE14  COX10	s and phospholipids  1-phosphatidylinositol-4,5-bisphosphate phosphodiesterase acyl-CoA oxidase phospholipase B (lysophospholipase) phospholipase D similarity to triacylglycerol lipase similarity to triacylglycerol lipases strong similarity to human esterase D strong similarity to phospholipases strong similarity to Plb1p triacylglycerol lipase stronglylglycerol lipase weak similarity to acylglycerol lipase weak similarity to acylglycerol lipase weak similarity to peroxisomal serineactive lipase  sterol utilization  acctyl-CoA C-acyltransferase, peroxisomal acyl-CoA synthase dolichol kinase essential for GPl-anchor attachment farnesyl cysteine carboxylmethyltransferase farnesyl transferase	metabolis YOL096c YDR232w YOL143c YGR204w YDR044w YDR044w YPL132w YNR068w YDR487c YOL066c YPL172c YOR176w YDL045c YGR267c YBR033c YBR033w YOR196c YHR042w YOR209c	## of vital  COQ3  HEM1 RIB4 BIO2 ADE3 MIS1  HEM13 COX11 BIO3 RIB2 COX10 FAD1 FAD1  FOL2 RIB1 RIB1 COQ1 RIB7 LIP5 NCP1 NPT1	mins, cofactors and prosthetic groups 3,4-dihydroxy-5-hexaprenylbenzoate methyltransferase 5-aminolevulinate synthase 6,7-dimethyl-8-ribityllumazine synthase biotin synthetase C1-tetrahydrofolate synthase, cytoplasmic C1-tetrahydrofolate synthase, cytoplasmic C1-tetrahydrofolate synthase, mitochondrial coproporphyrinogen III oxidase cytochrome c oxidase assembly protein DAPA aminotransferase DBP synthase DRAP deaminase farnesyl transferase ferrochelatase flavin adenine dinucleotide (FAD) synthetase GTP cyclohydrolase I GTP cyclohydrolase II hexaprenyl pyrophosphate synthetase HTP reductase lipoic acid synthase NADPH-cytochrome P450 reductase nicotinate phosphoribosyltransferase
YDL247w YIL170w YIL171w YJR158w YJR158w Ilpid, faty YML075c YLR450w YML126c YCR048w YNR019w YNR019w YJL099w YGR037c YBR222c	HXT12 HXT12 HXT16 HXT17 RGT2 tty-acid recid and HMG1 HMG2 HMGS ERG10 ACC1 ARE1 ARE2 FAA3 ACB1 PCS60	permease family strong similarity to sugar transport proteins sugar transport protein superssor of snf3 mutant suppressor suppressor snf3 mutant suppressor snf3 mutant suppressor snf3 mutant suppressor snf3 mutant snf3 mut	YPL268w YGL205w YMR008c YKR031c YLR020c YLL012w YJL068c YJL068c YJR107w YDR058c YJR107w YBR204c  Iipid, fatty YIL160c YIL099w YMR013c YDR331w YDR410c YPL172c YOR370c	PLC1 POX1 PLB1 SPO14  TGL1 TGL2  -acid and POT1 FAA3 SEC59 GPI8 STE14 COX10 MSI4	s and phospholipids  1-phosphatidylinositol-4,5-bisphosphate phosphodiesterase acyl-CoA oxidase phospholipase B (lysophospholipase) phospholipase D similarity to triacylglycerol lipase similarity to triacylglycerol lipase strong similarity to human esterase D strong similarity to hospholipases strong similarity to Plb1p triacylglycerol lipase stronglyerol lipase triacylglycerol lipase weak similarity to peroxisomal serine-active lipase  sterol utilization  acetyl-CoA C-acyltransferase, peroxisomal acyl-CoA synthase dolichol kimase essential for GPI-anchor attachment farnesyl cysteine carboxyl-methyltransferase farnesyl transferase geranylgeranyltransferase regulatory subunit	metabolis YOL096c YDR232w YOL143c YGR204w YBR084w YDR044w YPL132w YNR058w YDR487c YOL066c YPL172c YGR176w YDL045c YGR267c YBL033c YBR003w YBR153w YOR196c YHR042w	## of vital  COQ3  HEM1 RIB4 BIO2 ADE3 MIS1  HEM13 COX11 BIO3 RIB2 COX10 FAD1 FAD1  FOL2 RIB1 RIB1 COQ1 RIB7 LIP5 NCP1 NPT1	mins, cofactors and prosthetic groups 3,4-dihydroxy-5-hexaprenylbenzoate methyltransferase 5-aminolevulinate synthase 6,7-dimethyl-8-ribityllumazine synthase biotin synthetase C1-tetrahydrofolate synthase, cytoplasmic C1-tetrahydrofolate synthase, mitochondrial coproporphyrinogen III oxidase cytochrome c oxidase assembly protein DAPA aminotransferase DBP synthase DRAP deaminase farnesyl transferase flavin adenine dinucleotide (FAD) synthetase GTP cyclohydrolase I GTP cyclohydrolase I GTP cyclohydrolase II GTP reductase lipoic acid synthase NADPH-cychchrome P450 reductase nicotinate phosphoribosyltransferase para-aminobenzoate synthase para-aminobenzoate synthase para-hydroxybenzoate-
YDL247w YIL170w YIL171w YJR158w YNR072w YDL138w Ilpid, fatty YML075c YLR450w YML126c YPL028w YNR019w YIL090w YGR037c YBR222c YER061c	HXT12 HXT12 HXT16 HXT17 RGT2 tty-acid racid and HMG1 HMG2 HMGS ERG10 ACC1 ARE1 ARE1 ARE2 FAA3 ACB1 PCS60 CEM1	permease family strong similarity to sugar transport proteins sugar transport protein suppressor of snf3 mutant suppressor of snf3 mutant stand sterol metabolism sterol biosynthesis 3-hydroxy-3-methylglutaryl-CoA reductase 1 3-hydroxy-3-methylglutaryl-CoA reductase 2 3-hydroxy-3-methylglutaryl-CoA synthase acetyl-CoA carboxylase acetyl-CoA sterol acyltransferase acyl-CoA sterol acyltransferase acyl-CoA synthase acetyl-CoA printing protein (diazepambinding inhibitor) AMP-binding protein, peroxisomal β-keto-acyl-ACP synthase	YPL268w  YGL205w YMR008c YKR031c YLR020c YLL012w YJL088c Y0L011w YMR006c YKL140w YDR058c YJR107w YBR204c  Ilipid, fatty YIL160c YIL109w YMR013c YDR331w YDR311w YDR310c YPL172c YOR370c YGL155w	PLC1 POX1 PLB1 SPO14  TGL1 TGL2  -acid and POT1 FAA3 SEC59 GP18 STE14 COX10 MS14 CDC43	s and phospholipids  1-phosphatidylinositol-4,5-bisphosphate phosphodiesterase acyl-CoA oxidase phospholipase B (lysophospholipase) phospholipase B (lysophospholipase) phospholipase D similarity to triacylglycerol lipase similarity to triacylglycerol lipases strong similarity to phospholipases b strong similarity to phospholipases strong similarity to phospholipases strong similarity to pospholipases strong similarity to pospholipases strong similarity to pospholipases weak similarity to acylglycerol lipase weak similarity to acylglycerol lipase weak similarity to peroxisomal serineactive lipase  sterol utilization acetyl-CoA C-acyltransferase, peroxisomal acyl-CoA synthase dolichol kinase sesential for GPI-anchor attachment farnesyl cysteine carboxylmetyltransferase geranylgeranyltransferase regulatory subunit geranylgeranyltransferase type I β subunit	metabolis YOL096c YDR232w YOL143c YGR228ec YGR204w YBR084w YDR044w YPL132w YNR058w YDR487c YOL056c YPL172c YOR176w YDL045c YGR267c YGR267c YGR267c YGR196c YHR042w YOR196c YHR042w YOR296c YHR042w YOR296c	Im of vital COQ3 HEM1 RIB4 BIO2 ADE3 MIS1 HEM13 COX11 BIO3 RIB3 RIB2 COX10 HEM15 FAD1 FAD1 FOQ1 RIB1 COQ1 RIB1 RIB1 COQ1 RIB1 RIB1 RIB1 RIB1 RIB1 RIB1 RIB1 RIB	mins, cofactors and prosthetic groups 3,4-dihydroxy-5-hexaprenylbenzoate methyltransferase 5-aminolevulinate synthase 6,7-dimethyl-8-ribityllumazine synthase biotin synthetase C1-tetrahydrofolate synthase, cytoplasmic C1-tetrahydrofolate synthase, mitochondrial coproporphyrinogen III oxidase cytochrome c oxidase assembly protein DAPA aminotransferase DBP synthase DRAP deaminase farnesyl transferase ferrochelatase flavin adenine dinucleotide (FAD) synthetase GTP cyclohydrolase II hexaprenyl pyrophosphate synthetase HTP reductase lipoic acid synthase NADPH-cytochrome P450 reductase nicotinate phosphoribosyltransferase para-aminobenzoate synthase para-hydroxybenzoate- polyprenyltransferase
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PLB1 SPO14  TGL1 TGL2  -acid and POT1 FAA3 SEC59 GPI8 STE14  COX10 MSI4  CDC43 BET2 BET4 HSP12 COQ1 FOX2 FAA1 FAA2 FAA4 MDH3 NMT1 TOR1 RAM2 RAM1 ARD1 NAT1 of lipid, ACH1	s and phospholipids  1-phosphatidylinositol-4,5-bisphosphate phosphodiesterase acyl-CoA oxidase phospholipase B (lysophospholipase) phospholipase D similarity to triacylglycerol lipase similarity to triacylglycerol lipase similarity to triacylglycerol lipase strong similarity to phospholipases strong similarity to phospholipases strong similarity to plut ptriacylglycerol lipase triacylglycerol lipase weak similarity to acylglycerol lipase weak similarity to peroxisomal serine-active lipase  sterol utilization acetyl-CoA C-acyltransferase, peroxisomal acyl-CoA C-acyltransferase, peroxisomal acyl-CoA caryltransferase essential for GPl-anchor attachment farnesyl cysteine carboxyl-methyltransferase farnesyl transferase geranylgeranyltransferase type I β subunit geranylgeranyltransferase type I β subunit geranylgeranyltransferase, α subunit heat-shock protein hexaprenyl pyrophosphate synthetase hydratase-dehydrogenase-epimerase, peroxisomal long-chain-fatty-acid-CoA ligase long-chain-fatty-acid-CoA ligase malate dehydrogenase, peroxisomal N-myristoyltransferase protein farnesyltransferase subunit protein farnesyltransferase perotein farnesyltransferase protein farnesyltransferase perotein farnesyltransferase subunit protein farnesyltransferase subunit protein farnesyltransferase subunit protein N-acetyltransferase subunit fatty-acid and sterol biosynthesis acetyl-CoA hydrolase	metabolis YOL096c YDR232W YOL143c YGR2286c YGR204W YBR084W YDR044W YPL132W YNR058W YDR045C YOR176W YDL045c YGR176W YDL045c YGR267c YGR176W YDR045W YDR045W YDR045W YDR045W YDR045W YDR045W YDR045W YDR196C YHR042W YDR196C YHR042W YDR196C YHR042W YDR196C YHR042W YDR196C YHR042W YNR041c YOR196C YHR042W YNR057C YBR035C YBR256C YER014W YNR057C YBR035C YBR256C YER043C YKL027W YIL145C YGR255C YMR113W	## of vital  COQ3  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oxidase, mitochondrial putative dethiobiotin synthetase pyridoxamine-phosphate oxidase riboflavin synthase, a subunit S-adenosyl-L-homocysteine hydrolase similarity to bacterial dihydropteroate synthetase similarity to E. coli molybdopterin- converting factor chIN similarity to E. coli ubiH protein similarity to E. coli ubiH protein similarity to folylpolyglutamate synthetases and strong similarity to hypothetical protein YKL132c
YDL247w YIL170w YIL171w YJR158w YNR072w YDL138w Iipid, faty YML075c YLR450w YML126c YPL028w YNR019w YIL09w YIR016e YKR061c YKR061c YKR061c YMR202w YMR202w YMR0202w YMR0202w YMR0202w YMR0202w YMR066w YMR0202w YMR07007w YHR007c YHR139w YHR007c YHR190W YJL167w YDL052c	HXT12 HXT12 HXT16 HXT17 RGT2  tty-acid recid and HMG1 HMG2 HMGS ERG1 ARE1 ARE2 FAA3 ACB1 PCS00 CEM1 ERG24 ERG5 ERG3 ERG2 CAT2 PIS1 CH01 CDS1 CKI1 MUQ1 PCT1 CYB5 ERG11 ERG90 ERG90 SLC1	permease family strong similarity to sugar transport proteins sugar transport proteins sugar transport protein suppressor of sn/3 mutant  If and sterol metabolism  If sterol biosynthesis  3-hydroxy-3-methylglutaryl-CoA reductase 1 3-hydroxy-3-methylglutaryl-CoA reductase 2 3-hydroxy-3-methylglutaryl-CoA synthase acetyl-CoA carboxylase acetyl-CoA sterol acyltransferase acyl-CoA sterol acyltransferase acyl-CoA sterol acyltransferase acyl-CoA-binding protein (diazepambinding Inhibitor)  AMP-binding protein, peroxisomal β-keto-acyl-ACP synthase c-14 sterol methyl oxidase C-15 sterol desaturase C-25 sterol desaturase C-25 sterol desaturase C-3 sterol acylglycerol-inositol 3-phosphatidyltransferase CDP-diacylglycerol-serine C-phosphatidyltransferase CDP-diacylglycerol synthase choline kinase choline phosphate cytidylyltransferase choline phosphate cytidylyltransferase cytochrome P450 lanosterol 14a-demethylase farnesyl-diphosphate farnesyltransferase fatrs syltyransferase	YPL268w YGL205w YMR008c YKR031c YLR020c YLL012w YJL088c YOL011w YMR006c YKL140w YDR058c YJR107w YBR204c  Ipid, fatty YIL160c YIL029w YMR013c YDR331w YDR410c YPL172c YOR371c YPL172c YR1655w YPK176c YJL031c YPL1720c YR1655w YR176c YJL031c YFL014w YR109c YR179c YR1796c YL1796c YR179c	PLC1 POX1 PLB1 SPO14  TGL1 TGL2  TGL1 TGL2  -acid and POT1 FAA3 SEC59 GPI8 STE14  COX10 MSI4  CDC43 BET2 BET4 HSP12 COQ1 FOX2 FAA1 FAA2 FAA4 MDH3 NMT1 TOR1 RAMD2 RAM1 NAT1 TOR1 TOR1 TOR1 TOR1 TOR1 TOR1 TOR1 TO	s and phospholipids  1-phosphatidylinositol-4,5-bisphosphate phosphodiesterase acyl-CoA oxidase phospholipase B (lysophospholipase) phospholipase D similarity to triacylglycerol lipase similarity to triacylglycerol lipase similarity to triacylglycerol lipases strong similarity to human esterase D strong similarity to phospholipases strong similarity to Pib1p triacylglycerol lipase veak similarity to prospholipases strong similarity to Pib1p triacylglycerol lipase weak similarity to acylglycerol lipase weak similarity to peroxisomal serine-active lipase  sterol utilization  acetyl-CoA C-acyltransferase, peroxisomal acyl-CoA synthase dolichol kinase essential for GPl-anchor attachment farnesyl cysteine carboxyl-methyltransferase farnesyl transferase geranylgeranyltransferase type I β subunit geranylgeranyltransferase type I β subunit geranylgeranyltransferase se yell β subunit geranylgeranyltransferase, α subunit heat-shock protein hexaprenyl pyrophosphate synthetase hydratase-dehydrogenase-epimerase, peroxisomal long-chain-fatty-acid-CoA ligase long-chain-fatty-acid-CoA ligase malate dehydrogenase, peroxisomal N-myristoyltransferase  N-myristoyltransferase as ubunit protein farnesyltransferase, β subunit protein farnesyltransferase, a subunit protein farnesyltransferase, a subunit protein farnesyltransferase subunit protein N-acetyltransferase subunit protein N-acetyltransferase subunit fatty-acid and sterol biosynthesis acetyl-CoA hydrolase	metabolis YOL096c YDR232w YOL143c YGR2286c YGR204w YBR084w YDR044w YPL132w YNR058w YDR487c YOL066c YPL172c YOR176w YDL045c YGR267c YGR176w YOR196c YHR042w YOR196c YHR042w YOR209c YNR033w YNR041c YOR196c YHR042w YOR209c YNR033w YNR041c YOR196c YFR014w YNR057c YBR266c YFR043c YNL256w YKL027w YIL145c YGR255c	## of vital  COQ3  HEM1 RIB4 BIO2 ADE3 MIS1  HEM13 COX11 BIO3 RIB3 RIB2 COX10 HEM15 FAD1 FOLD FOLD FOLD SER1 HEM3 HEM14 BIO4 PDX3 RIB5 RIB7 BIO4 RIB7 BIO4 RIB7 BIO4 RIB7 RIB7 RIB7 RIB7 RIB7 RIB7 RIB7 RIB7	mins, cofactors and prosthetic groups 3,4-dihydroxy-5-hexaprenylbenzoate methyltransferase 5-aminolevulinate synthase 6,7-dimethyl-8-ribityllumazine synthase biotin synthetase C1-tetrahydrofolate synthase, cytoplasmic C1-tetrahydrofolate synthase, mitochondrial coproporphyrinogen III oxidase cytochrome c oxidase assembly protein DAPA aminotransferase DBP synthase DRAP deaminase farnesyl transferase flavin adenine dinucleotide (FAD) synthetase GTP cyclohydrolase I fTP cyclohydrolase II hexaprenyl pyrophosphate synthetase HTP reductase lipoic acid synthase NADPH-cytochrome P450 reductase nicotinate phosphoribosyltransferase para-aminobenzoate synthase para-pydroxybenzoate- polyprenyltransferase phosphoserine transaminase porphobilinogen deaminase porphobilinogen deaminase porphobilinogen synthase protoporphyrinogen oxidase, mitochondrial putative dethiobiotin synthetase pyridoxamine-phosphate oxidase riboflavin synthase, α subunit S-adenosyl-L-homocysteine hydrolase similarity to E. coli molybdopterin- converting factor chilx similarity to E. coli 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YDL247w YIL170w YIL171w YJR158w YJR158w YJDL138w Ilpid, faty YML075c YLR450w YML126c YCR048w YNR019c YJR109w YJL009w YNR016c YCR048w YNR019c YHR090c YMR015c YGR037c YBR222c YMR015c YGR060w YML280c YMR015c YGR060w YML02w YML042w YML042w YR113w YER026c YBR029c YSH139w YGR007w YGR020c YNL111c YHR007c YHR190w YJL1676w YDL056z YHR190w YJL1676w YDL052c	HXT12 HXT12 HXT16 HXT17 RGT2  tty-acid recid and HMG1 HMG2 HMG8 ERG10 ACC1 ARE1 ARE1 ARE2 FAA3 ACB1  PCS60 CEM11 ERG24 ERG5 ERG36 ERG2 CAT2 PIS1 CHO1 CDS1 CKI1 MUQ11 PCT1 CYB5 ERG11 ERG9 ERG20 SLC1 ERG9 ERG20 SLC1 FAS2	permease family strong similarity to sugar transport proteins sugar transport proteins sugar transport protein suppressor of sn/3 mutant  If and sterol metabolism  If sterol biosynthesis  3-hydroxy-3-methylglutaryl-CoA reductase 1 3-hydroxy-3-methylglutaryl-CoA reductase 2 3-hydroxy-3-methylglutaryl-CoA synthase acetyl-CoA carboxylase acetyl-CoA sterol acyltransferase acyl-CoA sterol acyltransferase acyl-CoA sterol acyltransferase acyl-CoA-binding protein (diazepambinding Inhibitor)  AMP-binding protein, peroxisomal β-keto-acyl-ACP synthase c-14 sterol methyl oxidase C-15 sterol desaturase C-25 sterol desaturase C-25 sterol desaturase C-3 sterol acylglycerol-inositol 3-phosphatidyltransferase CDP-diacylglycerol-serine C-phosphatidyltransferase CDP-diacylglycerol synthase choline kinase choline phosphate cytidylyltransferase choline phosphate cytidylyltransferase cytochrome P450 lanosterol 14a-demethylase farnesyl-diphosphate farnesyltransferase fatrs syltyransferase	YPL268w  YGL205w YMR008c YKR031c YLR020c YLL012w YJL080c YOL011w YMR006c YKL140w YBR204c  Iipid, fatty YIL160c YIL160c YIL160c YIL160c YPL172c YOR370c YGL155w YPR176c YJL031c YPL074w YBR003w YKR003w YKR003w YKR003w YKR005w YMR248w YDL079c YGR175w YGR175w YGR176c YJL031c YPL172c YGR176c YJL031c YPL172c YOR370c YPL172c YOR370c YR1655w YPR176c YJL031c YFL014w YBR003w YKR003w YKR003w YKR003w YKR005w YKR005w YHR015w YDL079c YLR195c YJR066w YLR195c YJR066c YHR013c YDL090c YHR013c YBL0156w	PLC1 POX1 PLB1 SPO14  TGL1 TGL2  -acid and POT1 FAA3 SEC59 GPI8 STE14  COX10 MSI4  CDC43 BET2 BET4 HSP12 COQ1 FOX2 FAA1 FAA2 FAA4 MDH3 NMT1 TOR1 RAM2 RAM1 ARD1 NAT1 of lipid, ACH1	s and phospholipids  1-phosphatidylinositol-4,5-bisphosphate phosphodiesterase acyl-CoA oxidase phospholipase B (lysophospholipase) phospholipase D similarity to triacylglycerol lipase similarity to triacylglycerol lipase similarity to triacylglycerol lipases strong similarity to human esterase D strong similarity to phospholipases strong similarity to Pib1p triacylglycerol lipase veak similarity to prospholipases strong similarity to Pib1p triacylglycerol lipase weak similarity to acylglycerol lipase weak similarity to peroxisomal serine-active lipase  sterol utilization  acetyl-CoA C-acyltransferase, peroxisomal acyl-CoA synthase dolichol kinase essential for GPl-anchor attachment farnesyl cysteine carboxyl-methyltransferase farnesyl transferase 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YHR042W YNR057C YBR035C YBR256C YER014W YNR057C YBR035C YBR256C YER043C YKL027W YIL145C YGR255C YMR113W	## of vital  COQ3  HEM1 RIB4 BIO2 ADE3 MIS1  HEM13 COX11 BIO3 RIB3 RIB2 COX10 HEM15 FAD1 FOLD FOLD FOLD SER1 HEM3 HEM14 BIO4 PDX3 RIB5 RIB7 BIO4 RIB7 BIO4 RIB7 BIO4 RIB7 RIB7 RIB7 RIB7 RIB7 RIB7 RIB7 RIB7	mins, cofactors and prosthetic groups 3,4-dihydroxy-5-hexaprenylbenzoate methyltransferase 5-aminolevulinate synthase 6,7-dimethyl-8-ribityllumazine synthase biotin synthetase C1-tetrahydrofolate synthase, cytoplasmic C1-tetrahydrofolate synthase, mitochondrial coproporphyrinogen III oxidase cytochrome c oxidase assembly protein DAPA aminotransferase DBP synthase DRAP deaminase farnesyl transferase flavin adenine dinucleotide (FAD) synthetase GTP cyclohydrolase I fTP cyclohydrolase II hexaprenyl pyrophosphate synthetase HTP reductase lipoic acid synthase NADPH-cytochrome P450 reductase nicotinate phosphoribosyltransferase para-aminobenzoate synthase para-pydroxybenzoate- polyprenyltransferase phosphoserine transaminase porphobilinogen deaminase porphobilinogen deaminase porphobilinogen synthase protoporphyrinogen oxidase, mitochondrial putative dethiobiotin synthetase pyridoxamine-phosphate oxidase riboflavin synthase, α subunit S-adenosyl-L-homocysteine hydrolase similarity to E. coli molybdopterin- converting factor chilx similarity to E. coli pantothenate synthetase similarity to E. coli pantothenate synthetase similarity to E. coli wilh protein similarity to E. coli wilh protein similarity to floylpolyglutamate synthetases and strong similarity to hypothetical protein YKL132c similarity to human

YLRA1175w C7R3   Copper transport protein   C7R3									
### STATES or prefixed to the boundaries of the control of the con	YPL023c			YOR031w	CRS5		YGR192c	TDH3	
Section of the Parties and the	YFR047c			YCL037c	SRO9		YOL059w	GPD3	
Description   Processing Control processing Contr	VHR111w			YMR243c	ZRC1	zinc- and cadmium-resistance protein	VER053c	HYK1	
Note of the state			proteins				YGL253w	HXK2	hexokinase II
ModRet   Mode	YOL151w			YDL128w	VCX1				
Secretary & prompty/propolescoped programs   Secretary & prompty/programs	YMR222c		similarity to S. pombe dihydrofolate			Ca <sup>2+</sup> -transporting P-type ATPase	YOL056w	GPM3	phosphoglycerate mutase
Systems of the property of the	YOR241w/						YER178w	PDA1	
Visible			synthase	YLR348c		dicarboxylate carrier protein	YBR221c	PDB1	pyruvate dehydrogenase (lipoamide)
VS-DIFF   VS-D							YGR193c	PDX1	
Post			methyltransferases	YJR121w	ATP2	F1F0-ATPase complex, F1 β subunit			X
PRINCESSON PROPERTY CONTROL OF CO	YGL039W							CDC19	
FEB.032   Storag amining to prohiphophophophophophophophophophophophophop	YBR176w						YDL021w	GPM2	
	YHR003c		strong similarity to molybdopterin-	YDR298c	ATP5	F1F0-ATPase complex, OSCP subunit	YMR323w		strong similarity to phosphopyruvate
VICLIDID	VDI 0360						VOR347c		
9.79.15 Hz stranspire faceplants preprintegraphics and in yethorogenic process of the process of	YOL049w		strong similarity to S. pombe Gsa1p	YEL017c-a	PMP2	H <sup>+</sup> -ATPase subunit, plasma membrane			strong similarity to S. pombe malate
and lytergoethydripolical kinesis in temporary control protection of victorial process of the protection of victorial protecti				YMR054W	SIVI		YMR125w	GCR3	
VPCIDING			and hydroxyethylthiazole kinase	YHR039c-a	VMA10	H <sup>+</sup> -ATPase V0 domain 13K subunit,	YDR050c		triose-phosphate isomerase
utilization of Valenths, conflorted and proteinated groups VPLISING PTP VPLISING PT				YEL027w	CUP5				
VEX.126 PC VICS VICS VICE VICE VICE VICE VICE VICE VICE VICE	utilization	of vitamin	ns. cofactors and prosthetic groups	YPI 234c	TFP3		YOR283w		
NALESE CYS WILLES AND AND STATE OF STATES AND	YDL141w	BPL1	biotin holocarboxylase synthetase			vacuolar			
Composition of Logical Public Public Published Public Published Pu				YLR447c	VMA6		giucone	eogene	SIS
NALES ADI Abbit-buchanea disconductase representation and protection and protecti			c haem lyase)	YOR270c	VPH1	H <sup>+</sup> -ATPase V0 domain 95K subunit,			
VRISSE Proc. repressible and phosphatase smillarly to a future for Cyneria and smillarly to a future for Cyneria and St. School. St. Proc. Proc. Proc. St. Proc. Proc. Proc. St. Proc. Pro				YGR020c	VMA7				
setong similarity to hypothetical protein hypotheti		PHO5	repressible acid phosphatase		\/\/\ <i>A</i>	vacuolar	YBR196c		glucose-6-phosphate isomerase
Feyblation of Villamine, confectors and prosthetic groups   VILL08W PROBLE   VILL08W PRO	INLIDZU		strong similarity to hypothetical protein			vacuolar	YKR097w	PCK1	phosphoenolpyruvate carboxykinase
Figure 1   Figure 2   Figure 3			YMR113w	YEL051w	VMA8				
of hypoic genes involved in glucoser repression (PRIZE Law Transport of vitamins, cofactors and prosthetic groups and the protein of the protein international protein internati				YKL080w	VMA5	H <sup>+</sup> -ATPase V1 domain 42K subunit,	YBR218c	PYC2	pyruvate carboxylase 2
VRH286 CATS Involved in glucose repression or transport of yellow plants and prosthetic group activities of the process of more of the process of the proces	YPR065w	ROX1		YPR036w	VMA13			SDL1	
Valuadie Zh. Va	YOR125c	CAT5				vacuolar		CAT8	transcription factor involved in
other vitamin, cofector and prosthetic-group activities TOR-IPC TOR-IP	transport	of vitamin	s, cofactors and prosthetic groups	YBR12/C	VIVIA2		YDR050c	TPI1	
other vitamin, oofsctor and prosthetic-group activities VDRSH0: VDRSH0: Smillarity to diffusionancial-reductases smillarity to furnifusionancial school signse VHLUSS FYERS VHLUSS FYERS VHLUSS VHLUSS FYERS VHLUSS VHLUSS FYERS VHLUSS FYERS VHLUSS FYERS VHLUSS FYERS VHLUSS FYERS FYERS VHLUSS FYERS F		FLX1		YDL185w	TFP1		nontos	a_nhosi	nhata nathway
VPBR3c   Similarity to £_gunni clannary al clobal dehydrogenses similarity to £_gunni clannary al clobal dehydrogenses similarity to £_gunni clannary al clobal dehydrogenses similarity to the fundamental potential similarity to fundamental potential protein similarity to fundamental potential potential similarity to fundamental potential potential potential potential similarity to fundamental potential potentia						H <sup>+</sup> -transporting P-type ATPase	_		
VERISSC Similarity to formyleterallydrofolate cycloligses similarity to formyleterallydrofolate sensitive to formyleterallydrofolate sensitive to formyleterallydrofolate cycloligses similarity to cycloridases sensitivity similarity to formyleterallydrofolate sensitivity cycloligy formyleterallydrofolates sensitivity cycloligidases similarity to cycloridases into formyleterallydrofolates sensitivity cycloligidases sonday in the formyleterallyd		min, cotac							
YER294w   Similarity to formyteteralydrofolate cyclo- ligase   Similarity to formyteteralydrofolate cyclo- ligase   Similarity to formyteteralydrofolate cyclo- ligase   Similarity to formyteteralydrofolate   Similarity to formyteteral			similarity to E. gunnii cinnamyl alcohol			symporter	YJL121c	POS18	D-ribulose-5-phosphate 3-epimerase
Highest   Hig	YER183c								
CR3Rieße willmitty to Rib2p  VGR144W 7H/H thismine-repressed protein  Ionic homeostasis  Nomeostasis of metal ions  YNL289c A7X1  Information in the protein and metal homeostasis factor  YNL289c A7X1  Information in the protein and metal homeostasis in the protein and metal homeostasis factor  YNL289c A7X1  Information in the protein and metal homeostasis in the protein associated with ferrir reductase activity  YNL289c A7X1  YNL289c A7X1  YNL289c A7X1  YNL289c A7X1  YNL289c A7X2  YNL289c A7X2  YNL289c A7X2  YNL289c A7X3  YNL289c A7X3  YNL289c A7X4  YNL289c YNL289c A7X4  YNL289c	VIII 010 a							TAL 1	strong similarity to transaldolase
YGRI/dw Tril# thiamine-repressed protein   Incinchomeostasis   Incinchomeostasis of metal   Ions   YIL0360 ATX1   antioxidant protein and metal   Ions   YIL0360 ATX1   antioxidant protein and metal   Ions   YIL0360 ATX1   antioxidant protein and metal   Ions   SPF1   YIR0760 ATX1   Antioxidant protein and metal   Ions   YIL0360 ATX1   Antioxidant protein   YIL0360 ATX1   YIL0							YPR074c	TKL1	transketolase 1
ionic homeostasis homeostasis of metal lons  NNL296 α / XY in antioxidant protein and metal homeostasis factor		THI4		YII 093c	TOK1		YBR117c	TKL2	transketolase 2
Nomeostasis of metal lons   YNL259c   ATX   antioxidant protein and metal homeostasis factor   YDR049c   Urital   ATX						phosphate transport protein,	tricarbo	oxylic-a	ncid pathway
Noneostasis for metal lons				YEL031w	SPF1		YIL125w	KGD1	2-oxoglutarate dehydrogenase complex
homestasis factor   MPR03e   LPA2   P-type ATPase involved in Na efflux   VPR03e   LPA5   VPR04F				YDR040c	ENA1		VDD1//00	VCD2	E1 component
VRR1058w FET3   Cell-surface ferroxidase   VRR138w   VLR138w   VLR14   VOR316c   COT1   colored ferroxidase   VRR138w   VLR14   COT2   Colored ferroxidase   VLR138w   VLR14   Colored ferroxidase   VLR14   Colored ferroxidase   VLR14   Colored ferroxidase   VLR14   Colored ferroxidase   VLR158w   VLR14   VRR158w   VLR14   Colored ferroxidase   VLR14   Colored ferroxidase   VLR158w   VLR14   Colored ferroxidase   VLR14   Colored ferroxidase   VLR14   Colored ferroxidase   VLR14   Colored ferroxidase   VLR14   VRR158w   VLR14   Colored ferroxidase   VLR158w   VLR158w   VLR158w   VLR158w   VLR158w   VLR158w   VLR158w   VLR158w   VLR158w   VLR154w   VLR158w			homeostasis factor			P-type ATPase involved in Na <sup>+</sup> efflux			E2 component
YOR316c   COT1   Cobalt accumulation protein   YPR-177c   CUP9   CUP9   CUP9   Promeostasis protein   Cup9   Copper homeostasis protein   Copper homeostasis protein   Copper transport protein   Copper transporting ATPase   Copper									
VPR154W   CTR   Copper transport protein   VPR154W   CTR	YOR316c	COT1	cobalt accumulation protein		747.07.17	similarity to burnetanide-sensitive Na <sup>+</sup> -K <sup>+</sup> -	YPR001w	CIT3	citrate (si)-synthase, mitochondrial
VPR124w CTR1   Cropper transport protein   VPR127bW VFR17bW CTR2   Cropper transport protein   Cropper transpor				YJL094c			YFL018c YPL262w		
YLR214w   YGL 166w   YCR176w   YCR270w   YCR270w YC	YPR124w	CTR1	copper transport protein			NapA	YNL009w		homology to isocitrate dehydrogenase
YL124w   FRE1   ferric (and cupric) reductase   FRE2   ferric (and cupric) reductase   YER03c   YER				YINKUI3C			YNLU3/C	IDH I	
YRL220c   FRE2   Fric (and cupric) reductase   YOR176w   YOR176							YOR136w	IDH2	
YGL256w ZRT1 VLL09c COX17 interacts genetically with SCO1 and SCO2 in cytochrome oxidase assembly YBR037c SCO1 involved in stabilization of Cox1p and Cox2p YGL071w RCS1 yLR130c ZRT2 VMR319c FET4 VOL122c SMF1 yR8290c BSD2 YKL064w MNR2 overexpression overcomes manganese toxicity YDR270w CCC2 YBR2950w PCA1 YDR370w GES Similarity to Fet3p Similarity to Subtage Fet3p PCR39w Fet3p Similarity to Inspection Strong similarity to Pho87p Strong similarity to Subtage strong similarity t	YKL220c	FRE2	ferric (and cupric) reductase			strong similarity to mitochondrial			isocitrate dehydrogenase, cytosolic
YLL009c COX17 interacts genetically with SCO1 and SCO2 in cytochrome oxidase assembly involved in stabilization of Cox1p and Cox2p involved in stabilizatio			high-affinity zinc-transport protein	YJL198w				MDH2	
YBR037c   SCO1   involved in stabilization of Cox1p and Cox2p   YGL07tw   RCS1   YLR130c   ZR12   YRM319c   YGL170tw   YMR319c   YGL170tw   YMR319c   YGL170tw   YGC170tw   YGL170tw   YGC170tw   YGC170tw   YGC170tw   YGC170tw   Y			interacts genetically with SCO1 and SCO2			strong similarity to phosphate-repressible	YJL200c		strong similarity to aconitate hydratase
VGL07tw   VGL	YBR037c	SCO1							
YLR130c   ZR12   VMR319c   FET4   VMR319c   VMR319			Cox2p			urea transport protein			strong similarity to Sdh4p
YOL122c SMF1   manganese transporter metal homeostasis protein overcomes manganese toxicity   YDR270w   CCC2   probable copper-transporting ATPase YBR299w   YPL041w   YDR370w   CCC2   Protein subunit   YDR506c   Similarity to copper homeostasis protein   Cup9p   YDR506c   YOL152w   Similarity to Fet3p   and Fre2p   YIR126c   YIR126c   YIR126c   YFL041w   Strong similarity to transferrin receptor protein   Strong similarity to transferrin receptor protein   YDR370w   CR290   YDR393w   ERR1   Energy   YDR377w   ATP17   ATPase symblase subunit   YDR132w   Atpase similarity to restance of the company of the content	YLR130c	ZRT2	low-affininty zinc transporter		GLII	voltage gated critoride challier protein			dehydrogenase
YBR290w BSD2   YKL064w MNR2   Overexpression overcomes manganese toxicity   YDR270w CCC2   YBR295w PCA1   P-type Cu²*-transporting ATPase   YGR240c PFK2   YGR296w   YGL096w   Similarity to Episoper homeostasis protein Cup9p   YDR506c   YGL152w YGL160w YGL162w YGL160w   YGL086w YGL160w   YGL086w YGL160w   YGL086w YGL160w YGL086w   YGL086w YGL160w YGL086w YGL086w YGL160w YGL086w YGL086w YGL160w YGL086w YGL086w YGL160w YGL086w				_			YJL045w		
toxicity YDR270w CCC2 YDR296w PCA1 YGL096w PCA1 YGL096w PCA1 YDR506c YOL152w YGL160w Similarity to Fre1p and Fre2p YIR126c YGL16w Strong similarity to transferrin receptor protein YFL041w Strong similarity to cell-surface ferroxidase YFL041w Strong similarity to cell-surface ferroxidase Fet3p  Toxicity YGR240c YGR240c PFK1 YMR205c PFK2 YGR240c PFK1 YMR205c PFK2 G-phosphofructokinase, β subunit G-phosphofructose-2-kinase, isoenzyme 1 G-phosphofructose-2-kinase, isoenzyme 2 Highlydrolipoamide S-acetyltransferase enolase I (2-phosphoglycerate dehydratase)  YMR28c YGR148c SDH1 YLL041c SDH2 YDR178w SDH4 Succinate dehydrogenase flavoprotein succinate dehydrogenase iron-sulphur yrotein subunit YDR178w SDH4 Succinate dehydrogenase flavoprotein yrotein subunit YDR178w SDH4 Succinate dehydrogenase flavoprotein yrotein subunit yDR178w SDH4 Succinate dehydrogenase iron-sulphur yrotein subunit yDR178w SDH4 Succinate dehydrogenase iron-sulphur yrotein subunit yDR178w SDH4 Succinate dehydrogenase flavoprotein yrotein subunit yDR178w SDH4 Succinate dehydrogenase flavoprotein yrotein subunit yDR178w SDH4 Succinate dehydrogenase flavoprotein yrotein subunit yDR178w SDH4 Succinate dehydrogenase iron-sulphur yrotein subunit yDR178w SDH4 Succinate dehydrogenase flavoprotein yrotein subunit yDR178w SDH4 Succinate dehydrogenase flavoprotein yrotein subunit yDR178w SDH4 Succinate dehydrogenase iron-sulphur yrotein subunit yDR178w SDH4 YLL041c SDH2 YDR178w SDH4 YLL041c SDH2 YDR178w SDH4 Succinate dehydrogenase iron-sulphur yrotein subunit yLL041c SDH2 YDR178w SDH4 YLL041c SDH2 YDR178w SDH4 YLL041c SDH2 YDR178w SDH4 YLL041c SDH2 YDR178w SDH4 YLL04	YBR290w	BSD2	metal homeostasis protein	Energ	Jy		YOR142w		strong similarity to succinate-CoA ligase
YDR270w CCC2   Probable copper-transporting ATPase   YBR295w PCA1   P-type Cu²*-transporting ATPase   YGR240c PFK1   YGR240c PFK2   Fybosphofructokinase, α subunit   YDR178w SDH4   Succinate dehydrogenase iron-sulphur protein subunit   YDR178w SDH4   Succinate dehydrogenase iron-sulphur   Y	YKLU64W	IVIINK2		glycolv	sis		YKL148c	SDH1	
YGL096w similarity to copper homeostasis protein Cup9p YDR506c similarity to Fet3p YOL136w yGL162w similarity to Fre1p and Fre2p YGL160w similarity to transferrin receptor protein YFL041w strong similarity to cell-surface ferroxidase Fet3p YOR393w ERR1  YMR205c PFK2 6-phosphofructose-2-kinase, isoenzyme 1 6-phosphofructose-2-kinase, isoenzyme 2 7 VDL136c PFK2 6-phosphofructose-2-kinase, isoenzyme 2 6-phosphofructose-2-kinase, isoenzyme 2 7 VDL162w similarity to Fre1p and Fre2p YNL071w LAT1 YGR254w ENO1 VGR393w ERR1  YDR178w SDH4 succinate dehydrogenase membrane anchor subunit for Sdh2p YDR178w SDH4 succinate dehydrogenase membrane anchor subunit for Sdh2p YDR178w SDH4 succinate dehydrogenase membrane anchor subunit for Sdh2p YESPITATION FRESP YMR28c AEP2 YGR080s STF2 YGR080s STF2 YGR080s STF2 YGR30w-a STF1 ATPase stabilizing factor YDR377w ATP17 ATPase synthase subunit f						6 phoophofy intokinggo as culturait	YLL041c	SDH2	succinate dehydrogenase iron-sulphur
Cup9p YDR506c similarity to Fet3p YOL152w YGL160w YGL160w YGL160w YGL160w YRL041w YFL041w YFL041w YFL041w YFL041w YGR393w YGR393w YGR393w YGR393w YGR393w YGR395b YIL107c PFK26 6-phosphofructose-2-kinase, isoenzyme 1 6-phosphofructose-2-kinase, isoenzyme 2 dihydrotlipoamide S-acetyltransferase enolase (2-phosphoglycerate dehydratase) YMR28c YGR008c YFL041w Arpase stabilizing factor YDR377w Arpase synthase subunit for Sdh2p YMR28c YGR008c YFL041w YDR377w Arpase synthase subunit for Sdh2p		FUMI	similarity to copper homeostasis protein	YMR205c	PFK2	6-phosphofructokinase, β subunit	YDR178w	SDH4	succinate dehydrogenase membrane
YOL152w Similarify to Fre1p and Fre2p YGL160w Similarity to hypothetical protein YLR04rc and Fre2p YR126c Similarity to transferrin receptor protein YFL041w Strong similarity to cell-surface ferroxidase Fet3p YOR393w ERR1 VGR393w ERR1 dihydrolipoamide S-acetyltransferase enolase (12-phosphoglycerate dehydratase) YMR28c AEP2 2'-O-ribosyl phosphate transferase YGR008c STF2 ATPase stabilizing factor YDL130w-a STF1 ATPase symbolic for the YOR393w ERR1 enolase-related protein YDR377w ATP17 ATPase symboli f	YDR5060								
and Fre2p YJR126c similarity to transferrin receptor protein YFL041w strong similarity to cell-surface ferroxidase YHR174w ENO2 enolase II (2-phosphoglycerate dehydratase) YHR174w ENO2 enolase II (2-phosphoglycerate dehydratase) YDL130w-a STF1 ATPase stabilizing factor YDR377w ATP17 ATPase synthase subunit f	YOL152w		similarity to Fre1p and Fre2p	YNL071w	LAT1	dihydrolipoamide S-acetyltransferase	respira	tion	
YJR126c similarity to transferrin receptor protein YFL041w strong similarity to cell-surface ferroxidase YFL041w strong similarity to cell-surface ferroxidase YRR174w ENO2 enoíase II (2-phosphoglycerate dehydratase) YGR008c STF2 ATPase stabilizing factor YDL130w-a STF1 ATPase synthase subunit f YOR393w ERR1 enoíase-related protein YDR377w ATP17 ATPase synthase subunit f	YGL160w			YGR254w	ENO1		YMR282c	AEP2	2'-O-ribosyl phosphate transferase
Fet3p YOR393w ERR1 enolase-related protein YDR377w ATP17 ATPase synthase subunit f			similarity to transferrin receptor protein	YHR174w	ENO2	enolase II (2-phosphoglycerate	YGR008c	STF2	ATPase stabilizing factor
	YFLU41W			YOR393w	ERR1				ATPase synthase subunit f
YOR381w strong similarity to ferric reductase Fre2p YKL060c FBA1 fructose-bisphosphate aldolase YIL043c CBR1 cytochrome b5 reductase			strong similarity to ferric reductase Fre2p	YPL281c	ERR2	enolase-related protein	YER061c	CEM1	β-keto-acyl-ACP synthase
YOR384w strong similarity to ferric reductase Fre2p YBR196c PGI1 glucose-6-phosphate isomerase YKL150w MCR1 cytochrome b5 reductase	YOR384w		strong similarity to ferric reductase Fre2p	YBR196c	PGI1	glucose-6-phosphate isomerase	YKL150w	MCR1	cytochrome b5 reductase
	YNR060w		strong similarity to Fre2p and hypothetical	YJL052w	TDH1		YKL141w	SDH3	cytochrome b560 subunit of respiratory
YBR024w SCO2 strong similarity to Sco1p YJR009c TDH2 glyceraldehyde-3-phosphate YJR048w CYC1 cytochrome c isoform 1	YBR024w	SCO2		YJR009c	TDH2	glyceraldehyde-3-phosphate			cytochrome c isoform 1
dehydrogenase 2 YEL039c CYC7 cytochrome c isoform 2						denydrogenase 2	YEL039c	CYC7	cytochrome c isoform 2

VMI 100~	COV14	ovtochrome a ovidese essembly protein	V D104.4	PDOF	nyruwata dagarhayylaga isazyma 2	VHD170	OVE?	NAPDH dehydrogenase (old yellow
YML129c YDR079w YGL187c	COX14 PET100 COX4	cytochrome c oxidase assembly protein cytochrome c oxidase assembly protein cytochrome c oxidase subunit IV	YLR134w YGR087c YAL060w	PDC5 PDC6 FUN49	pyruvate decarboxylase, isozyme 2 pyruvate decarboxylase, isozyme3 similarity to alcohol/sorbitol	YHR179w YPL171c	OYE3	enzyme), isoform 1
YGL187c YNL052w		cytochrome c oxidase subunit IV cytochrome c oxidase subunit V.A	TALUOUW	ruiv49	similarity to alcohol/sorbitol dehydrogenase	TFLI/IC	UTES	NAPDH dehydrogenase (old yellow enzyme), isoform 3
YIL111w	COX5B	cytochrome c oxidase subunit Vb	YAL061w	FUN50	similarity to alcohol/sorbitol		ICL2	non-functional isocitrate lyase
YHR051w YGL191w	COX6 COX13	cytochrome c oxidase subunit VI cytochrome c oxidase subunit VIa	YMR318c		dehydrogenase similarity to alcohol-dehydrogenase	YOL079w YEL020c		similarity to NADH dehydrogenase similarity to <i>O. formigenes</i> oxalyl-CoA
YLR038c	COX12	cytochrome c oxidase subunit VIB	YHR039c		similarity to aldehyde dehydrogenases			decarboxylase
YMR256c YDL067c	COX7 COX9	cytochrome c oxidase subunit VII cytochrome c oxidase subunit VIIA	YPL088w YMR285c		similarity to aryl-alcohol dehydrogenases similarity to Ccr4p	YDR384c		strong similarity to Y. lipolytica GPR1
YLR395c	COX8	cytochrome c oxidase subunit VIII	YHL008c		similarity to M. formicicum formate			gene
YOR065w YER154w	CYT1 OXA1	cytochrome cytoase biogenesis protein	YKR096w		dehydrogenase similarity to mitochondrial aldehyde			
YER 154W YGR207c	ETF-β	cytochrome oxidase biogenesis protein electron-transferring flavoprotein,			dehydrogenase Ald1p	Cellg	rowt	h, cell division and
YKL016c	ATP7	β subunit	YDR380w		similarity to pyruvate decarboxylases	DNA:	synth	nesis
YKL016C YBL099w	ATP1	F1F0-ATPase complex, F0 D subunit F1F0-ATPase complex, F1 α subunit	YNL331c YCR107w		strong similarity aryl-alcohol reductase strong similarity aryl-alcohol reductases		•	
YJR121w	ATP2	F1F0-ATPase complex, F1 β subunit	YCR105w		strong similarity to alcohol	cell gro	wth	
YDL004w YPL078c	ATP4	F1F0-ATPase complex, F1 δ subunit F1F0-ATPase complex, F1 δ subunit	YMR169c	ALD4	dehydrogenases strong similarity to aldehyde	YPL268w	PLC1	1-phosphatidylinositol-4,5-bisphosphate
YPL271w		F1F0-ATPase complex, F1 ε subunit			dehydrogenase			phosphodiesterase
YBR039w YDR298c	ATP3 ATP5	F1F0-ATPase complex, F1 γ subunit F1F0-ATPase complex, OSCP subunit	YDL243c		strong similarity to aryl-alcohol dehydrogenase	YCR088w YDL029w	ABP1 ACT2	actin-binding protein actin-like protein
YLR295c	ATP14	F1F0-ATPase complex, subunit h	YJR155w		strong similarity to aryl-alcohol	YOL052c	SPE2	adenosylmethionine decarboxylase
YEL053c YLL009c	MAK10 COX17	glucose-repressible protein interacts genetically with SCO1 and SCO2	YFL056c		dehydrogenase strong similarity to aryl-alcohol	YNL138w YER170w	SRV2 ADK2	adenylate cyclase-associated protein, 70K adenylate kinase, mitochondrial
		in cytochrome oxidase assembly			dehydrogenases	YBR109c	CMD1	calmodulin
YJR034w	PET191	involved in assembly of cytochrome oxidase	YFL057c		strong similarity to aryl-alcohol dehydrogenases	YHR135c YNL154c	YCK1 YCK2	casein kinase I isoform casein kinase I isoform
YMR165c	SMP2	involved in plasmid maintenance,	YOL165c		strong similarity to aryl-alcohol	YJL174w	KRE9	cell-wall synthesis protein
YML054c	CYB2	respiration and cell proliferation lactate dehydrogenase cytochrome b2	YOR388c		dehydrogenases strong similarity to <i>H. polymorpha</i> formate	YNL327w YLR175w	EGT2 CBF5	cell-cycle regulation protein centromere/microtubule binding protein
YBR192w	RIM2	mitochondrial carrier protein (MCF)	1010000		dehydrogenase	YGR167w	CLC1	clathrin light chain
YMR089c	YTA12	protease of the SEC18/CDC48/PAS1 family of ATPases (AAA)	metaho	lism of	energy reserves (glycogen and	YDR251w	PAM1	coiled-coil protein multicopy suppressor of loss of PP2A
YLR044c	PDC1	pyruvate decarboxylase, isozyme 1	trehalo		chargy reserves (grycogen and	YBL007c	SLA1	cytoskeleton assembly control protein
YGR062c	COX18	required for activity of mitochondrial	VEI 044	GI CO	14 alugan branchina annurs (shissess	YFL001w	DEG1	depressed growth-rate protein
YBR185c	MBA1	cytochrome oxidase respiratory chain assembly protein	YEL011w	GLC3	1,4-glucan branching enzyme (glycogen branching enzyme)	YLR300w YDR261c	EXG1 EXG2	exo-1,3glucanase (I/II), major isoform exo-1,3glucanase minor isoform
YDL107w	MSS2	ser/thr protein kinase	YBR001c	NTH2	α,α-trehalase	YPR159w	KRE6	glucan synthase subunit
YPR048w		similarity to M. domestica NADPH- ferrihemoprotein reductase and	YDR074w	TPS2	α,α-trehalose-phosphate synthase, 105K subunit	YBR212w YOR043w	NGR1 WHI2	glucose-repressible RNA-binding protein growth regulation protein
VOL 000		mammalian nitric-oxide synthases	YMR261c	TPS3	α,α-trehalose-phosphate synthase, 115K	YKL021c	MAK11	involved in cell growth and replication of
YGL226w		similarity to <i>N. crassa</i> cytochrome c oxidase subunit V	YML100w	TSL1	subunit α,α-trehalose-phosphate synthase, 123K	YMR165c	SMP2	M1 dsRNA virus involved in plasmid maintenance,
YMR244w		similarity to NCA3 and SUN4 protein			subunit			respiration and cell proliferation
YML087c		strong similarity to cytochrome b5- and nitrate reductases	YBR126c	TPS1	α,α-trehalose-phosphate synthase, 56K subunit	YNL197c YDR293c	WHI3 SSD1	involved in regulation of cell size involved in the tolerance to high
YML125c		strong similarity to cytochrome b5- and	YPR026w	ATH1	acid trehalase, vacuolar			concentration of Ca2+
YPR004c		nitrate reductases strong similarity to electron transfer	YBR299w YHR047c	MAL32 AAP1	α-glucosidase alanine/arginine aminopeptidase	YOR336w YDR480w	KRE5 DIG2	killer toxin-resistance protein MAP kinase-associated protein
		flavoproteins α subunit	YPL031c	PHO85	cyclin-dependent protein kinase	YJR032w	CPR7	member of the cyclophilin family
YOR356w		strong similarity to human electron transfer flavoprotein-ubiquinone	YLR071c	RGR1	DNA-directed RNA polymerase II holoenzyme subunit	YGR029w	ERV1	mitochondrial biogenesis and cell viability protein
		oxidoreductase	YER054c	GIP2	Glc7p-interacting protein	YBR089c-a		nonhistone chromosomal protein
YDL085w		strong similarity to NADH dehydrogenase	YBR229c	ROT2 GPH1	glucosidase II, catalytic subunit	YPR052c	NHP6A	nonhistone chromosomal protein related
YMR145c		(ubiquinone) strong similarity to NADH dehydrogenase	YPR160w YPL240c	HSP82	glycogen phosphorylase heat-shock protein	YKL203c	TOR2	to mammalian HMG1 phosphatidylinositol 3-kinase
		(ubiquinone)	YKL128c	PMU1	high copy suppressor of ts tps2 mutant	YCR034w	GNS1	probable 1,3glucan synthase subunit
YDL080c		strong similarity to pyruvate decarboxylases	YDR001c	NTH1	phenotype neutral trehalase (α,α-trehalase)	YOR149c YPL140c	SMP3 MKK2	protein kinase C pathway protein protein kinase of the MAP kinase kinase
YDR178w	SDH4	succinate dehydrogenase membrane	YMR105c	PGM2	phosphoglucomutase, major isoform			(MEK) family
YNL118c	PSU1	anchor subunit for Sdh2p suppressor protein of a yeast <i>pet</i> mutant	YKL127w YNR032w	PGM1 PPG1	phosphoglucomutase, minor isoform phosphoprotein phosphatase PPG	YDR151c	CTH1	protein of the inducible CCCH zinc-finger family
YFR033c	QCR6	ubiquinol-cytochrome c reductase 17K			catalytic subunit		PPH3	protein ser/thr phosphatase
YPR191w	QCR2	protein ubiquinol-cytochrome c reductase 40K	YBL058w YLR273c	SHP1 PIG1	potential regulatory subunit for Glc7p protein interacting with Gsy2p	YDL006w YDL134c	PTC1 PPH21	protein ser/thr phosphatase 2c protein ser/thr phosphatase PP2A-1
		subunit II	YIL045w	PIG2	protein interacting with Gsy2p	YDL188c	PPH22	protein ser/thr phosphatase PP2A-2
YBL045c	COR1	ubiquinol-cytochrome c reductase 44K core protein	YJL137c	GLG2	self-glucosylating initiator of glycogen synthesis	YDR137w YJR090c	RGP1 GRR1	reduced growth phenotype protein required for glucose repression and for
YHR001w-a	a QCR10	ubiquinol-cytochrome c reductase 8.5K	YKR058w	GLG1	self-glycosylating initiator of glycogen			glucose and cation transport
YGR174c	CBP4	subunit ubiquinol-cytochrome c reductase	YER133w	GLC7	synthesis ser/thr phosphoprotein phosphatase 1,	YGL190c	CDC55	ser/thr phosphatase 2A regulatory subunit B
		assembly factor			catalytic subunit	YAL016w	TPD3	ser/thr phosphatase 2A, regulatory
YGL119w	ABC1	ubiquinol-cytochrome c reductase	YOR178c	GAC1	ser/thr phosphoprotein phosphatase 1,		NAVV+	subunit A
YEL024w	RIP1	complex assembly protein ubiquinol-cytochrome c reductase iron-	YPR184w		regulatory subunit similarity to glycogen debranching	YOR231w YPR161c	MKK1 SGV1	ser/thr protein kinase ser/thr protein kinase
		sulphur protein		EOD?	enzymes	YHR030c	SLT2	ser/thr protein kinase of MAP kinase
YDR529c	QCR7	ubiquinol-cytochrome c reductase subunit 7	YJL221c YOL157c	FSP2	strong similarity to α-D-glucosidase strong similarity to α-glucosidases	YJL095w	BCK1	family ser/thr protein kinase of the MEKK family
YGR183c	QCR9	ubiquinol-cytochrome c reductase	YIL172c		strong similarity to Fsp2p		BCK2	ser/thr protein kinase of the protein
YJL166w	QCR8	subunit 9 ubiquinol-cytochrome c reductase	YJL216c YFR015c	GSY1	strong similarity to Mal62p UDP glucose-starch glucosyltransferase,	YNL180c		kinase C pathway similarity to S. pombe Cdc42p and other
		subunit VIII			isoform 1		OT: :	GTP-binding proteins
YMR073c		weak similarity to C-terminal part of cytochrome b5 and b2	YLR258w	GSY2	UDP-glucose-starch glucosyltransferase, isoform 2	YOR027w YGL106w	STI1	stress-induced protein strong similarity to calmodulins
YNL237w	YTP1	weak similarity to mitochondrial electron	YKL035w	UGP1	UTP-glucose-1-phosphate	YER177w	ВМН1	strong similarity to mammalian 14-3-3
		transport proteins			uridylyltransferase	YPL032c		proteins
fermen	tation		other e	nergy-d	generation activities	YPL032c YKL161c		strong similarity to Pam1p strong similarity to ser/thr-specific protein
		alach al dahi dasa asa a						kinase Slt2p
YOL086c YMR303c		alcohol dehydrogenase I alcohol dehydrogenase II	YIL160c YGL205w	POT1 POX1	acetyl-CoA C-acyltransferase, peroxisomal acyl-CoA oxidase	YDL224c YDR099w	ВМН2	strong similarity to WHI3 protein suppressor of clathrin deficiency
YMR083w	ADH3	alcohol dehydrogenase III	YMR170c	ALD5	aldehyde dehydrogenase 2 (NAD+),	YJR075w	HOC1	suppressor of pkc1
YGL256w YBR145w		alcohol dehydrogenase IV alcohol dehydrogenase V	YML035c	AMD1	mitochondrial AMP deaminase	YOR075w YHR206w		syntaxin (T-SNARE) of the ER transcription factor with similarity to Hsf1p
YER073w		aldehyde dehydrogenase (NAD+)	YCR005c	CIT2	citrate (si)-synthase, peroxisomal	YNL079c	TPM1	tropomyosin 1
YPL061w YDL174c	ALD6 DLD1	aldehyde dehydrogenase, cytosolic D-lactate ferricytochrome c	YKR009c	FOX2	hydratase-dehydrogenase-epimerase, peroxisomal	YLR337w YLR403w	VRP1 SFP1	verprolin zinc-finger protein
		oxidoreductase (D-LCR)	YMR267w		inorganic pyrophosphatase, mitochondrial			
YML004c YOR126c	GLO1 EST2	glyoxalase I isoamyl acetate hydrolytic enzyme	YDL066w	IDP1	isocitrate dehydrogenase (NADP⁺), mitochondrial	budding	, cell po	plarity and filament formation
YPL275w	LUIL	putative formate dehydrogenase/putative	YER065c	ICL1	isocitrate lyase	YFL039c		actin
YPL276w		pseudogene putative formate dehydrogenase/putative	YKL085w YDL078c	MDH1 MDH3	malate dehydrogenase, mitochondrial malate dehydrogenase, peroxisomal	YDR129c YCR088w		actin filament bundling protein, fimbrin actin-binding protein
		pseudogene	YNL117w	MLS1	malate synthase 1	YDL029w	ACT2	actin-like protein
YDR081c YLR044c	PDC2 PDC1	pyruvate decarboxylase regulatory protein pyruvate decarboxylase, isozyme 1	YIR031c	DAL7	malate synthase 2	YNL138w YOR304c-a		adenylate cyclase-associated protein, 70K AIP3 binding protein
						1011304C-8	UNIC	, a biliding protein
NIATELIDE	TIOT OOM	CLIDD   90 MAN 1007						41

YBL085w BOI1	BEM1 protein-binding protein	YDL135c	RDI1	RHO GDP dissociation inhibitor with	YBR253w	SRB6	DNA-directed RNA polymerase II
YBR200w BEM1	bud emergence mediator			activity toward Rho1p		MSG5	suppressor protein
YPL161c BEM4 YDR351w SBE2	bud emergence protein bud growth protein	YOR127w	RGA1	RHO-type GTPase-activating protein for Cdc42p	YNL053w YNL238w	KEX2	dual-specifity protein phosphatase endoproteinase of late Golgi
YLR319c BUD6 YNL271c BNI1	bud site selection protein budding protein	YKL181w YJR076c	PRPS1 CDC11	ribose-phosphate pyrophosphokinase septin	YLR300w	EXG1	compartment exo-1,3—glucanase (I/II), major isoform
YER114c BOI2	budding protein	YHR107c	CDC12	septin	YDR261c	EXG2	exo-1,3glucanase minor isoform
YJR092w BUD4 YLR353w BUD8	budding protein budding protein	YGL190c	CDC55	ser/thr phosphatase 2A regulatory subunit B	YKL007w YIL034c	CAP1 CAP2	F-actin capping protein, α subunit F-actin capping protein, β subunit
YGR041w BUD9	budding protein	YAL016w	TPD3	ser/thr phosphatase 2A, regulatory	YJL157c	FAR1	factor arrest protein
YBR109c CMD1 YHR135c YCK1	calmodulin casein kinase I isoform	YER133w	GLC7	subunit A ser/thr phosphoprotein phosphatase 1,	YAL041w YGL097w	CDC24 SRM1	GDP/GTP exchange factor for Cdc42p GDP/GTP exchange factor for
YNL154c YCK2	casein kinase I isoform			catalytic subunit			Gsp1p/Gsp2p
YPL255w BBP1 YDR182w CDC1	cell division control protein cell division control protein	YOR178c	GAC1	ser/thr phosphoprotein phosphatase 1, regulatory subunit	YNL236w YHL025w	SIN4 SNF6	global regulator protein global transcription activator
YLR314c CDC3 YFL009w CDC4	cell division control protein cell division control protein	YKL048c YOR231w	ELM1 MKK1	ser/thr protein kinase ser/thr protein kinase	YKL104c	GFA1	glucosamine-fructose-6-phosphate transaminase
YJL174w KRE9	cell-wall synthesis protein	YBL105c	PKC1	ser/thr protein kinase	YPL115c	BEM3	GTPase-activating protein for Cdc42p and
YBR038w CHS2 YBR023c CHS3	chitin synthase II chitin synthase III	YHR030c	SLT2	ser/thr protein kinase of MAP kinase family	YHR005c	GPA1	Rho1p GTP-binding protein α subunit of the
YLR330w CHS5	chitin synthesis protein	YJL095w	BCK1	ser/thr protein kinase of the MEKK family			pheromone pathway
YLL050c COF1 YDR251w PAM1	cofilin, actin binding and severing protein coiled-coil protein multicopy suppressor	YLR362w YER167w	STE11 BCK2	ser/thr protein kinase of the MEKK family ser/thr protein kinase of the protein	YOR212w	STE4	GTP-binding protein β subunit of the pheromone pathway
YPL256c CLN2	of loss of PP2A cyclin, G1/S specific	YDL159w	STE7	kinase C pathway ser/thr/tyr protein kinase of MAP kinase	YJR086w	STE18	GTP-binding protein γ subunit of the pheromone pathway
YBR160w CDC28	cyclin-dependent protein kinase		OTLY	kinase family	YLR229c	CDC42	GTP-binding protein of RAS superfamily
YNL243w SLA2 YLR071c RGR1	cytoskeleton assembly control protein DNA-directed RNA polymerase II	YDL225w		similarity to Cdc11p, Cdc3p and human CDC10 protein	YNL173c	MDG1	GTP-binding protein of the pheromone pathway
YKL007w CAP1	holoenzyme subunit	YGL054c YCR009c	RVS161	similarity to D. melanogaster cni protein	YER020w	GPA2	guanine nucleotide-binding regulatory
YIL034c CAP2	F-actin capping protein, α subunit F-actin capping protein, β subunit			similarity to human amphiphysin and Rvs167p	YDL227c	НО	protein homothallic switching endonuclease
YJL157c FAR1 YAL041w CDC24	factor arrest protein GDP/GTP exchange factor for Cdc42p	YDR208w YDR409w	MSS4	similarity to human PI P 5-kinase similarity to Nfi1p	YNL291c YLL021w	MID1 SPA2	involved in Ca <sup>2+</sup> influx during mating involved in cell polarity
YCR038c BUD5	GDP/GTP exchange factor for	YDL125c	YHI1	similarity to protein kinase C inhibitor-I	YLR452c	SST2	involved in desensitization to α-factor
YGR070w ROM1	Rsr1p/Bud1p GDP/GTP exchange protein for Rho1p	YDR245w	MNN10	similarity to <i>S. pombe</i> galactosyltransferase	YDR085c	AFR1	pheromone involved in morphogenesis of the mating
YLR371w ROM2 YGL155w CDC43	GDP/GTP exchange protein for Rho1p geranylgeranyltransferase type I ß subunit	YFR040w YKR028w	SAP155 SAP190	Sit4p-associated protein Sit4p-associated protein	YER149c	PEA2	projection involved in oriented growth toward mating
YER155c BEM2	GTPase-activating protein	YJL098w	SAP 190 SAP 185	Sit4p-associating protein	1 EN 1490	FEAZ	partner
YKL092c BUD2	GTPase-activating protein for Bud1p/Rsr1p	YLR372w YHR103w	SUR4 SBE22	sterol isomerase strong similarity to budding protein Sbe2p	YMR052w	FAR3	involved in pheromone-mediated cell cycle arrest
YPL115c BEM3	GTPase-activating protein for Cdc42p and	YGL106w	OBLLL	strong similarity to calmodulins	YMR127c	SAS2	involved in silencing at HMR
YGR152c RSR1	Rho1p GTP-binding protein	YBR210w		strong similarity to <i>D. melanogaster</i> cornichon protein	YPR141c YPL187w	KAR3 MFα1	kinesin-related protein mating pheromone α-1 factor
YLR229c CDC42 YIL118w RHO3	GTP-binding protein of RAS superfamily GTP-binding protein of the RHO family	YPL032c YNL320w		strong similarity to Pam1p strong similarity to S. pombe Bem46p	YGL089c YDR461w	MFα2 MFA1	mating pheromone α-2 factor mating pheromone a-factor 1
YKR055w RHO4	GTP-binding protein of the RHO family	YKL161c		strong similarity to ser/thr-specific protein	YNL145w	MFA2	mating pheromone a-factor 2
YPR165w RHO1	GTP-binding protein of the RHO subfamily of RAS-like proteins	YBR161w		kinase Slt2p strong similarity to Sur1p	YLR332w YHR066w	MID2 SSF1	mating process protein mating protein
YNL090w RHO2	GTP-binding protein of the RHO subfamily of RAS-like proteins	YJR075w YDR297w	HOC1 SUR2	suppressor of pkc1 suppressor of rvs161 and rvs167	YDR143c YCR040w	SAN1 MATα1	mating type regulatory protein mating type regulatory protein (expressed
YOR156c NFI1	interacts with Cdc12p in 2-hybrid assay			mutations			copy at MAT locus)
YKR063c LAS1	involved in cell morphogenesis, cytoskeletal regulation and bud formation	YPL057c	SUR1	suppressor of rvs161, rvs167, and cls2 mutations	YCR039c	MATα2	mating type regulatory protein (expressed copy at MAT locus)
YLL021w SPA2 YDR085c AFR1	involved in cell polarity involved in morphogenesis of the mating	YKL043w YGL181w	PHD1 GTS1	transcription factor transcription factor of the	YCL066w	α1	mating type regulatory protein (silenced copy at HML locus)
YMR273c ZDS1	projection involved in negative regulation of cell	YHR084w	STE12	Gcs1p/Glo3p/Sps18p family transcriptional activator	YCL067c	α2	mating type regulatory protein (silenced copy at HML locus)
	polarity	YNL079c	TPM1	tropomyosin 1 tropomyosin 2	YCR097w	A1	mating type regulatory protein (silenced
YER149c PEA2	involved in oriented growth towards mating partner	YIL138c YBR083w	TPM2 TEC1	Ty transcription activator	YCR096c	A2	copy at HMR locus) mating type regulatory protein (silenced
YDR293c SSD1	involved in the tolerance to high concentration of Ca <sup>2+</sup>	YGL095c	VPS45	vacuolar protein sorting-associated protein	YIL047c	SYG1	copy at HMR locus) member of the major facilitator
YKL079w SMY1 YOR198c BFR1	kinesin-related protein maintenance of normal ploidy	YLR337w	VRP1	verprolin	YBL016w	FUS3	superfamily mitogen-activated protein kinase (MAP
YJL158c	member of the Pir1p/Hsp150p/Pir3p			sponse and mating-type			kinase)
YJL159w	family member of the Pir1p/Hsp150p/Pir3p	determ	ination		YGL151w YPR168w	NUT1 NUT2	negative regulator of HO endonuclease negative regulator of HO endonuclease
YJL160c	family member of the Pir1p/Hsp150p/Pir3p	YJR004c YNR044w	SAG1	α-agglutinin α-agglutinin anchor subunit	YKL185w YCL029c	ASH1 BIK1	negative regulator of HO expression nuclear fusion protein
	family	YGL032c	AGA2	α-agglutinin binding subunit	YML065w	ORC1	origin recognition complex, 104K subunit
YOR188w MSB1 YGR014w MSB2	morphogenesis-related protein multicopy suppressor of a cdc24 bud	YDR264c YKL209c	AKR1 STE6	ankyrin repeat-containing protein ATP-binding cassette transporter protein	YNL261w YHR118c	ORC5 ORC6	origin recognition complex, 50K subunit origin recognition complex, 50K subunit
YHR023w MYO1	emergence defect	YIL015w	BAR1	barrier pepsin	YPR162c	ORC4	origin recognition complex, 56K subunit
	myosin 1 isoform (type II myosin) heavy chain	YBR200w YPL161c	BEM4	bud emergence mediator bud emergence protein	YLL004w YBR060c	ORC3 RRR1	origin recognition complex, 62K subunit origin recognition complex, 72K subunit
YOR326w MYO2 YAL029c MYO4	myosin heavy chain myosin heavy chain, unconventional	YML057w YLR433c	CMP2 CNA1	calcineurin B, catalytic subunit calcineurin B, catalytic subunit	YFL026w YKL178c	STE2 STE3	pheromone α-factor receptor pheromone α-factor receptor
	(class V) isoform	YKL190w	CNB1	calcineurin B, regulatory subunit	YCL032w	STE50	pheromone response pathway protein
YMR109w <i>MYO5</i> YKL129c <i>MYO3</i>	myosin I myosin type I	YBR109c YCR002c	CMD1 CDC10	calmodulin cell division control protein	YDR103w	STE5	pheromone signal transduction pathway protein
YBR089c-a NHP6B YPR052c NHP6A	nonhistone chromosomal protein nonhistone chromosomal protein related	YLR314c YNL188w	CDC3 KAR1	cell division control protein cell division control protein	YCR034w YLR389c	GNS1 STE23	probable 1,3—glucan synthase subunit protease involved in α-factor processing
	to mammalian HMG1	YCL027w	FUS1	cell fusion protein	YML032c	RAD52	recombination and DNA repair protein
YCR057c PWP2 YBL058w SHP1	periodic tryptophan protein potential regulatory subunit for Glc7p	YJL174w YNL192w	KRE9 CHS1	cell-wall synthesis protein chitin synthase I	YDR392w YCL055w	SPT3 KAR4	regulatory protein regulatory protein required for pheromone
YCR034w GNS1	probable 1,3—glucan synthase subunit probable transcriptional activator of Flo1p	YBR023c	CHS3	chitin synthase III	YMR232w		induction of karyogamy genes
YER108c FLO8 YOR122c PFY1	probable transcriptional activator of FioTp profilin	YLR330w YDR073w	CHS5 SNF11	chitin synthesis protein component of SWI/SNF transcription	YBR040w	FIG1	required for cell fusion during mating required for efficient mating
YPR122w AXL1 YOR149c SMP3	protease protein kinase C pathway protein	YOR290c	SNF2	activator complex component of SWI/SNF transcription	YCR089w YNL084c	FIG2 END3	required for efficient mating required for endocytosis and cytoskeletal
YPL140c MKK2	protein kinase of the MAP kinase kinase			activator complex			organization
YDL047w SIT4	(MEK) family protein ser/thr phosphatase	YBR289w	SNF5	component of SWI/SNF transcription activator complex	YKL130c	SHE2	required for mother cell-specific expression of HO
YDL006w PTC1 YDL134c PPH21	protein ser/thr phosphatase 2c protein ser/thr phosphatase PP2A-1	YPL016w	SWI1	component of SWI/SNF transcription activator complex	YOR035c	SHE4	required for mother cell-specific gene expression
YDL188c PPH22	protein ser/thr phosphatase PP2A-2	YPL256c	CLN2	cyclin, G1/S specific	YOR127w	RGA1	RHO-type GTPase-activating protein for
YDR388w RVS167 YMR016c SOK2	reduced viability upon starvation protein regulatory protein in the PKA signal	YNL243w YER095w	RAD51	cytoskeleton assembly control protein DNA repair protein	YLR441c	RP10A	Cdc42p ribosomal protein S3a.e
YCL014w BUD3	transduction pathway required for axial budding	YDR076w YDR004w		DNA repair protein DNA repair protein	YJR076c YHR107c	CDC11 CDC12	septin septin
YIL140w SRO4	required for axial pattern of budding	YAR007c	RFA1	DNA replication factor A, 69K subunit	YPR161c	SGV1	ser/thr protein kinase
YER109c FLO8 YNL084c END3	required for diploid filamentous growth required for endocytosis and cytoskeletal	YOL051w	GAL11	DNA-directed RNA polymerase II holoenzyme and Kornberg's mediator	YGR040w	KSS1	ser/thr protein kinase of the MAP kinase family
	organization	1		(SRB) subcomplex subunit	YLR362w	STE11	ser/thr protein kinase of the MEKK family
YJR090c GRR1	required for glucose repression and for	YLR071c	RGR1	DNA-directed RNA polymerase II	YHL007c	STE20	ser/thr protein kinase of the pheromone

YDL159w	STE7	ser/thr/tyr protein kinase of MAP kinase	YBR078w		strong similarity to sporulation-specific	YJR094c	IME1	transcription factor required for
YOL068c	HST1	kinase family silencing protein	YCL048w		Sps2p strong similarity to sporulation-specific	YGR044c	RME1	sporulation zinc-finger transcription factor
YBL052c	SAS3	silencing protein	\/DDoce		Sps2p	DN/4	4.l t	-
YKR101w YDL042c	SIR1 SIR2	silencing regulatory protein silencing regulatory protein	YDR055w YOR075w	UFE1	strong similarity to Sps2p syntaxin (T-SNARE) of the ER	DIVA SY	ntnesis	and replication
YLR442c	SIR3	silencing regulatory protein	YMR043w		transcription factor of the MADS box	YKL112w	ABF1	ARS-binding factor
YDR227w YNL283c	SIR4	silencing regulatory protein similarity to a-agglutinin core protein	YJR094c	IME1	family transcription factor required for	YFL009w YDR364c	CDC4 CDC40	cell division control protein cell division control protein
		Aga1p			sporulation	YLR274w	CDC46	cell division control protein
YDL225w		similarity to Cdc11p, Cdc3p and human	YNL330c	RPD3	transcription modifier protein	YBR202w	CDC47 CDC6	cell division control protein
YDR191w	HST4	CDC10 protein similarity to Hst3p,Hst1p and Sir2p	YOL004w YNL012w	SIN3 SPO1	transcription regulatory protein transcriptional regulator involved in	YJL194w YML102w	CAC2	cell division control protein chromatin assembly complex, subunit
YGR023w		similarity to Mid2p			sporulation	YBR195c	MSI1	chromatin assembly complex, subunit
YHR146w		similarity to pheromone-response G- protein YNL173c	YLL039c YGL058w	UBI4 RAD6	ubiquitin ubiquitin-conjugating enzyme	YPR018w	RLF2	p50 chromatin assembly complex, subunit
YKL117w		Ste5p-associated protein	YDR177w	UBC1	ubiquitin-conjugating enzyme			p90
YGL106w YJL212c		strong similarity to calmodulins strong similarity to <i>S. pombe</i> isp4 protein	YER125w YML115c	RSP5 VAN1	ubiquitin-protein ligase vanadate resistance protein	YPR120c YGR109c	CLB5 CLB6	cyclin, B-type cyclin, B-type
YDR312w	SSF2	strong similarity to 3. pornoe isp4 protein	TIVILIIOC	VAIVI	variadate resistance protein	YPL256c	CLB6 CLN2	cyclin, G1/S specific
YPL129w	ANC1	TFIIF subunit (transcription initiation	meiosis	•		YBR160w	CDC28	cyclin-dependent protein kinase
YDR146c	SWI5	factor), 30K transcription factor	YPR103w	PRE2	26S proteasome subunit	YER176w YHR164c	DNA2	DNA dependent ATPase/DNA helicase DNA helicase
YMR043w		transcription factor of the MADS box	YGR253c	PUP2	26S proteasome subunit	YDL164c	CDC9	DNA ligase
YNL330c	RPD3	family transcription modifier protein	YKL112w YFL037w	ABF1 TUB2	ARS-binding factor β-tubulin	YJL173c YNL312w	RFA3 RFA2	DNA replication factor A, 13K subunit DNA replication factor A, 36K subunit
YOL004w	SIN3	transcription regulatory protein	YOR265w	RBL2	β-tubulin binding protein	YAR007c	RFA1	DNA replication factor A, 69K subunit
YJL176c YHR084w	SWI3 STE12	transcription regulatory protein transcriptional activator	YPL204w YBR136w		casein kinase I, ser/thr/tyr protein kinase cell cycle checkpoint protein	YOL094c YNL290w	RFC4 RFC3	DNA replication factor C, 37K subunit DNA replication factor C, 40K subunit
YER068w		transcriptional repressor	YPL255w		cell division control protein	YBR087w	RFC5	DNA replication factor C, 40K subunit
YNL079c	TPM1	tropomyosin 1	YDL220c	CDC13	cell division control protein	YJR068w	RFC2	DNA replication factor C, 41K subunit
YOR219c YMR022w	STE13 ORI8	type IV dipeptidyl aminopeptidase ubiquitin-conjugating enzyme	YPL042c YOR368w	SSN3 RAD17	cyclin-dependent ser/thr protein kinase DNA damage checkpoint control protein	YOR217w YJR006w	RFC1 HUS2	DNA replication factor C, 95K subunit DNA replication protein
YBR082c	UBC4	ubiquitin-conjugating enzyme	YMR224c		DNA repair and meiotic recombination	YOL006c	TOP1	DNA topoisomerase I
YDR059c	UBC5	ubiquitin-conjugating enzyme	YNL250w	DADEO	protein	YNL088w YNL102w	TOP2	DNA topoisomerase II (ATP-hydrolysing)
YER100w YJR117w	UBC6 STE24	ubiquitin-conjugating enzyme zinc metallo-protease	YNL250W YDR076W		DNA repair protein DNA repair protein	Y INL IUZW	CDC17	DNA-directed DNA polymerase α, 180K subunit
			YDR004w	RAD57	DNA repair protein	YIR008c	PRI1	DNA-directed DNA polymerase α, 48K
sporula	ation an	d germination	YDR369c YLR234w	XRS2 TOP3	DNA repair protein DNA topoisomerase III	YKL045w	PRI2	subunit (DNA primase) DNA-directed DNA polymerase α, 58K
YGR032w		1,3-D-glucan synthase, subunit	YGL163c	RAD54	DNA-dependent ATPase of the Snf2p			subunit (DNA primase)
YPR103w YGR253c	PRE2 PUP2	26S proteasome subunit 26S proteasome subunit	YNL025c	SSN8	family DNA-directed RNA polymerase II	YPR135w	POB1	DNA-directed DNA polymerase α-binding protein
YBL015w		acetyl-CoA hydrolase	TIVEUZUC	00110	holoenzyme and Kornberg's mediator	YDL102w	CDC2	DNA-directed DNA polymerase δ,
YCR048w		acyl-CoA sterol acyltransferase			(SRB) subcomplex subunit, cyclin C	VAII 000	DOL 2	catalytic 125K subunit
YNR019w YOL052c	ARE2 SPE2	acyl-CoA sterol acyltransferase adenosylmethionine decarboxylase	YKL017c	DIP1	homolog Dom34p Interacting Protein	YNL262w	POL2	DNA-directed DNA polymerase ε, catalyt subunit A
YDR173c	ARG82	arginine metabolism transcription factor	YLR129w	DIP2	Dom34p-interacting protein	YPR175w	DPB2	DNA-directed DNA polymerase ε, subun
YIL033c	SRA1	cAMP dependent protein kinase, regulatory subunit	YBR045c YPL240c	GIP1 HSP82	Glc7-interacting protein heat-shock protein	YBR278w	DPB3	B DNA-directed DNA polymerase ε, subun
YDR182w	CDC1	cell division control protein	YJL146w	IDS2	IME2-dependent signaling protein	IBINETOW	D1 D0	C
YFL009w		cell division control protein	YOR198c YHL022c	BFR1 SPO11	maintenance of normal ploidy	YOR330c	MIP1	DNA-directed DNA polymerase γ, catalyt
YNL192w YBR023c	CHS3	chitin synthase I chitin synthase III	YER179w	DMC1	meiosis-specific protein meiosis-specific protein	YPL167c	REV3	subunit, mitochondrial DNA-directed DNA polymerase ζ
YDR402c	DIT2	cytochrome P450 56	YIL072w	HOP1	meiosis-specific protein	YFL036w	RPO41	DNA-directed RNA polymerase,
YML110c YOL051w	DBI56 GAL11	DBF2 interacting protein	YER180c YER044c-a		meiosis-specific protein	YMR072w	ADEO	mitochondrial
TOLUSIW	GALII	DNA-directed RNA polymerase II holoenzyme and Kornberg's mediator	YDL154w		meiosis-specific protein meiosis-specific protein	YJL090c	DPB11	high-mobility group protein involved in DNA replication and S-phase
VDDOEO	0000	(SRB) subcomplex subunit	YHR124w		meiosis-specific protein	V/DD0000	D004	checkpoint
YBR253w	SRB6	DNA-directed RNA polymerase II suppressor protein	YHR157w YLR263w		meiosis-specific protein meiosis-specific protein	YDR068w YMR001c	DOS1 CDC5	involved in genome stability involved in regulation of DNA replication
YMR013c		dolichol kinase	YHR079c-a	SAE3	meiosis-specific protein	YPR019w	CDC54	member of the Cdc46p/Mcm2p/Mcm3p
YOR190w YLR300w		exo-1,3—glucanase exo-1,3—glucanase (I/II), major isoform	YHR014w YPL121c	SPO13 MEI5	meiosis-specific protein meiotic protein	YBL023c	МСМ2	family member of the Mcm2p,Mcm3p,Cdc46p
YDR261c	EXG2	exo-1,3—glucanase minor isoform	YBR057c	MUM2	meiotic protein	IDLUZGO	IVICIVIZ	family
YBR045c	GIP1	Glc7p-interacting protein	YAL009w		meiotic protein	YML065w		origin recognition complex, 104K subunit
YNL236w YDL240w		global regulator protein GTPase-activating protein of the	YNL210w YHR086w		meiotic recombination protein meiotic recombination protein	YNL261w YHR118c	ORC5 ORC6	origin recognition complex, 50K subunit origin recognition complex, 50K subunit
		RHO/RAC family	YLR329w	REC102	meiotic recombination protein	YPR162c	ORC4	origin recognition complex, 56K subunit
YNL098c	RAS2 HSP82	GTP-binding protein	YJR021c YMR133w	REC107	meiotic recombination protein	YLL004w	ORC3 RRR1	origin recognition complex, 62K subunit
YPL240c YJL146w	HSP82 IDS2	heat-shock protein  IME2-dependent signaling protein	YMR133W YGL175c		meiotic recombination protein meiotic recombination protein	YBR060c YGR132c	KKK1 PHB1	origin recognition complex, 72K subunit prohibitin, antiproliferative protein
YER044c-a	a <i>MEI4</i>	meiosis-specific protein	YHL027w	RIM101	meiotic regulatory protein	YBR088c	POL30	proliferating cell nuclear antigen (PCNA)
YBR057c YAL009w		meiotic protein meiotic protein	YDR207c YBL058w		negative transcriptional regulator potential regulatory subunit for Glc7p	YDL017w YFR028c	CDC7 CDC14	protein kinase protein-tyrosine-phosphatase
YLR025w	SNF7	nuclear protein	YMR076c	PDS5	precocious dissociation of sister	YDR052c	DBF4	regulatory subunit for Cdc7p protein
YKR031c	SPO14	phospholipase D			chromatids			kinase
YGL192w YCR034w		positive transcription factor for IME2 probable 1,3—glucan synthase subunit	YDL017w YIR026c	CDC7 YVH1	protein kinase protein tyrosine phosphatase	YEL032w YIL139c	MCM3 REV7	replication initiation protein required for DNA damage-induced
YIR026c	YVH1	protein tyrosine phosphatase	YOR208w	PTP2	protein tyrosine phosphatase			mutagenesis
YOR208w YBL066c	PTP2 SEF1	protein-tyrosine-phosphatase putative transcription factor	YBR073w YER133w	RDH54 GLC7	required for meiosis ser/thr phosphoprotein phosphatase 1,	YLR103c	CDC45	required for minichromosome maintenance and initiation of
YBLU66C YNR052c	POP2	required for glucose derepression	I EN ISSW	GLU/	catalytic subunit			chromosomal DNA replication
	SPR28	septin-related sporulation protein	YOR178c	GAC1	ser/thr phosphoprotein phosphatase 1,	YIL150c	DNA43	required for S-phase initiation or
YDR218c	IME2 SPS1	ser/thr protein kinase ser/thr protein kinase	YJL106w	IME2	regulatory subunit ser/thr protein kinase	YER070w	RNR1	completion ribonucleoside-diphosphate reductase,
YJL106w		ser/thr/tyr protein kinase	YMR139w	MDS1	ser/thr protein kinase			large subunit
YJL106w YDR523c YNL307c	MCK1		YOR351c		ser/thr protein kinase	YJL026w	RNR2	ribonucleoside-diphosphate reductase,
YJL106w YDR523c YNL307c YDR403w	MCK1 DIT1	spore-wall maturation protein				I .		small subunit
YJL106w YDR523c YNL307c YDR403w YBR148w	MCK1 DIT1	spore-wall maturation protein spore-specific protein sporulation protein	YDR523c YNL307c		ser/thr protein kinase ser/thr/tyr protein kinase	YIL066c	RNR3	ribonucleotide reductase, renair inducible
YJL106w YDR523c YNL307c YDR403w YBR148w YKL165c YLR399c	MCK1 DIT1 YSW1 BDF1	spore-specific protein sporulation protein sporulation protein	YDR523c YNL307c YDL028c	MCK1 MPS1	ser/thr/tyr protein kinase ser/thr/tyr protein kinase	YIL066c YJL065c	RNR3	similarity to DNA-directed DNA
YJL106w YDR523c YNL307c YDR403w YBR148w YKL165c YLR399c YHR152w	MCK1 DIT1 YSW1 BDF1 SPO12	spore-specific protein sporulation protein sporulation protein sporulation protein	YDR523c YNL307c	MCK1 MPS1	ser/thr/tyr protein kinase ser/thr/tyr protein kinase similarity to <i>D. melanogaster</i> pelota	YJL065c	RNR3	similarity to DNA-directed DNA polymerase II subunit C
YJL106w YDR523c YNL307c YDR403w YBR148w YKL165c YLR399c YHR152w YHR153c	MCK1 DIT1 YSW1 BDF1	spore-specific protein sporulation protein sporulation protein	YDR523c YNL307c YDL028c	MCK1 MPS1	ser/thr/tyr protein kinase ser/thr/tyr protein kinase		RNR3	similarity to DNA-directed DNA polymerase II subunit C similarity to EST1 protein
YJL106w YDR523c YNL307c YDR403w YBR148w YKL165c YLR399c YHR152w YHR153c YIL099w	MCK1 DIT1 YSW1 BDF1 SPO12 SPO16 SGA1	spore-specific protein sporulation protein sporulation protein sporulation protein sporulation protein sporulation specific glucan 1,4—glucosidase	YDR523c YNL307c YDL028c YNL001w YFL003c YHR152w	MCK1 MPS1 DOM34 MSH4 SPO12	ser/thr/tyr protein kinase ser/thr/tyr protein kinase similarity to <i>D. melanogaster</i> pelota protein similarity to MSH proteins sporulation protein	YJL065c YDR206w YOR005c	RNR3	similarity to DNA-directed DNA polymerase II subunit C similarity to EST1 protein similarity to human mRNA for DNA ligas IV
YJL106W YDR523c YNL307c YDR403W YBR148W YKL165c YLR399c YHR152W YHR153c YIL099W YDR108W	MCK1 DIT1 YSW1 BDF1 SPO12 SPO16 SGA1 GSG1	spore-specific protein sporulation specific glucan 1,4—glucosidase sporulation-specific protein	YDR523c YNL307c YDL028c YNL001w YFL003c YHR152w YHR153c	MCK1 MPS1 DOM34 MSH4 SPO12 SPO16	ser/thr/tyr protein kinase ser/thr/tyr protein kinase similarity to <i>D. melanogaster</i> pelota protein similarity to MSH proteins sporulation protein sporulation protein	YJL065c YDR206w	RNR3	similarity to DNA-directed DNA polymerase II subunit C similarity to EST1 protein similarity to human mRNA for DNA ligas IV similarity to <i>S. aureus</i> DNA helicase
YJL106W YDR523c YNL307c YDR403W YBR148W YKL165c YLR399c YHR152W YHR153c YIL099W YDR108W YER096W	MCK1 DIT1 YSW1 BDF1 SPO12 SPO16 SGA1 GSG1 SHC1	spore-specific protein sporulation protein sporulation protein sporulation protein sporulation protein sporulation specific glucan 1,4—glucosidase	YDR523c YNL307c YDL028c YNL001w YFL003c YHR152w	MCK1 MPS1 DOM34 MSH4 SPO12 SPO16 GSG1	ser/thr/tyr protein kinase ser/thr/tyr protein kinase similarity to <i>D. melanogaster</i> pelota protein similarity to MSH proteins sporulation protein	YJL065c YDR206w YOR005c	RNR3	similarity to DNA-directed DNA polymerase II subunit C similarity to EST1 protein similarity to human mRNA for DNA ligas IV
YJL106W YDR523c YNL307c YDR403W YBR148W YKL165c YLR399c YHR152W YHR153c YIL099W YDR108W YER096W YLR307W YLR308W	MCK1 DIT1 YSW1 BDF1 SPO12 SPO16 SGA1 GSG1 SHC1 CDA1 CDA2	spore-specific protein sporulation specific glucan 1,4—glucosidase sporulation-specific protein sporulation-specific protein sporulation-specific chitin deacetylase sporulation-specific chitin deacetylase sporulation-specific hitin deacetylase	YDR523c YNL307c YDL028c YNL001w YFL003c YHR152w YHR153c YDR108w YNL202w YDR522c	MCK1 MPS1 DOM34 MSH4 SPO12 SPO16 GSG1 SPS19 SPS2	ser/thr/tyr protein kinase ser/thr/tyr protein kinase ser/thr/tyr protein kinase similarity to <i>D. melanogaster</i> pelota protein similarity to MSH proteins sporulation protein sporulation-specific protein sporulation-specific protein sporulation-specific protein	YJL065c YDR206w YOR005c YOL095c YGL201c		similarity to DNA-directed DNA polymerase II subunit C similarity to EST1 protein similarity to human mRNA for DNA ligas IV similarity to <i>S. aureus</i> DNA helicase PCRA similarity with rat intestinal DNA replication protein
YJL106W YDR523c YDR403W YBR148W YKL165c YJR399c YHR152W YHR153c YIL099W YDR108W YER096W YLR307W YLR308W YPR054W YPR054W	MCK1 DIT1 YSW1 BDF1 SPO12 SPO16 SGA1 GSG1 SHC1 CDA1 CDA2 SMK1	spore-specific protein sporulation protein sporulation protein sporulation protein sporulation protein sporulation protein sporulation specific glucan 1,4—glucosidase sporulation-specific protein sporulation-specific protein sporulation-specific chitin deacetylase sporulation-specific chitin deacetylase sporulation-specific chitin deacetylase sporulation-specific MAP kinase	YDR523c YNL307c YDL028c YNL001w YFL003c YHR152w YHR153c YDR108w YNL202w YDR522c YNL204c	MCK1 MPS1 DOM34 MSH4 SPO12 SPO16 GSG1 SPS19	ser/thr/tyr protein kinase ser/thr/tyr protein kinase similarity to <i>D. melanogaster</i> pelota protein similarity to MSH proteins sporulation protein sporulation protein sporulation-specific protein sporulation-specific protein sporulation-specific protein sporulation-specific protein	YJL065c YDR206w YOR005c YOL095c	RNR3 RAD27	similarity to DNA-directed DNA polymerase II subunit C similarity to EST1 protein similarity to human mRNA for DNA ligas IV similarity to S. aureus DNA helicase PCRA similarity with rat intestinal DNA replication protein ssDNA endonuclease and
YJL106W YDR523c YNL307c YDR403W YBR148W YKL165c YLR399c YHR152W YHR153c YIL099W YDR108W YER096W YLR307W YLR308W YPR054W YPR054W YPR054W YPR156C YNL202W	MCK1 DIT1 YSW1 BDF1 SPO12 SPO16 SGA1 GSG1 SHC1 CDA1 CDA2 SMK1 SPR6 SPS19	spore-specific protein sporulation protein sporulation protein sporulation protein sporulation protein sporulation protein sporulation specific glucan 1.4—glucosidase sporulation-specific protein sporulation-specific protein sporulation-specific chitin deacetylase sporulation-specific MAP kinase sporulation-specific protein sporulation-specific protein sporulation-specific protein sporulation-specific protein	YDR523c YNL307c YDL028c YNL001w YFL003c YHR152w YHR153c YDR108w YNL202w YDR522c YNL204c YBR078w	MCK1 MPS1 DOM34 MSH4 SPO12 SPO16 GSG1 SPS19 SPS2	ser/thr/tyr protein kinase ser/thr/tyr protein kinase ser/thr/tyr protein kinase similarity to <i>D. melanogaster</i> pelota protein similarity to MSH proteins sporulation protein sporulation protein sporulation-specific protein sporulation-specific protein sporulation-specific protein sporulation-specific zinc-finger protein strong similarity to sporulation-specific Sps2p	YJL065c YDR206w YOR005c YOL095c YGL201c YKL113c YCR028c-a	RAD27	similarity to DNA-directed DNA polymerase II subunit C similarity to EST1 protein similarity to human mRNA for DNA ligas IV similarity to <i>S. aureus</i> DNA helicase PCRA similarity with rat intestinal DNA replication protein ssDNA endonuclease and 5°-3'exonuclease ssDNA-binding protein, mitochondrial
YJL106W YDR523c YNL307c YDR403W YBA148W YKL165c YLR399c YHR152W YHR152W YHR152W YHR152W YLR307W YLR307W YLR308W YPR054W YPR054W YPR054W YPR054W YDR522c	MCK1 DIT1 YSW1 BDF1 SPO12 SPO16 SGA1 GSG1 SHC1 CDA1 CDA2 SMK1 SPR6 SPS19 SPS2	spore-specific protein sporulation protein sporulation protein sporulation protein sporulation protein sporulation sporulation specific sporulation specific glucan 1,4—glucosidase sporulation-specific protein sporulation-specific protein sporulation-specific chitin deacetylase sporulation-specific chitin deacetylase sporulation-specific protein sporulation-specific protein sporulation-specific protein sporulation-specific protein sporulation-specific protein	YDR523c YNL307c YDL028c YNL001w YFL003c YHR152w YHR153c YDR108w YNL202w YDR522c YNL204c	MCK1 MPS1 DOM34 MSH4 SPO12 SPO16 GSG1 SPS19 SPS2	ser/thr/tyr protein kinase ser/thr/tyr protein kinase similarity to <i>D. melanogaster</i> pelota protein similarity to MSH proteins sporulation protein sporulation protein sporulation-specific protein strong similarity to sporulation-specific Sps2p strong similarity to sporulation-specific	YJL065c  YDR206w YOR005c  YOL095c  YGL201c  YKL113c  YCR028c-a YGR231c	RAD27 RIM1	polymerase II subunit C similarity to EST1 protein similarity to human mRNA for DNA ligas IV similarity to <i>S. aureus</i> DNA helicase PCRA similarity with rat intestinal DNA replication protein ssDNA endonuclease and 6'-3'exonuclease ssDNA-binding protein, mitochondrial strong similarity to prohibitins
YJL 106W YDR523c YNL307c YDR403W YBR148W YKL166c YLR399c YHR152W YHR153c YIL099W YER096W YLR307W YLR308W YPR054W YER115c YNL202W YDR522c YOR313c	MCK1 DITI YSW1 BDF1 SPO16 SGA1 GSG1 SHC1 CDA1 CDA2 SMK1 SPR6 SPS19 SPS2 SPS4	spore-specific protein sporulation specific glucan 1,4—glucosidase sporulation-specific protein sporulation-specific protein sporulation-specific chitin deacetylase sporulation-specific chitin deacetylase sporulation-specific fichitin deacetylase sporulation-specific protein sporulation-specific protein sporulation-specific protein sporulation-specific protein sporulation-specific protein sporulation-specific protein	YDR523c YNL307c YDL028c YNL001w YFL003c YHR152w YHR153c YDR108w YNL202w YDR522c YNL204c YBR078w YCL048w	MCK1 MPS1 DOM34 MSH4 SPO12 SPO16 GSG1 SPS19 SPS2	ser/thr/tyr protein kinase ser/thr/tyr protein kinase ser/thr/tyr protein kinase similarity to <i>D. melanogaster</i> pelota protein similarity to MSH proteins sporulation protein sporulation protein sporulation-specific protein sporulation-specific protein sporulation-specific protein sporulation-specific zinc-finger protein strong similarity to sporulation-specific Sps2p strong similarity to sporulation-specific Sps2p	YJL065c YDR206w YOR005c YOL095c YGL201c YKL113c YCR028c-a	RAD27	similarity to DNA-directed DNA polymerase II subunit C similarity to EST1 protein similarity to human mRNA for DNA ligas IV similarity to S. aureus DNA helicase PCRA similarity with rat intestinal DNA replication protein ssDNA endonuclease and 5°-3'exonuclease ssDNA-binding protein, mitochondrial strong similarity to prohibitins subunit of DNA polymerase ac-primase
YJL106W YDR523c YDR523c YDR403W YBR148W YBR148W YHR152w YHR153c YHL999W YDR108W YER096W YLR307W YLR307W YLR305W YPR054W YYLR305W YPR054W YYLR305W YDR522c	MCK1 DITI YSW1 BDF1 SPO16 SGA1 GSG1 SHC1 CDA1 CDA2 SMK1 SPR6 SPS19 SPS2 SPS4	spore-specific protein sporulation protein sporulation protein sporulation protein sporulation protein sporulation sporulation specific sporulation specific glucan 1,4—glucosidase sporulation-specific protein sporulation-specific protein sporulation-specific chitin deacetylase sporulation-specific chitin deacetylase sporulation-specific protein sporulation-specific protein sporulation-specific protein sporulation-specific protein sporulation-specific protein	YDR523c YNL307c YDL028c YNL001w YFL003c YHR152w YHR153c YDR108w YNL202w YDR522c YNL204c YBR078w	MCK1 MPS1 DOM34 MSH4 SPO12 SPO16 GSG1 SPS19 SPS2	ser/thr/tyr protein kinase ser/thr/tyr protein kinase similarity to <i>D. melanogaster</i> pelota protein similarity to MSH proteins sporulation protein sporulation protein sporulation-specific protein strong similarity to sporulation-specific Sps2p strong similarity to sporulation-specific	YJL065c  YDR206w YOR005c  YOL095c  YGL201c  YKL113c  YCR028c-a YGR231c	RAD27 RIM1	similarity to DNA-directed DNA polymerase II subunit C similarity to EST1 protein similarity to human mRNA for DNA ligas IV similarity to S. aureus DNA helicase PCRA similarity with rat intestinal DNA replication protein ssDNA endonuclease and 6-3-exonuclease ssDNA-binding protein, mitochondrial strong similarity to prohibitins

YLR182w	SWI6	transcription factor	YOR026w	BUB3	cell-cycle arrest protein	YGR140w	CBF2	kinetochore protein complex CBF3, 110K
YDR054c YGL058w	CDC34 RAD6	ubiquitin-conjugating enzyme ubiquitin-conjugating enzyme	YPL178w YBR136w	SAE1 ESR1	cell-cycle block in meiotic prophase cell-cycle checkpoint protein	YMR094w	CTF13	subunit kinetochore protein complex CBF3, 58K
		and DNA repair	YPR111w YDR113c	DBF20 PDS1	cell-cycle protein kinase related to Dbf2p cell-cycle regulator	YMR168c	CEP3	subunit kinetochore protein complex CBF3, 71K
		•	YBR215w	HPC2	cell-cycle regulatory protein			subunit
YGL127c YBR136w		allows hpr1 null mutant to grow at 37°C cell-cycle checkpoint protein	YOR373w YPL255w	BBP1	cell-cycle regulatory protein cell division control protein	YDR328c	SKP1	kinetochore protein complex CBF3, subunit D
YER173w YDR182w		cell-cycle checkpoint protein cell-division control protein	YDR182w YCR002c	CDC1 CDC10	cell division control protein cell division control protein	YOR198c YLR332w	BFR1 MID2	maintenance of normal ploidy mating process protein
YMR106c	HDF2	component of DNA end-joining repair	YDL220c	CDC13 CDC20	cell division control protein	YER179w	DMC1	meiosis-specific protein
YKL011c	CCE1	pathway cruciform-cutting endonuclease,	YGL116w YLR314c	CDC3	cell division control protein cell division control protein	YHR079c-a YPR019w	CDC54	meiosis-specific protein member of the Cdc46p/Mcm2p/Mcm3p
YER176w		mitochondrial DNA-dependent ATPase/DNA helicase B	YDR168w YFL009w		cell division control protein cell division control protein	YDL126c	CDC48	family microsomal protein of
YLR032w YMR190c	RAD5 SGS1	DNA helicase DNA helicase	YDR364c YLR274w	CDC40 CDC46	cell division control protein	YOR058c	ASE1	CDC48/PAS1/SEC18 family of ATPases microtubule-associated protein
YML061c	PIF1	DNA helicase involved in mitochondrial	YBR202w	CDC47	cell division control protein	YNL064c	YDJ1	mitochondrial and ER import protein
YDL164c	CDC9	DNA repair and telomere length DNA ligase	YJL194w YNL188w	CDC6 KAR1	cell division control protein cell division control protein	YGR029w	ERV1	mitochondrial biogenesis and regulation of cell cycle
YMR167w YOL090w		DNA mismatch repair protein DNA mismatch repair protein	YDL226c YNL327w	GCS1 EGT2	cell proliferation zinc-finger protein cell-cycle regulation protein	YBL016w	FUS3	mitogen-activated protein kinase (MAP kinase)
YNL082w	PMS1	DNA mismatch repair protein	YHR129c	ACT5	centractin	YMR294w	JNM1	mitosis protein, involved in nuclear
YHR120w		DNA mismatch repair protein, mitochondrial	YLR175w YDR254w		centromere/microtubule binding protein chromosome segregation protein	YMR036c	MIH1	migration M-phase inducing protein tyrosine
YCR014c YMR224c	POL4 MRF11	DNA polymerase DNA repair and meiotic recombination	YOR349w YFL008w		chromosome segregation protein chromosome segregation protein	YGL178w	MPT5	phosphatase multicopy suppressor of pop2
		protein	YFR031c YMR028w	SMC2	chromosome segregation protein	YML109w	ZDS2	multicopy suppressor of sin4
YJR035w YEL019c	RAD26 MMS21	DNA repair and recombination protein DNA repair protein	YIL106w	MOB1	component of the Tor signalling pathway conditional mutants arrest in late mitosis	YGL173c YDR207c	KEM1 UME6	multifunctional nuclease negative transcriptional regulator
YML095c YCR066w		DNA repair protein DNA repair protein	YDL132w YPR120c	CDC53 CLB5	controls G1/S transition cyclin, B-type	YBL020w YNL299w	RFT1 TRF5	nuclear division protein nuclear division protein
YNL250w	RAD50	DNA repair protein	YGR109c	CLB6	cyclin, B-type	YML031w	NDC1	nuclear envelope protein
YER095w YDR076w	RAD55	DNA repair protein DNA repair protein	YMR199w YPL256c	CLN2	cyclin, G1/S specific cyclin, G1/S specific	YJR112w YCL029c	NNF1 BIK1	nuclear envelope protein nuclear fusion protein
YDR004w YDR369c	RAD57 XRS2	DNA repair protein DNA repair protein	YAL040c YNL289w	CLN3 PCL1	cyclin, G1/S specific cyclin, G1/S specific	YJL034w YDR150w	KAR2 NUM1	nuclear fusion protein nuclear migration protein
YAR007c YOL006c	RFA1 TOP1	DNA replication factor A, 69K subunit	YDL127w YGR108w	PCL2	cyclin, G1/S specific	YAL025c YKR048c	MAK16 NAP1	nuclear viral propagation protein
YNL088w	TOP2	DNA topoisomerase I DNA topoisomerase II (ATP-hydrolysing)	YPR119w	CLB2	cyclin, G2/M-specific cyclin, G2/M-specific	YLR079w	SIC1	nucleosome assembly protein I p40 inhibitor of Cdc28p-Clb protein kinase
YGL163c	RAD54	DNA-dependent ATPase of the Snf2p family	YDL155w YLR210w	CLB3 CLB4	cyclin, G2/M-specific cyclin, G2/M-specific	YJR066w	TOR1	complex phosphatidylinositol 3-kinase
YFR023w	PES4	DNA-directed DNA polymerase ε suppressor	YBR135w	CKS1	cyclin-dependent kinase regulatory subunit	YKL203c YLR305c	TOR2 STT4	phosphatidylinositol 3-kinase phosphatidylinositol-4-kinase
YPL167c	REV3	DNA-directed DNA polymerase ζ	YBR160w	CDC28	cyclin-dependent protein kinase	YCL004w	PEL1	phosphatidylserine synthase
YCR092c YKR056w	MSH3 RNC1	DNA-repair protein endo-exonuclease	YPL031c YDL108w	PHO85 KIN28	cyclin-dependent protein kinase cyclin-dependent ser/thr protein kinase	YBL058w YGL238w	SHP1 CSE1	potential regulatory subunit for Glc7p probable kinetochore protein
YOR033c YLR288c	DHS1 MEC3	exonuclease, interacting with Msh2p G2-specific checkpoint protein	YGL215w YOR368w		cyclin-like protein DNA damage checkpoint control protein	YGR132c YDL017w	PHB1 CDC7	prohibitin, antiproliferative protein protein kinase
YMR284w YDR138w	HDF1	high-affinity DNA-binding protein	YDR217c YOR217w	RAD9	DNA repair checkpoint protein	YOR149c	SMP3 MKK2	protein kinase C pathway protein
		hyperrecombination protein related to Top1p	YLR234w	TOP3	DNA replication factor C, 95K subunit DNA topoisomerase III	YPL140c		protein kinase of the MAP kinase kinase (MEK) family
YHL022c YER179w	SPO11 DMC1	meiosis-specific protein meiosis-specific protein	YKL017c YLR129w	DIP1 DIP2	Dom34p-interacting protein Dom34p-interacting protein	YAR019c	CDC15	protein kinase of the MAP kinase kinase kinase kinase family
YIL072w YHR157w	HOP1 RFC104	meiosis-specific protein meiosis-specific protein	YNL053w YKR054c	MSG5 DYN1	dual-specifity protein phosphatase dynein heavy chain, cytosolic	YHR013c YPL008w	ARD1 CHL1	protein N-acetyltransferase subunit protein of the DEAH box family
YLR263w YPL121c		meiosis-specific protein	YDR172w	SUP35	eukaryotic peptide chain release factor GTP-binding subunit	YDL047w YDL134c	SIT4 PPH21	protein ser/thr phosphatase
YNL210w	MER1	meiotic protein meiotic recombination protein	YNL292w		exit from mitosis	YDL188c	PPH22	protein ser/thr phosphatase PP2A-1 protein ser/thr phosphatase PP2A-2
YHR086w YLR329w		meiotic recombination protein meiotic recombination protein	YDL087c YJL157c	EXM2 FAR1	exit from mitosis factor arrest protein	YBR267w YFR028c	PPS1 CDC14	protein tyrosine phosphatase protein-tyrosine-phosphatase
YJR021c YGL175c	REC107 SAE2	meiotic recombination protein	YLR212c YLR288c	TUB4 MEC3	γ tubulin G2-specific checkpoint protein	YOL021c YDR137w	DIS3 RGP1	Ran binding protein reduced growth phenotype protein
YBR114w	RAD16	nucleotide excision repair protein	YAL024c	LTE1	GDP/GTP exchange factor	YDR052c	DBF4	regulatory subunit for Cdc7p protein
YGL025c YBR088c	PGD1 POL30	probable transcription factor proliferating cell nuclear antigen (PCNA)	YLL016w YAL041w	SDC25 CDC24	GDP/GTP exchange factor GDP/GTP exchange factor for Cdc42p	YKL193c	SDS22	kinase regulatory subunit for the mitotic function
YML032c YDL059c	RAD52 RAD59	recombination and DNA repair protein recombination and DNA repair protein	YLR310c	CDC25	GDP/GTP exchange factor for Ras1p and Ras2p	YMR078c	CHL12	of type I protein phosphatase required for accurate chromosome
YLR383w YBR073w	RHC18 RDH54	recombination repair protein required for meiosis	YGL207w YGL155w		general chromatin factor geranylgeranyltransferase type I β subunit			transmission in mitosis and maintenance of normal telomere length
YIL066c	RNR3	ribonucleotide reductase, repair inducible	YER155c	BEM2	GTPase-activating protein	YOL145c	CTR9	required for G1 cyclin expression
YMR228w	MIF1	RNA polymerase specific factor, mitochondrial	YMR138w YNL098c	CIN4 RAS2	GTP-binding protein GTP-binding protein	YLR103c	CDC45	required for minichromosome maintenance and initiation of
YOR351c YPL164c	MEK1	ser/thr protein kinase similarity to mismatch repair protein	YLR229c YML064c	CDC42 TEM1	GTP-binding protein of RAS superfamily GTP-binding protein of the RAS	YKL089w	MIF2	chromosomal DNA replication required for normal chromosome
YOR077w	RTC2	MIh1p similarity to mouse KIN17 protein	YNL007c	SIS1	superfamily heat-shock protein	YGR098c	ESP1	segregation and spindle integrity required for normal spindle structure
YFL003c	MSH4	similarity to MSH proteins	YBR133c	HSL7	histone synthetic lethality	YIL150c	DNA43	required for S-phase initiation or
YDR097c YHR031c	MSH6	similarity to MSH proteins similarity to Pif1p	YJL080c YOL076w		histone-like protein interacts genetically with CIN8	YJL074c	SMC3	completion required for structural maintenance of
YGL043w YCR077c	DST1 (PAT1)	TFIIS (transcription elongation factor) topoisomerase II-associated protein	YOR156c YNR010w	NFI1 CSE2	interacts with Cdc12p in 2-hybrid assay interacts with centromeric element CDEII	YGR078c	PAC10	chromosomes required in the absence of Cin8p
YGR063c	SPT4	transcription initiation protein	YML104c		intermediate filament protein involved in cell cycle-specific gene	YDR488c YLR075w	PAC11 GRC5	required in the absence of Cin8p
YGR116w YML021c		uracil-DNA glycosylase	YKR072c		expression	YJR076c	CDC11	ribosomal protein septin
cell-cy	cle cont	rol and mitosis	YKR063c	LAS1	involved in cell morphogenesis, cytoskeletal regulation and bud formation	YHR107c YAL016w	CDC12 TPD3	septin ser/thr phosphatase 2A, regulatory
YFR052w	NIN1	26S proteasome regulatory subunit	YPL241c YPL018w	CIN2 CTF19	involved in chromosome segregation involved in chromosome segregation	YER133w	GLC7	subunit A ser/thr phosphoprotein phosphatase 1,
YPR103w	PRE2	26S proteasome subunit	YJL090c	DPB11	involved in DNA replication and S-phase			catalytic subunit
YGL048c YKL145w		26S proteasome subunit 26S proteasome subunit	YMR273c	ZDS1	checkpoint involved in negative regulation of cell	YOR178c	GAC1	ser/thr phosphoprotein phosphatase 1, regulatory subunit
YJL005w YPL239w	CYR1 YAR1	adenylate cyclase ankyrin repeat-containing protein	YMR052w	FAR3	polarity involved in pheromone-mediated cell	YGR188c YKL048c	BUB1 ELM1	ser/thr protein kinase ser/thr protein kinase
YHR101c YHR208w	BIG1 TWT1	big cells phenotype branched-chain amino-acid	YMR052w		cycle arrest involved in pheromone-mediated cell	YJL106w YPL209c	IME2 IPL1	ser/thr protein kinase ser/thr protein kinase
		aminotransferase, mitochondrial			cycle arrest	YOR231w	MKK1	ser/thr protein kinase
YFL037w YBR200w	BEM1	β-tubulin bud emergence mediator	YMR001c YMR127c	SAS2	involved in regulation of DNA replication involved in silencing at HMR	YBL105c YPR161c	PKC1 SGV1	ser/thr protein kinase ser/thr protein kinase
YBR109c YOR061w	CMD1 CKA2	calmodulin casein kinase II α' subunit	YKR042w YDR293c	UTH1 SSD1	involved in the aging process involved in the tolerance to high	YJL141c YMR104c	YAK1 YPK2	ser/thr protein kinase ser/thr protein kinase
YIL035c YER123w	CKA1 YCK3	casein kinase II, catalytic α subunit casein kinase, isoform 3	YNL189w		concentration of Ca <sup>2+</sup> karyopherin-α or importin	YHR030c	SLT2	ser/thr protein kinase of MAP kinase family
YER123W YLR178c	TFS1	cdc25-dependent nutrient- and ammonia-	YEL061c	CIN8	kinesin-related protein	YJL095w	BCK1	ser/thr protein kinase of the MEKK family
YGR049w		response cell-cycle regulator cdc4 suppressor	YPR141c YBL063w	KAR3 KIP1	kinesin-related protein kinesin-related protein	YER167w	BCK2	ser/thr protein kinase of the protein kinase C pathway
YFL029c YMR055c	CAK1 BUB2	cdk-activating protein kinase cell-cycle arrest protein	YJR060w	CBF1	kinetochore protein	YGR092w	DBF2	ser/thr protein kinase related to Dbf20p
	DUDL	22 2,010 G11001 p1010111	l					

YKL101w	HSL1	ser/thr protein kinase that interacts	cytokine	esis		YPR186c	TFC2	TFIIIA subunit (transcription initiation
		genetically with histone mutations	-					factor)
YHR102w	NRK1	ser/thr protein kinase that interacts with Cdc31p	YDL029w YPL255w		actin-like protein cell division control protein	YGR246c YNL039w	BRF1 TFC5	TFIIIB subunit, 70K TFIIIB subunit, 90K
YNL307c		ser/thr/tyr protein kinase	YCR002c	CDC10	cell division control protein	YGR047c	TFC4	TFIIIC subunit (transcription initiation
YDL028c YPL153c	MPS1 SPK1	ser/thr/tyr protein kinase ser/thr/tyr protein kinase		CDC3 EGT2	cell division control protein cell-cycle regulation protein	YAL001c	TFC3	factor), 131K TFIIIC subunit (transcription initiation
YJL187c	SWE1	ser/tyr dual-specifity protein kinase	YNL192w	CHS1	chitin synthase I			factor), 138K
YGL003c		similarity to <i>C. elegans</i> CDC20 protein and human p55CDC		CTS1 NFI1	endochitinase interacts with Cdc12p in 2-hybrid assay	YBR123c	TFC1	TFIIIC subunit (transcription initiation factor), 95K
YDL225w		similarity to Cdc11p, Cdc3p and human	YNL225c		involved in cytokinesis	YBR049c	REB1	transcription factor
YDL179w		CDC10 protein similarity to cyclin G1 homologue HCS26		ACE2 MYO4	metallothionein expression activator myosin heavy chain, unconventional	rRNA pi	rocossi	na
YNL001w	DOM34	similarity to Cyclin an Homologue 110320 similarity to <i>D. melanogaster</i> pelota			(class V) isoform	_		ng .
YNL246w		protein similarity to <i>D. melanogaster</i> SET protein	YHR023w	MYO1	myosin-1 isoform (type II myosin) heavy chain	YOR048c YBR142w	RAT1 MAK5	5'-3' exoribonuclease ATP-dependent RNA helicase
YAR003w	FUN16	similarity to b. melanogaster 321 protein similarity to human RB protein binding		PWP2	periodic tryptophan protein	YNL112w	DBP2	ATP-dependent RNA helicase of DEAD
YKL179c		protein similarity to Nuf1p		PIK1 CDC11	phosphatidylinositol 4-kinase septin	YFL002c	SPB4	box family ATP-dependent RNA helicase of DEAH
YDL125c	YHI1	similarity to North		CDC12	septin			box family
YMR262w YLR356w		similarity to S. pombe scn1 protein similarity to SCM4 protein	YGL190c	CDC55	ser/thr phosphatase 2A regulatory subunit B	YPL029w	SUV3	ATP-dependent RNA helicase, mitochondrial
YIL095w	PRK1	similarity to ser/thr protein kinase	YAL016w	TPD3	ser/thr phosphatase 2A, regulatory	YJL033w	HCA4	can suppress the U14 snoRNA rRNA
YLR179c YOL080c		similarity to Tfs1p and Nsp1p similarity to X. laevis XPMC2 protein	YNL298w	CLAA	subunit A ser/thr protein kinase	YMR239c	RNT1	processing function double-stranded ribonuclease
YFR040w	SAP155	Sit4p-associated protein	YDL225w	OLA	similarity to Cdc11p, Cdc3p and human	YDL014w	NOP1	fibrillarin
YKR028w YGL229c	SAP190 SAP4	Sit4p-associated protein Sit4p-associated protein	YMR197c		CDC10 protein similarity to Nuf1p	YGL097w	SRM1	GDP/GTP exchange factor for Gsp1p/Gsp2p
YJL098w	SAP185	Sit4p-associating protein				YMR235c	RNA1	GTPase-activating protein
YGL086w YMR198w		spindle assembly checkpoint protein spindle pole body associated protein	synthes		vth, cell-division and DNA-	YLL011w YGR158c	SOF1 MTR3	involved in 18S pre-rRNA production involved in mRNA transport
YDR356w	NUF1	spindle pole body component				YGL173c	KEM1	multifunctional nuclease
YKL042w YNL126w		spindle pole body component spindle pole body component	YLR248w	RCK2	Ca <sup>2+</sup> /calmodulin-dependent ser/thr protein kinase	YGR159c	NSR1	nuclear localization sequence binding protein
YOR257w	CDC31	spindle pole body component, centrin	YOR101w		GTP-binding protein	YPL043w		nucleolar protein
YOL069w YJL030w	NUF2 MAD2	spindle pole body protein spindle-assembly checkpoint protein		RAS2 HDR1	GTP-binding protein high-dosage reductional segregation	YDR432w YCR018c	NPL3 SRD1	nucleolar protein nucleolar protein
YJL013c	MAD3	spindle-assembly checkpoint protein			defective	YHR089c	GAR1	nucleolar rRNA processing protein
YGL106w YHR205w	SCH9	strong similarity to calmodulins strong similarity to cAMP-dependent		LAG1 MCD1	longevity-assurance protein mitotic chromosome determinant	YLR223c	IFH1	pre-rRNA processing machinery control protein
		protein kinase	YGL091c	NBP35	nucleotide-binding protein	YMR229c	RRP5	processing of pre-ribosomal RNA
YER066w		strong similarity to cell division control protein Cdc4p		SHR5 RCK1	RAS suppressor ser/thr protein kinase	YNL221c	POP1	protein component of ribonuclease P and ribonuclease MRP
YLR117c		strong similarity to D. melanogaster	YKL189w		similarity to mouse MO25 gene	YHR065c	RRP3	required for maturation of the 35S primary
YIR012w		putative cell-cycle control protein crn strong similarity to Dbf8p				YLL008w	DRS1	transcript RNA helicase of the DEAD box family
YBR238c		strong similarity to general chromatin	Trans	crinti	ion	YPL266w	DIM1	rRNA (adenine-N6,N6-)-
YKL049c	CSE4	factor Spt16p strong similarity to histone H3		-		YOR201c	PET56	dimethyltransferase rRNA (guanosine-2'-O-)-methyltransferase
YGR231c YLR215c		strong similarity to prohibitins strong similarity to rat cell cycle	rRNA sy	nthesis	5	YPL021w YHL034c	SRD2 SBP1	similarity to Srd1p single-strand nucleic acid binding protein
		progression related D123 protein		RPA12	DNA-directed RNA polymerase I, 13.7K	YLR059c	YNT20	suppressor of rna12 yme2
YKL161c		strong similarity to ser/thr-specific protein kinase Slt2p	YPR010c	RPA135	DNA-directed RNA polymerase I, 135K	othory	2N/A +==	magnintian activities
YNL172w	APC1	subunit of anaphase-promoting complex	YOR341w	RPA190	subunit DNA-directed RNA polymerase I, 190K			nscription activities
		subunit of anaphase-promoting complex (cyclosome)		RPA190 RPA43	DNA-directed RNA polymerase I, 190K $\alpha$ subunit	YNL216w	RAP1	DNA-binding protein with repressor and
YKL022c	CDC16	subunit of anaphase-promoting complex (cyclosome) subunit of anaphase-promoting complex (cyclosome)	YOR340c	RPA43	DNA-directed RNA polymerase I, 190K α subunit DNA-directed RNA polymerase I, 36K subunit		RAP1	•
		subunit of anaphase-promoting complex (cyclosome) subunit of anaphase-promoting complex	YOR340c		DNA-directed RNA polymerase I, 190K α subunit DNA-directed RNA polymerase I, 36K	YNL216w	RAP1 PRP12	DNA-binding protein with repressor and activator activity involved in early maturation of pre-rRNA
YKL022c	CDC16	subunit of anaphase-promoting complex (cyclosome) subunit of anaphase-promoting complex	YOR340c YNL248c	RPA43	DNA-directed RNA polymerase I, 190K α subunit DNA-directed RNA polymerase I, 36K subunit DNA-directed RNA polymerase I, 49K α subunit DNA-directed RNA polymerase I, 414	YNL216w YMR302c tRNA sy	RAP1 PRP12 <b>/nthesi</b> :	DNA-binding protein with repressor and activator activity involved in early maturation of pre-rRNA
YKL022c YHR166c	CDC16 CDC23	subunit of anaphase-promoting complex (cyclosome) subunit of anaphase-promoting complex output of anaphase-promoting complex subunit of anaphase-promoting complex	YOR340c YNL248c YDR156w	RPA43 RPA49	DNA-directed RNA polymerase I, 190K α subunit DNA-directed RNA polymerase I, 36K subunit DNA-directed RNA polymerase I, 49K α subunit DNA-directed RNA polymerase I, A14 subunit DNA-directed RNA polymerase I, II, III 16K	YNL216w YMR302c <i>tRNA</i> sy YGL019w	RAP1 PRP12 <b>/nthesi</b> :	DNA-binding protein with repressor and activator activity involved in early maturation of pre-rRNA s  casein kinase II, β subunit DNA-directed RNA polymerase I, II, III 16K
YKL022c YHR166c YFR036w YBL084c	CDC16 CDC23 CDC26	subunit of anaphase-promoting complex (cyclosome)	YOR340c YNL248c YDR156w YOR224c	RPA43 RPA49 RPA14 RPB8	DNA-directed RNA polymerase I, 190K α subunit DNA-directed RNA polymerase I, 36K subunit DNA-directed RNA polymerase I, 49K α subunit DNA-directed RNA polymerase I, 414 subunit DNA-directed RNA polymerase I, II, III 16K subunit	YNL216w YMR302c tRNA sy YGL019w YOR224c	RAP1 PRP12 <b>/nthesi</b> : CKB1 RPB8	DNA-binding protein with repressor and activator activity involved in early maturation of pre-rRNA  s  casein kinase II, β subunit DNA-directed RNA polymerase I, II, III 16K subunit
YKL022c YHR166c YFR036w YBL084c YOR213c YCR052w	CDC16 CDC23 CDC26 CDC27 RSC6	subunit of anaphase-promoting complex (cyclosome) subunit of the RSC complex subunit of the RSC complex subunit of the RSC complex	YOR340c YNL248c YDR156w YOR224c YPR187w	RPA43 RPA49 RPA14 RPB8 RPO26	DNA-directed RNA polymerase I, 190K α subunit DNA-directed RNA polymerase I, 36K subunit DNA-directed RNA polymerase I, 49K α subunit DNA-directed RNA polymerase I, 414 subunit DNA-directed RNA polymerase I, II, III 16K subunit DNA-directed RNA polymerase I, II, III 18K subunit	YNL216w YMR302c <i>tRNA sy</i> YGL019w YOR224c YPR187w	RAP1 PRP12 /nthesi: CKB1 RPB8 RPO26	DNA-binding protein with repressor and activator activity involved in early maturation of pre-rRNA  S  casein kinase II, β subunit DNA-directed RNA polymerase I, II, III 16K subunit DNA-directed RNA polymerase I, II, III 18K subunit
YKL022c YHR166c YFR036w YBL084c YOR213c	CDC16 CDC23 CDC26 CDC27	subunit of anaphase-promoting complex (cyclosome) subunit of the RSC complex	YOR340c YNL248c YDR156w YOR224c	RPA43 RPA49 RPA14 RPB8 RPO26	DNA-directed RNA polymerase I, 190K α subunit DNA-directed RNA polymerase I, 36K subunit DNA-directed RNA polymerase I, 49K α subunit DNA-directed RNA polymerase I, 414 subunit DNA-directed RNA polymerase I, II, III 16K subunit DNA-directed RNA polymerase I, II, III 16K subunit DNA-directed RNA polymerase I, II, III 18K	YNL216w YMR302c tRNA sy YGL019w YOR224c	RAP1 PRP12 /nthesi: CKB1 RPB8 RPO26	DNA-binding protein with repressor and activator activity involved in early maturation of pre-rRNA s  casein kinase II, β subunit DNA-directed RNA polymerase I, II, III 16K subunit DNA-directed RNA polymerase I, II, III 18K
YKL022c YHR166c YFR036w YBL084c YOR213c YCR052w YFR037c YLR321c YIL126w	CDC16 CDC23 CDC26 CDC27  RSC6 RSC8 SFH1 STH1	subunit of anaphase-promoting complex (cyclosome) subunit of the RSC complex	YOR340c YNL248c YDR156w YOR224c YPR187w	RPA43 RPA49 RPA14 RPB8 RPO26 RPB5	DNA-directed RNA polymerase I, 190K α subunit DNA-directed RNA polymerase I, 36K subunit DNA-directed RNA polymerase I, 49K α subunit DNA-directed RNA polymerase I, 414 subunit DNA-directed RNA polymerase I, II, III 16K subunit DNA-directed RNA polymerase I, II, III 18K subunit DNA-directed RNA polymerase I, II, III 18K subunit DNA-directed RNA polymerase I, II, III 25K subunit DNA-directed RNA polymerase I, II, III 77K	YNL216w YMR302c <i>tRNA sy</i> YGL019w YOR224c YPR187w	RAP1 PRP12 /nthesis CKB1 RPB8 RPO26 RPB5	DNA-binding protein with repressor and activator activity involved in early maturation of pre-rRNA  S  casein kinase II, β subunit DNA-directed RNA polymerase I, II, III 16K subunit DNA-directed RNA polymerase I, II, III 18K subunit DNA-directed RNA polymerase I, II, III 25K subunit
YKL022c YHR166c YFR036w YBL084c YOR213c YCR052w YFR037c YLR321c YIL126w YJR091c	CDC16 CDC23 CDC26 CDC27 RSC6 RSC8 SFH1 STH1 JSN1	subunit of anaphase-promoting complex (cyclosome) subunit of the RSC complex subunit of the	YOR340c YNL248c YDR156w YOR224c YPR187w YBR154c YHR143w-a	RPA43 RPA49 RPA14 RPB8 RPO26 RPB5	DNA-directed RNA polymerase I, 190K α subunit DNA-directed RNA polymerase I, 36K subunit DNA-directed RNA polymerase I, 49K α subunit DNA-directed RNA polymerase I, 414 subunit DNA-directed RNA polymerase I, II, III 16K subunit DNA-directed RNA polymerase I, II, III 16K subunit DNA-directed RNA polymerase I, II, III 18K subunit DNA-directed RNA polymerase I, II, III 25K subunit DNA-directed RNA polymerase I, II, III 77K subunit DNA-directed RNA polymerase I, II, III 77K subunit DNA-directed RNA polymerase I, II, III	YNL216W YMR302c <i>tRNA</i> sy YGL019W YOR224c YPR187W YBR154c	RAP1 PRP12 /nthesis CKB1 RPB8 RPO26 RPB5	DNA-binding protein with repressor and activator activity involved in early maturation of pre-rRNA  S  casein kinase II, β subunit DNA-directed RNA polymerase I, II, III 16K subunit DNA-directed RNA polymerase I, II, III 18K subunit DNA-directed RNA polymerase I, II, III 25K subunit DNA-directed RNA polymerase I, II, III 7.7K subunit DNA-directed RNA polymerase I, II, III 7.7K subunit
YKL022c YHR166c YFR036w YBL084c YOR213c YCR052w YFR037c YLR321c YIL126w	CDC16 CDC23 CDC26 CDC27  RSC6 RSC8 SFH1 STH1	subunit of anaphase-promoting complex (cyclosome) subunit of the RSC complex suppresses the high-temperature lethality of tub2-150 suppressor of mil2 temperature-sensitive	YOR340c YNL248c YDR156w YOR224c YPR187w YBR154c YHR143w-a YOR210w	RPA43 RPA49 RPA14 RPB8 RPO26 RPB5 RPC10 RPB10	DNA-directed RNA polymerase I, 190K α subunit DNA-directed RNA polymerase I, 36K subunit DNA-directed RNA polymerase I, 49K α subunit DNA-directed RNA polymerase I, 414 subunit DNA-directed RNA polymerase I, II, III 16K subunit DNA-directed RNA polymerase I, II, III 18K subunit DNA-directed RNA polymerase I, II, III 25K subunit DNA-directed RNA polymerase I, II, III 7.7K subunit DNA-directed RNA polymerase I, II, III 7.7K subunit DNA-directed RNA polymerase I, II, III 7.7K subunit DNA-directed RNA polymerase I, II, III 8.3K subunit	YNL216W YMR302c <i>tRNA</i> sy YGL019W YOR224c YPR187W YBR154c YHR143W-4 YOR210W	RAP1 PRP12 /nthesis CKB1 RPB8 RP026 RPB5 a RPC10 RPB10	DNA-binding protein with repressor and activator activity involved in early maturation of pre-rRNA  S  casein kinase II, β subunit DNA-directed RNA polymerase I, II, III 16K subunit DNA-directed RNA polymerase I, II, III 18K subunit DNA-directed RNA polymerase I, II, III 25K subunit DNA-directed RNA polymerase I, II, III 77K subunit DNA-directed RNA polymerase I, II, III 77K subunit DNA-directed RNA polymerase I, II, III 8.3K subunit
YKL022c YHR166c YFR036w YBL084c YOR213c YCR052w YFR037c YLR321c YIL126w YJR091c YIL031w YDR285w	CDC16 CDC23 CDC26 CDC27  RSC6 RSC8 SFH1 STH1 JSN1 SMT4 ZIP1	subunit of anaphase-promoting complex (cyclosome) subunit of the RSC complex suppresses the high-temperature lethality of tub2-150 suppressor of mif2 temperature-sensitive mutation synaptonemal complex protein	YOR340c YNL248c YDR156W YOR224c YPR187W YBR154c YHR143W-a YOR210W YPR110c	RPA43 RPA49 RPA14 RPB8 RPO26 RPB5 RPC10 RPB10 RPC40	DNA-directed RNA polymerase I, 190K α subunit DNA-directed RNA polymerase I, 36K subunit DNA-directed RNA polymerase I, 49K α subunit DNA-directed RNA polymerase I, 414 subunit DNA-directed RNA polymerase I, II, III 16K subunit DNA-directed RNA polymerase I, II, III 16K subunit DNA-directed RNA polymerase I, II, III 18K subunit DNA-directed RNA polymerase I, II, III 25K subunit DNA-directed RNA polymerase I, II, III 77K subunit DNA-directed RNA polymerase I, II, III 8.3K subunit DNA-directed RNA polymerase I, II, III 8.3K subunit DNA-directed RNA polymerase I, III 40K subunit	YNL216w YMR302c <i>tRNA</i> sy YGL019w YOR224c YPR187w YBR154c YHR143w-4 YOR210w YPR110c	RAP1 PRP12 //nthesis CKB1 RPB8 RP026 RPB5 a RPC10 RPB10 RPC40	DNA-binding protein with repressor and activator activity involved in early maturation of pre-rRNA s  casein kinase II, β subunit DNA-directed RNA polymerase I, II, III 16K subunit DNA-directed RNA polymerase I, II, III 18K subunit DNA-directed RNA polymerase I, II, III 25K subunit DNA-directed RNA polymerase I, II, III 77K subunit DNA-directed RNA polymerase I, II, III 8.3K subunit DNA-directed RNA polymerase I, II, III 8.4K subunit DNA-directed RNA polymerase I, III, III 8.4K subunit DNA-directed RNA polymerase I, III 40K subunit
YKL022c YHR166c YFR036w YBL084c YOR213c YCR052w YFR037c YLR321c YIL126w YJR091c YIL031w	CDC16 CDC23 CDC26 CDC27 RSC6 RSC8 RSC8 SFH1 JSN1 SMT4	subunit of anaphase-promoting complex (cyclosome) subunit of the RSC complex suppresses the high-temperature lethality of tub2-150 suppressor of mil/2 temperature-sensitive mutation synaptonemal complex protein TFIIF subunit (transcription initiation	YOR340c YNL248c YDR156W YOR224c YPR187W YBR154c YHR143W-a YOR210W YPR110c	RPA43 RPA49 RPA14 RPB8 RPO26 RPB5 RPC10 RPB10	DNA-directed RNA polymerase I, 190K α subunit DNA-directed RNA polymerase I, 36K subunit DNA-directed RNA polymerase I, 49K α subunit DNA-directed RNA polymerase I, 49K α subunit DNA-directed RNA polymerase I, 11, 111 16K subunit DNA-directed RNA polymerase I, II, III 16K subunit DNA-directed RNA polymerase I, II, III 18K subunit DNA-directed RNA polymerase I, II, III 25K subunit DNA-directed RNA polymerase I, II, III 7.7K subunit DNA-directed RNA polymerase I, II, III 8.3K subunit DNA-directed RNA polymerase I, II, III 8.3K subunit DNA-directed RNA polymerase I, III 40K subunit DNA-directed RNA polymerase I, III 40K subunit	YNL216W YMR302c <i>tRNA</i> sy YGL019W YOR224c YPR187W YBR154c YHR143W-4 YOR210W	RAP1 PRP12 /nthesis CKB1 RPB8 RP026 RPB5 a RPC10 RPB10	DNA-binding protein with repressor and activator activity involved in early maturation of pre-rRNA  S  casein kinase II, β subunit DNA-directed RNA polymerase I, II, III 16K subunit DNA-directed RNA polymerase I, II, III 18K subunit DNA-directed RNA polymerase I, II, III 25K subunit DNA-directed RNA polymerase I, II, III 77K subunit DNA-directed RNA polymerase I, II, III 83K subunit DNA-directed RNA polymerase I, II, III 80K subunit DNA-directed RNA polymerase I, III 40K subunit DNA-directed RNA polymerase I, III 40K subunit
YKL022c YHR166c YFR036w YBL084c YOR213c YCR052w YFR037c YLR321c YIL126w YJR091c YIL031w YDR285w	CDC16 CDC23 CDC26 CDC27  RSC6 RSC8 SFH1 STH1 JSN1 SMT4 ZIP1	subunit of anaphase-promoting complex (cyclosome) subunit of the RSC complex suppresses the high-temperature lethality of tub2-160 suppressor of mif2 temperature-sensitive mutation synaptonemal complex protein TFIIF subunit (transcription initiation factor), 30K	YOR340c YNL248c YDR156w YOR224c YPR187w YBR154c YHR143w-a YOR210w YPR110c YNL113w	RPA43 RPA49 RPA14 RPB8 RPO26 RPB5 RPC10 RPB10 RPC40	DNA-directed RNA polymerase I, 190K α subunit DNA-directed RNA polymerase I, 36K subunit DNA-directed RNA polymerase I, 49K α subunit DNA-directed RNA polymerase I, 49K α subunit DNA-directed RNA polymerase I, II, III 16K subunit DNA-directed RNA polymerase I, II, III 16K subunit DNA-directed RNA polymerase I, II, III 18K subunit DNA-directed RNA polymerase I, II, III 25K subunit DNA-directed RNA polymerase I, II, III 77K subunit DNA-directed RNA polymerase I, II, III 83K subunit DNA-directed RNA polymerase I, III 40K subunit DNA-directed RNA polymerase I, III 16K subunit DNA-directed RNA polymerase I, III, 16K subunit DNA-directed RNA polymerase II, III, 16K subunit	YNL216w YMR302c <i>tRNA</i> sy YGL019w YOR224c YPR187w YBR154c YHR143w-4 YOR210w YPR110c	RAP1 PRP12 //nthesis CKB1 RPB8 RP026 RPB5 a RPC10 RPB10 RPC40	DNA-binding protein with repressor and activator activity involved in early maturation of pre-rRNA  S  casein kinase II, β subunit DNA-directed RNA polymerase I, II, III 16K subunit DNA-directed RNA polymerase I, II, III 18K subunit DNA-directed RNA polymerase I, II, III 25K subunit DNA-directed RNA polymerase I, II, III 77K subunit DNA-directed RNA polymerase I, II, III 8.3K subunit DNA-directed RNA polymerase I, III, III 9.3K subunit DNA-directed RNA polymerase I, III, III 9.3K subunit DNA-directed RNA polymerase I, III, 16K subunit DNA-directed RNA polymerase II, III, 16K subunit DNA-directed RNA polymerase III, 130K
YKL022c YHR166c YFR036w YBL084c YOR213c YCR052w YFR037c YLR321c YIL126w YJR091c YIL031w YDR285w YPL129w YPR025c YLR043c	CDC16 CDC23 CDC26 CDC27 RSC6 RSC8 RSC8 RSCH1 STH1 JSN1 SMT4 ZIP1 ANC1 CCL1 TRX1	subunit of anaphase-promoting complex (cyclosome) subunit of the RSC complex subpresses the high-temperature lethality of tub2-150 suppressor of mil2 temperature-sensitive mutation synaptonemal complex protein TFIIF subunit (transcription initiation factor), 30K	YOR340c YNL248c YDR156w YOR224c YPR187w YBR154c YHR143w-a YOR210w YPR110c YNL113w YOR207c	RPA43 RPA49 RPA14 RPB8 RPO26 RPB5 RPC10 RPB10 RPC40 RPC19	DNA-directed RNA polymerase I, 190K α subunit DNA-directed RNA polymerase I, 36K subunit DNA-directed RNA polymerase I, 49K α subunit DNA-directed RNA polymerase I, 49K α subunit DNA-directed RNA polymerase I, II, III 16K subunit DNA-directed RNA polymerase I, II, III 16K subunit DNA-directed RNA polymerase I, II, III 18K subunit DNA-directed RNA polymerase I, II, III 25K subunit DNA-directed RNA polymerase I, II, III 77K subunit DNA-directed RNA polymerase I, II, III 8.3K subunit DNA-directed RNA polymerase I, III 118 8.3K subunit DNA-directed RNA polymerase I, III 40K subunit DNA-directed RNA polymerase I, III 40K subunit	YNL216w YMR302c <i>tRNA</i> sy YGL019w YOR224c YPR187w YBR154c YHR143w-4 YOR210w YPR110c YNL113w	RAP1 PRP12 //nthesis CKB1 RPB8 RPO26 RPB5 a RPC10 RPB10 RPC40 RPC19	DNA-binding protein with repressor and activator activity involved in early maturation of pre-rRNA  S  casein kinase II, β subunit DNA-directed RNA polymerase I, II, III 16K subunit DNA-directed RNA polymerase I, II, III 18K subunit DNA-directed RNA polymerase I, II, III 25K subunit DNA-directed RNA polymerase I, II, III 77K subunit DNA-directed RNA polymerase I, II, III 8.3K subunit DNA-directed RNA polymerase I, II, III 8.4 subunit DNA-directed RNA polymerase I, III 40K subunit DNA-directed RNA polymerase I, III 40K subunit
YKL022c YHR166c YFR036w YBL084c YOR213c YCR052w YFR037c YLR321c YIL126w YJR091c YIL031w YDR285w YPL129w YPR025c YLR043c YGR209c	CDC16 CDC23 CDC26 CDC27 RSC6 RSC8 SFH1 JSN1 SMT4 ZIP1 ANC1 CCL1 TRX1 TRX2	subunit of anaphase-promoting complex (cyclosome) subunit of the RSC complex subunit of the RSC	YOR340c YNL248c YDR156w YOR224c YPR187w YBR154c YHR143w-a YOR210w YPR110c YNL113w YOR207c YOR116c	RPA43 RPA49 RPA14 RPB8 RPO26 RPB5 RPC10 RPB10 RPC40 RPC19 RPC128 RPO31	DNA-directed RNA polymerase I, 190K α subunit DNA-directed RNA polymerase I, 36K subunit DNA-directed RNA polymerase I, 49K α subunit DNA-directed RNA polymerase I, 49K α subunit DNA-directed RNA polymerase I, II, III 16K subunit DNA-directed RNA polymerase I, II, III 16K subunit DNA-directed RNA polymerase I, II, III 15K subunit DNA-directed RNA polymerase I, II, III 25K subunit DNA-directed RNA polymerase I, II, III 27K subunit DNA-directed RNA polymerase I, II, III 40K subunit DNA-directed RNA polymerase I, III 40K subunit DNA-directed RNA polymerase I, III, 16K subunit DNA-directed RNA polymerase III, 16K subunit DNA-directed RNA polymerase III, 130K subunit DNA-directed RNA polymerase III, 160K subunit	YNL216w YMR302c <i>tRNA</i> sy YGL019w YOR224c YPR187w YBR154c YHR143w-4 YOR210w YPR110c YNL113w YOR207c YOR216c	RAP1 PRP12 /nthesis CKB1 RPB8 RPO26 RPB5 a RPC10 RPB10 RPC40 RPC19 RPC128 RPO31	DNA-binding protein with repressor and activator activity involved in early maturation of pre-rRNA  S  casein kinase II, β subunit DNA-directed RNA polymerase I, II, III 16K subunit DNA-directed RNA polymerase I, II, III 18K subunit DNA-directed RNA polymerase I, II, III 25K subunit DNA-directed RNA polymerase I, II, III 77K subunit DNA-directed RNA polymerase I, II, III 8.3K subunit DNA-directed RNA polymerase I, III 40K subunit DNA-directed RNA polymerase I, III 16K subunit DNA-directed RNA polymerase II, III 16K subunit DNA-directed RNA polymerase III, 16K subunit DNA-directed RNA polymerase III, 16K subunit DNA-directed RNA polymerase III, 16K subunit
YKL022c YHR166c YFR036w YBL084c YOR213c YCR052w YFR037c YLR321c YIL126w YJR091c YIL031w YDR285w YPL129w YPR025c YLR043c YGR209c YOL116w YDL166w YDL166w	CDC16 CDC23 CDC26 CDC27  RSC6 RSC8 RSC8 RSCH1 STH1 JSN1 SMT4 ZIP1 ANC1 CCL1 TRX1 TRX2 TRF4 CDC36	subunit of anaphase-promoting complex (cyclosome) subunit of the RSC complex subunit of the RSC	YOR340c YNL248c YDR156W YOR224c YPR187W YBR154c YHR143W-a YOR210W YPR110c YNL113W YOR207c YOR116c YKL144c	RPA43 RPA49 RPA14 RPB8 RPO26 RPB5 RPC10 RPB10 RPC40 RPC19 RPC128 RPO31 RPC25	DNA-directed RNA polymerase I, 190K α subunit DNA-directed RNA polymerase I, 36K subunit DNA-directed RNA polymerase I, 49K α subunit DNA-directed RNA polymerase I, 49K α subunit DNA-directed RNA polymerase I, II, III 16K subunit DNA-directed RNA polymerase I, II, III 16K subunit DNA-directed RNA polymerase I, II, III 18K subunit DNA-directed RNA polymerase I, II, III 25K subunit DNA-directed RNA polymerase I, II, III 77K subunit DNA-directed RNA polymerase I, II, III 8.3K subunit DNA-directed RNA polymerase I, III, III 8.3K subunit DNA-directed RNA polymerase I, III, 16K subunit DNA-directed RNA polymerase III, 16K subunit DNA-directed RNA polymerase III, 130K subunit DNA-directed RNA polymerase III, 16K subunit DNA-directed RNA polymerase III, 16K subunit DNA-directed RNA polymerase III, 16K subunit DNA-directed RNA polymerase III, 25K subunit	YNL216W YMR302c tRNA sy YGL019W YOR224c YPR187W YBR154c YHR143W-4 YOR210W YPR110c YNL113W YOR207c YOR116c YKL144c	RAP1 PRP12 /nthesis: CKB1 RPB8 RP026 RPB5 a RPC10 RPC40 RPC19 RPC128 RPO31 RPC25	DNA-binding protein with repressor and activator activity involved in early maturation of pre-rRNA  S  casein kinase II, β subunit DNA-directed RNA polymerase I, II, III 16K subunit DNA-directed RNA polymerase I, II, III 18K subunit DNA-directed RNA polymerase I, II, III 25K subunit DNA-directed RNA polymerase I, II, III 77K subunit DNA-directed RNA polymerase I, II, III 8.3K subunit DNA-directed RNA polymerase I, III, III 8.1 (100 NA-directed RNA polymerase I, III, III 100 NA-directed RNA polymerase I, III, 16K subunit DNA-directed RNA polymerase III, 130K subunit DNA-directed RNA polymerase III, 160K subunit DNA-directed RNA polymerase III, 160K subunit DNA-directed RNA polymerase III, 25K subunit
YKL022c YHR166c YFR036w YBL084c YOR213c YCR052w YFR037c YLR321c YIL126w YJR091c YIL031w YDR286w YPL129w YPR025c YLR043c YGR209c YOL115w YDL165w YDL165w YER1111c	CDC16 CDC23 CDC26 CDC27  RSC6 RSC8 SFH1 STH1 JSN1 SMT4 ZIP1 ANC1 CCL1 TRX1 TRX2 TRF4 CSSCS SWW4	subunit of anaphase-promoting complex (cyclosome) subunit of the RSC complex subunit of the RSC	YOR340c YNL248c YDR156W YOR224c YPR187W YBR154c YHR143W-a YOR210W YPR110c YNL113W YOR207c YOR116c YKL144c	RPA43 RPA49 RPA14 RPB8 RPO26 RPB5 RPC10 RPB10 RPC40 RPC19 RPC128 RPO31	DNA-directed RNA polymerase I, 190K α subunit DNA-directed RNA polymerase I, 36K subunit DNA-directed RNA polymerase I, 49K α subunit DNA-directed RNA polymerase I, 49K α subunit DNA-directed RNA polymerase I, 1I, III 16K subunit DNA-directed RNA polymerase I, II, III 16K subunit DNA-directed RNA polymerase I, II, III 15K subunit DNA-directed RNA polymerase I, II, III 25K subunit DNA-directed RNA polymerase I, II, III 25K subunit DNA-directed RNA polymerase I, II, III 40K subunit DNA-directed RNA polymerase I, III, III 8.3K subunit DNA-directed RNA polymerase I, III, 16K subunit DNA-directed RNA polymerase III, 16K subunit DNA-directed RNA polymerase III, 16K subunit DNA-directed RNA polymerase III, 160K subunit DNA-directed RNA polymerase III, 160K subunit DNA-directed RNA polymerase III, 25K subunit DNA-directed RNA polymerase III, 25K subunit	YNL216w YMR302c <i>tRNA</i> sy YGL019w YOR224c YPR187w YBR154c YHR143w-4 YOR210w YPR110c YNL113w YOR207c YOR216c	RAP1 PRP12 /nthesis CKB1 RPB8 RPO26 RPB5 a RPC10 RPB10 RPC40 RPC19 RPC128 RPO31	DNA-binding protein with repressor and activator activity involved in early maturation of pre-rRNA  S  casein kinase II, β subunit DNA-directed RNA polymerase I, II, III 16K subunit DNA-directed RNA polymerase I, II, III 18K subunit DNA-directed RNA polymerase I, II, III 25K subunit DNA-directed RNA polymerase I, II, III 25K subunit DNA-directed RNA polymerase I, II, III 7.7K subunit DNA-directed RNA polymerase I, II, III 40K subunit DNA-directed RNA polymerase I, III, 16K subunit DNA-directed RNA polymerase III, 15K subunit DNA-directed RNA polymerase III, 25K subunit DNA-directed RNA polymerase III, 25K subunit
YKL022c YHR166c YFR036w YBL084c YOR213c YCR052w YFR037c YLR321c YIL126w YJR091c YIL031w YDR285w YPL129w YPR025c YLR043c YGR209c YOL116w YDL166w YDL166w	CDC16 CDC23 CDC26 CDC27  RSC6 RSC8 RSC8 RSCH1 STH1 JSN1 SMT4 ZIP1 ANC1 CCL1 TRX1 TRX2 TRF4 CDC36	subunit of anaphase-promoting complex (cyclosome) subunit of the RSC complex suppresses the high-temperature lethality of tub2-150 suppressor of mif2 temperature-sensitive mutation synaptonemal complex protein TFIIF subunit (transcription initiation factor), cyclin C component thioredoxin I thioredoxin I thioredoxin I thioredoxin I thioredoxin I transcription factor of the	YOR340c YNL248c YDR156W YOR224c YPR187W YBR154c YHR143W-a YOR210W YPR110c YNL113W YOR207c YOR116c YKL144c YNL151c	RPA43 RPA49 RPA14 RPB8 RPO26 RPB5 RPC10 RPB10 RPC40 RPC19 RPC128 RPO31 RPC25	DNA-directed RNA polymerase I, 190K α subunit DNA-directed RNA polymerase I, 36K subunit DNA-directed RNA polymerase I, 49K α subunit DNA-directed RNA polymerase I, 49K α subunit DNA-directed RNA polymerase I, II, III 16K subunit DNA-directed RNA polymerase I, II, III 16K subunit DNA-directed RNA polymerase I, II, III 18K subunit DNA-directed RNA polymerase I, II, III 25K subunit DNA-directed RNA polymerase I, II, III 77K subunit DNA-directed RNA polymerase I, II, III 8.3K subunit DNA-directed RNA polymerase I, III, III 8.3K subunit DNA-directed RNA polymerase I, III, 16K subunit DNA-directed RNA polymerase III, 25K subunit DNA-directed RNA polymerase III, 25K subunit DNA-directed RNA polymerase III, 31K subunit DNA-directed RNA polymerase III, 31K subunit DNA-directed RNA polymerase III, 31K subunit	YNL216W YMR302c tRNA sy YGL019W YOR224c YPR187W YBR154c YHR143W-4 YOR210W YPR110c YNL113W YOR207c YOR116c YKL144c	RAP1 PRP12 /nthesis: CKB1 RPB8 RP026 RPB5 a RPC10 RPC40 RPC19 RPC128 RPO31 RPC25	DNA-binding protein with repressor and activator activity involved in early maturation of pre-rRNA  S  casein kinase II, β subunit DNA-directed RNA polymerase I, II, III 16K subunit DNA-directed RNA polymerase I, II, III 18K subunit DNA-directed RNA polymerase I, II, III 25K subunit DNA-directed RNA polymerase I, II, III 25K subunit DNA-directed RNA polymerase I, II, III 7.7K subunit DNA-directed RNA polymerase I, II, III 8.3K subunit DNA-directed RNA polymerase I, III, 16K subunit DNA-directed RNA polymerase II, 16K subunit DNA-directed RNA polymerase III, 16K subunit DNA-directed RNA polymerase III, 16K subunit DNA-directed RNA polymerase III, 25K subunit DNA-directed RNA polymerase III, 25K subunit DNA-directed RNA polymerase III, 31K subunit DNA-directed RNA polymerase III, 31K subunit
YKL022c YHR166c YFR036w YBL084c YOR052w YFR037c YLR321c YIL126w YJR091c YIL031w YDR285w YPR025c YLR043c YGR209c YOL115w YDL165w YER111c YLR182w	CDC16 CDC23 CDC26 CDC27 RSC6 RSC8 SFH1 STH1 JSN1 SMT4 ZIP1 ANC1 CCL1 TRX1 TRX2 TRF4 CDC36 SW44 SW6 GTS1	subunit of anaphase-promoting complex (cyclosome) subunit of the RSC complex suppresses the high-temperature lethality of tub2-150 suppressor of mil2 temperature-sensitive mutation synaptonemal complex protein TFIIF subunit (transcription initiation factor), cyclin C component thioredoxin I thioredoxin I thioredoxin I thoreodxin I transcription factor transcription factor transcription factor transcription factor transcription factor	YOR340c YNL248c YDR156w YOR224c YPR187w YBR154c YHR143w-a YOR210w YPR110c YNL113w YOR207c YOR116c YKL144c YNL151c YNR003c	RPA43 RPA49 RPA14 RPB8 RPO26 RPB5 RPC10 RPC19 RPC40 RPC19 RPC128 RPO31 RPC25 RPC31	DNA-directed RNA polymerase I, 190K α subunit DNA-directed RNA polymerase I, 36K subunit DNA-directed RNA polymerase I, 49K α subunit DNA-directed RNA polymerase I, 49K α subunit DNA-directed RNA polymerase I, II, III 16K subunit DNA-directed RNA polymerase I, II, III 16K subunit DNA-directed RNA polymerase I, II, III 18K subunit DNA-directed RNA polymerase I, II, III 25K subunit DNA-directed RNA polymerase I, II, III 77K subunit DNA-directed RNA polymerase I, II, III 8.3K subunit DNA-directed RNA polymerase I, III, III 8.3K subunit DNA-directed RNA polymerase I, III, 16K subunit DNA-directed RNA polymerase III, 130K subunit DNA-directed RNA polymerase III, 160K subunit DNA-directed RNA polymerase III, 160K subunit DNA-directed RNA polymerase III, 25K subunit DNA-directed RNA polymerase III, 25K subunit DNA-directed RNA polymerase III, 25K subunit	YNL216W YMR302c tRNA sy YGL019W YOR224c YPR187W YBR154c YHR143W-4 YOR210W YPR110c YNL113W YOR207c YOR116c YKL144c YNL151c	RAP1 PRP12 Interest CKB1 RPB8 RP026 RPB5 RPC10 RPB10 RPC19 RPC19 RPC19 RPC128 RPO31 RPC25 RPC31	DNA-binding protein with repressor and activator activity involved in early maturation of pre-rRNA  S  casein kinase II, β subunit DNA-directed RNA polymerase I, II, III 16K subunit DNA-directed RNA polymerase I, II, III 18K subunit DNA-directed RNA polymerase I, II, III 25K subunit DNA-directed RNA polymerase I, II, III 27K subunit DNA-directed RNA polymerase I, II, III 8.3K subunit DNA-directed RNA polymerase I, II, III 8.1K subunit DNA-directed RNA polymerase I, III, 16K subunit DNA-directed RNA polymerase II, 16K subunit DNA-directed RNA polymerase III, 25K subunit DNA-directed RNA polymerase III, 25K subunit
YKL022c YHR166c YFR036w YBL084c YOR213c YCR052w YFR037c YLR321c YIL126w YJR091c YIL031w YDR285w YPL129w YPR025c YLR043c YGR209c YOL115w YDL165w YDL165w YDL165w YGL181w YMR043w	CDC16 CDC23 CDC26 CDC27 RSC6 RSC8 SFH1 JSN1 SMT4 ZIP1 ANC1 CCL1 TRX1 TRX2 TRF4 CDC36 SW14 SW16 GTS1 MCM1	subunit of anaphase-promoting complex (cyclosome) subunit of the RSC complex suppresses the high-temperature lethality of tub2-150 suppressor of mif2 temperature-sensitive mutation synaptonemal complex protein TFIIF subunit (transcription initiation factor), cyclin C component thioredoxin I thioredoxin I thioredoxin I thioredoxin I thioredoxin I thioredoxin factor transcription factor of the Gcs Ip/Glo3p/Sps18p family transcription factor of the MADS box family	YOR340c YNL248c YDR156w YOR224c YPR187w YBR154c YHR143w-a YOR210w YPR110c YNL113w YOR207c YOR116c YKL144c YNL151c YNR003c YDL150w	RPA43 RPA49 RPA14 RPB8 RPO26 RPB5 RPC10 RPB10 RPC40 RPC19 RPC128 RPC31 RPC25 RPC31 RPC34 RPC53	DNA-directed RNA polymerase I, 190K α subunit DNA-directed RNA polymerase I, 36K subunit DNA-directed RNA polymerase I, 49K α subunit DNA-directed RNA polymerase I, 49K α subunit DNA-directed RNA polymerase I, II, III 16K subunit DNA-directed RNA polymerase I, II, III 16K subunit DNA-directed RNA polymerase I, II, III 18K subunit DNA-directed RNA polymerase I, II, III 25K subunit DNA-directed RNA polymerase I, II, III 77K subunit DNA-directed RNA polymerase I, II, III 83K subunit DNA-directed RNA polymerase I, III, III 83K subunit DNA-directed RNA polymerase I, III, 16K subunit DNA-directed RNA polymerase III, 15K subunit DNA-directed RNA polymerase III, 31K subunit DNA-directed RNA polymerase III, 31K subunit DNA-directed RNA polymerase III, 34K subunit DNA-directed RNA polymerase III, 34K subunit	YNL216W YMR302c tRNA sy YGL019W YOR224c YPR187W YBR154c YHR143W-4 YOR210W YPR110c YNL113W YOR207c YOR116c YNL151c YNR003c YDL150W	RAP1 PRP12 //nthesis CKB1 RPB8 RP026 RPB5 a RPC10 RPP10 RPC40 RPC19 RPC128 RPO31 RPC25 RPC31 RPC34 RPC34 RPC53	DNA-binding protein with repressor and activator activity involved in early maturation of pre-rRNA  S  casein kinase II, β subunit DNA-directed RNA polymerase I, II, III 16K subunit DNA-directed RNA polymerase I, II, III 18K subunit DNA-directed RNA polymerase I, II, III 25K subunit DNA-directed RNA polymerase I, II, III 25K subunit DNA-directed RNA polymerase I, II, III 7.7K subunit DNA-directed RNA polymerase I, II, III 8.3K subunit DNA-directed RNA polymerase I, III, 16K subunit DNA-directed RNA polymerase II, 16K subunit DNA-directed RNA polymerase III, 16K subunit DNA-directed RNA polymerase III, 16K subunit DNA-directed RNA polymerase III, 25K subunit DNA-directed RNA polymerase III, 25K subunit DNA-directed RNA polymerase III, 31K subunit DNA-directed RNA polymerase III, 34K subunit DNA-directed RNA polymerase III, 34K subunit
YKL022c YHR166c YFR036w YBL084c YOR213c YCR052w YFR037c YLR321c YIL126w YJR091c YIL031w YDR286w YPL129w YPR025c YLR043c YGR209c YOL115w YDL165w YDL165w YDL165w YGL181w YGL181w	CDC16 CDC23 CDC26 CDC27 RSC6 RSC8 SFH1 JSN1 SMT4 ZIP1 ANC1 CCL1 TRX1 TRX2 TRF4 CDC36 SW14 SW16 GTS1 MCM1	subunit of anaphase-promoting complex (cyclosome) subunit of the RSC complex suppresses the high-temperature lethality of tub2-150 suppressor of mil2 temperature-sensitive mutation synaptonemal complex protein TFIIF subunit (transcription initiation factor), cyclin C component thioredoxin I thioredoxin I thioredoxin I thioredoxin I thioredoxin I transcription factor transcription factor transcription factor transcription factor transcription factor of the Gcs1p/Glo3p/Sps18p family transcription factor of the MADS box	YOR340c YNL248c YDR156W YOR224c YPR187W YBR154c YHR143W-a YOR210W YPR110c YNL113W YOR207c YOR116c YKL144c YNL151c YNR003c YDL150W YPR190c	RPA43 RPA49 RPA14 RPB8 RPO26 RPB5 RPC10 RPC40 RPC40 RPC31 RPC25 RPC31 RPC25 RPC31 RPC34 RPC53 RPC82	DNA-directed RNA polymerase I, 190K α subunit DNA-directed RNA polymerase I, 36K subunit DNA-directed RNA polymerase I, 49K α subunit DNA-directed RNA polymerase I, 49K α subunit DNA-directed RNA polymerase I, II, III 16K subunit DNA-directed RNA polymerase I, II, III 16K subunit DNA-directed RNA polymerase I, II, III 18K subunit DNA-directed RNA polymerase I, II, III 25K subunit DNA-directed RNA polymerase I, II, III 25K subunit DNA-directed RNA polymerase I, II, III 8.3K subunit DNA-directed RNA polymerase I, II, III 8.3K subunit DNA-directed RNA polymerase I, III, 16K subunit DNA-directed RNA polymerase III, 130K subunit DNA-directed RNA polymerase III, 16K subunit DNA-directed RNA polymerase III, 16K subunit DNA-directed RNA polymerase III, 25K subunit DNA-directed RNA polymerase III, 25K subunit DNA-directed RNA polymerase III, 31K subunit DNA-directed RNA polymerase III, 31K subunit DNA-directed RNA polymerase III, 34K subunit DNA-directed RNA polymerase III, 47K	YNL216W YMR302c tRNA sy YGL019W YOR224c YPR187W YBR154c YHR143W-4 YOR210W YPR110C YNL113W YOR207c YOR116c YKL144c YNL151c YNR003c	RAP1 PRP12 Interest Control PRP12 Interest Control PRP8 RP026 RPB6 RPC10 RPC10 RPC10 RPC19 RPC128 RPC31 RPC25 RPC31 RPC34 RPC34 RPC34 RPC53 RPC82	DNA-binding protein with repressor and activator activity involved in early maturation of pre-rRNA  S  casein kinase II, β subunit DNA-directed RNA polymerase I, II, III 16K subunit DNA-directed RNA polymerase I, II, III 18K subunit DNA-directed RNA polymerase I, II, III 25K subunit DNA-directed RNA polymerase I, II, III 27K subunit DNA-directed RNA polymerase I, II, III 27K subunit DNA-directed RNA polymerase I, II, III 40K subunit DNA-directed RNA polymerase I, III, 16K subunit DNA-directed RNA polymerase III, 25K subunit DNA-directed RNA polymerase III, 31K subunit DNA-directed RNA polymerase III, 31K subunit DNA-directed RNA polymerase III, 34K subunit DNA-directed RNA polymerase III, 34K subunit
YKL022c YHR166c YFR036w YBL084c YOR213c YCR052w YFR037c YLR321c YIL126w YJR091c YIL031w YDR285w YPL129w YPR025c YLR043c YGR209c YOL115w YDL165w YER111c YLR182w YGL181w YMR043w YHR206w YDL056w	CDC16 CDC23 CDC26 CDC27 RSC6 RSC8 SFH1 JSN1 SMT4 ZIP1 ANC1 CCL1 TRX1 TRX2 TRF4 CDC36 GTS1 MCM1 SKN7 MBP1	subunit of anaphase-promoting complex (cyclosome) subunit of the RSC complex suppresses the high-temperature lethality of tub2-150 suppressor of mif2 temperature-sensitive mutation synaptonemal complex protein TFIIF subunit (transcription initiation factor), cyclin C component thioredoxin I thioredoxin I thioredoxin I thioredoxin I thioredoxin I thioredoxin factor transcription factor transcription factor transcription factor transcription factor transcription factor transcription factor the Gcstp/Glo3p/Sps18p family transcription factor with similarity to Hsf1p transcription factor, subunit of the MBF factor	YOR340c YNL248c YDR156W YOR224c YPR187W YBR154c YHR143W-a YOR210W YPR110c YNL113W YOR207c YOR116c YKL144c YNL151c YNR003c YDL150W YPR190c	RPA43 RPA49 RPA14 RPB8 RPO26 RPB5 RPC10 RPB10 RPC40 RPC19 RPC128 RPC31 RPC25 RPC31 RPC34 RPC53	DNA-directed RNA polymerase I, 190K α subunit DNA-directed RNA polymerase I, 36K subunit DNA-directed RNA polymerase I, 49K α subunit DNA-directed RNA polymerase I, 49K α subunit DNA-directed RNA polymerase I, II, III 16K subunit DNA-directed RNA polymerase I, II, III 16K subunit DNA-directed RNA polymerase I, II, III 18K subunit DNA-directed RNA polymerase I, II, III 125K subunit DNA-directed RNA polymerase I, II, III 25K subunit DNA-directed RNA polymerase I, II, III 77K subunit DNA-directed RNA polymerase I, II, III 8.3K subunit DNA-directed RNA polymerase I, III, 16K subunit DNA-directed RNA polymerase III, 25K subunit DNA-directed RNA polymerase III, 31K subunit DNA-directed RNA polymerase III, 31K subunit DNA-directed RNA polymerase III, 34K subunit DNA-directed RNA polymerase III, 47K subunit DNA-directed RNA polymerase III, 82K subunit INA-directed RNA polymerase III, 82K subunit INA-directed RNA polymerase III, 82K subunit Involved in transcription of ribosomal	YNL216W YMR302c tRNA s) YGL019W YOR224c YPR187W YBR154c YHR143W-4 YOR210W YPR110c YNL113W YOR207c YNL115tc YNL151c YNR003c YDL150W YPR190c YER148W	RAP1 PRP12 (Inthesis CKB1 RPB8 RP026 RPB5 A RPC10 RPB10 RPC40 RPC128 RPC31 RPC25 RPC31 RPC34 RPC63 RPC82 SPT15	DNA-binding protein with repressor and activator activity involved in early maturation of pre-rRNA  S  casein kinase II, β subunit DNA-directed RNA polymerase I, II, III 16K subunit DNA-directed RNA polymerase I, II, III 18K subunit DNA-directed RNA polymerase I, II, III 25K subunit DNA-directed RNA polymerase I, II, III 25K subunit DNA-directed RNA polymerase I, II, III 77K subunit DNA-directed RNA polymerase I, II, III 8.3K subunit DNA-directed RNA polymerase I, III, 16K subunit DNA-directed RNA polymerase II, 16K subunit DNA-directed RNA polymerase III, 16K subunit DNA-directed RNA polymerase III, 16K subunit DNA-directed RNA polymerase III, 25K subunit DNA-directed RNA polymerase III, 25K subunit DNA-directed RNA polymerase III, 31K subunit DNA-directed RNA polymerase III, 34K subunit DNA-directed RNA polymerase III, 47K subunit DNA-directed RNA polymerase III, 47K subunit DNA-directed RNA polymerase III, 82K subunit TFIID and TFIIIB subunit
YKL022c YHR166c YFR036w YBL084c YOR213c YCR052w YFR037c YLR321c YIL126w YJR091c YIL031w YDR285w YPL129w YPR025c YLR043c YGR209c YOL115w YDL165w YDL165w YDL165w YGL181w YMR043w YHR043w YHR043w	CDC16 CDC23 CDC26 CDC27  RSC6 RSC8 SFH1 JSN1 SMT4 ZIP1 ANC1 CCL1 TRX1 TRX2 TRF4 CDC36 SW44 SW6 GTS1 MCM1 SKN7	subunit of anaphase-promoting complex (cyclosome) subunit of the RSC complex subunit (transcription initiation factor), got of component thioredoxin I thioredoxin I thioredoxin I thioredoxin I transcription factor transcription factor transcription factor transcription factor of the Gcs Ip/Glo3p/Sps18p family transcription factor of the MADS box family transcription factor with similarity to Hsf1p transcription factor, subunit of the MBF factor transcriptional activator transcriptional regulator involved in	YOR340c YNL248c YDR156w YOR224c YPR187w YBR154c YHR143w-a YOR210w YPR110c YNL113w YOR207c YOR116c YKL144c YNL151c YNR003c YDL150w YPR190c YLR039c	RPA43 RPA49 RPA14 RPB8 RPO26 RPB5 RPC10 RPC40 RPC40 RPC31 RPC25 RPC31 RPC25 RPC31 RPC34 RPC53 RPC82	DNA-directed RNA polymerase I, 190K α subunit DNA-directed RNA polymerase I, 36K subunit DNA-directed RNA polymerase I, 49K α subunit DNA-directed RNA polymerase I, 49K α subunit DNA-directed RNA polymerase I, II, III 16K subunit DNA-directed RNA polymerase I, II, III 16K subunit DNA-directed RNA polymerase I, II, III 18K subunit DNA-directed RNA polymerase I, II, III 25K subunit DNA-directed RNA polymerase I, II, III 77K subunit DNA-directed RNA polymerase II, III 18K subunit DNA-directed RNA polymerase I, II, III 8.3K subunit DNA-directed RNA polymerase II, III 16K subunit DNA-directed RNA polymerase II, III 16K subunit DNA-directed RNA polymerase III, 25K subunit DNA-directed RNA polymerase III, 31K subunit DNA-directed RNA polymerase III, 34K subunit DNA-directed RNA polymerase III, 47K subunit DNA-directed RNA polymerase III, 47K subunit DNA-directed RNA polymerase III, 82K subunit involved in transcription of ribosomal proteins and ribosomal RNA RNA polymerase I specific transcription	YNL216W YMR302c tRNA sy YGL019W YOR224c YPR187W YBR154c YHR143W-4 YOR210W YPR110c YNL113W YOR207c YOR116c YKL144c YNL151c YNR003c YDL150W YPR190c YER148W YPR186c	RAP1 PRP12 Interest of the property of the pro	DNA-binding protein with repressor and activator activity involved in early maturation of pre-rRNA  S  casein kinase II, β subunit DNA-directed RNA polymerase I, II, III 16K subunit DNA-directed RNA polymerase I, II, III 18K subunit DNA-directed RNA polymerase I, II, III 25K subunit DNA-directed RNA polymerase I, II, III 25K subunit DNA-directed RNA polymerase I, II, III 77K subunit DNA-directed RNA polymerase I, II, III 8.3K subunit DNA-directed RNA polymerase I, III, 16K subunit DNA-directed RNA polymerase II, 16K subunit DNA-directed RNA polymerase III, 25K subunit DNA-directed RNA polymerase III, 31K subunit DNA-directed RNA polymerase III, 34K subunit DNA-directed RNA polymerase III, 34K subunit DNA-directed RNA polymerase III, 47K subunit TFIIIA subunit (transcription initiation factor)
YKL022c YHR166c YFR036w YBL084c YOR213c YCR052w YFR037c YLR321c YIL126w YJR091c YIL031w YDR285w YPL129w YPR025c YLR043c YGR209c YOL115w YDL165w YDL165w YGL181w YMR043w YHR206w YDL056w YOR028c YNL012w	CDC16 CDC23 CDC26 CDC27 RSC6 RSC8 SFH1 STH1 JSN1 SMT4 ZIP1 ANC1 CCL1 TRX1 TRX2 TRF4 CDC36 SW46 GTS1 MCM1 SKN7 MBP1 CIN5 SPO1	subunit of anaphase-promoting complex (cyclosome) subunit of the RSC complex suppresses the high-temperature lethality of tub2-150 suppressor of mif2 temperature-sensitive mutation synaptonemal complex protein TFIIF subunit (transcription initiation factor), 30K TFIIH subunit (transcription initiation factor), 30K TFIIH subunit (transcription initiation factor), yotlin C component thioredoxin I thioredoxin I thioredoxin I thopoisomerase I-related protein transcription factor transcription factor transcription factor transcription factor transcription factor the GCs1p/Glo3p/Sps18p family transcription factor with similarity to Hsf1p transcription factor with similarity to Hsf1p transcriptional activator transcriptional regulator involved in sporulation	YOR340c YNL248c YDR156w YOR224c YPR187w YBR154c YHR143w-a YOR210w YPR110c YNL113w YOR207c YOR116c YKL144c YNL151c YNR003c YDL150w YPR190c YLR039c YKL125w	RPA43 RPA49 RPA14 RPB8 RPO26 RPB5 RPC10 RPB10 RPC40 RPC19 RPC28 RPO31 RPC25 RPC31 RPC34 RPC34 RPC53 RPC82 RIC1 RRN3	DNA-directed RNA polymerase I, 190K α subunit DNA-directed RNA polymerase I, 36K subunit DNA-directed RNA polymerase I, 49K α subunit DNA-directed RNA polymerase I, 414 subunit DNA-directed RNA polymerase I, II, III 16K subunit DNA-directed RNA polymerase I, II, III 16K subunit DNA-directed RNA polymerase I, II, III 18K subunit DNA-directed RNA polymerase I, II, III 125K subunit DNA-directed RNA polymerase I, II, III 7.7K subunit DNA-directed RNA polymerase I, II, III 8.3K subunit DNA-directed RNA polymerase I, II, III 8.3K subunit DNA-directed RNA polymerase I, III, III 6K subunit DNA-directed RNA polymerase II, III, 16K subunit DNA-directed RNA polymerase III, 31K subunit DNA-directed RNA polymerase III, 31K subunit DNA-directed RNA polymerase III, 34K subunit DNA-directed RNA polymerase III, 47K subunit DNA-directed RNA polymerase III, 82K subunit DNA-directed RNA polymerase III, 82K subunit involved in transcription of ribosomal proteins and ribosomal RNA RNA polymerase I specific transcription factor	YNL216W YMR302c tRNA sy YGL019W YOR224c YPR187W YBR164c YHR143W-4 YOR210W YPR110C YNL113W YOR207c YOR116c YKL144c YNL151c YNR003c YDL150W YPR190C YER148W YPR186c YGR246c	RAP1 PRP12 (Inthesis CKB1 RPB8 RP026 RPB5 A RPC10 RPB10 RPC40 RPC128 RPC31 RPC25 RPC31 RPC34 RPC34 RPC53 RPC82 SPT15 TFC2 BRF1	DNA-binding protein with repressor and activator activity involved in early maturation of pre-rRNA  S  casein kinase II, β subunit DNA-directed RNA polymerase I, II, III 16K subunit DNA-directed RNA polymerase I, II, III 18K subunit DNA-directed RNA polymerase I, II, III 25K subunit DNA-directed RNA polymerase I, II, III 7.7K subunit DNA-directed RNA polymerase I, II, III 7.7K subunit DNA-directed RNA polymerase I, II, III 8.3K subunit DNA-directed RNA polymerase I, III, 16K subunit DNA-directed RNA polymerase II, 16K subunit DNA-directed RNA polymerase III, 16K subunit DNA-directed RNA polymerase III, 16K subunit DNA-directed RNA polymerase III, 150K subunit DNA-directed RNA polymerase III, 25K subunit DNA-directed RNA polymerase III, 31K subunit DNA-directed RNA polymerase III, 34K subunit DNA-directed RNA polymerase III, 47K subunit DNA-directed RNA polymerase III, 82K subunit DNA-directed RNA polymerase III, 82K subunit TRIID and TFIIIB subunit TFIII a subunit, 70K
YKL022c YHR166c YFR036w YBL084c YOR213c YCR052w YFR037c YLR321c YIL126w YJR091c YIL031w YDR285w YPL129w YPR025c YLR043c YGR209c YLR043c YGR111c YLR182w YGL181w YMR043w YHR206w YDL056w YOR028c	CDC16 CDC23 CDC26 CDC27 RSC6 RSC8 SFH1 STH1 JSN1 SMT4 ZIP1 ANC1 CCL1 TRX1 TRX2 TRF4 CDC36 SW46 GTS1 MCM1 SKN7 MBP1 CIN5	subunit of anaphase-promoting complex (cyclosome) subunit of the RSC complex subunit (transcription initiation factor), cyclin C component thioredoxin I thoredoxin I thoredoxin I the subunit of the RSC complex transcription factor transcription factor transcription factor transcription factor of the Csc Ip/Glo3p/Sps18p family transcription factor of the MADS box family transcription factor with similarity to Hsf1p transcription factor, subunit of the MBF factor transcriptional activator transcriptional regulator involved in sporulation translation initiation factor eIF3 subunit U5 snRNP protein, pre-mRNA splicing	YOR340c YNL248c YDR156w YOR224c YPR187w YBR154c YHR143w-a YOR210w YPR110c YNL113w YOR207c YOR116c YKL144c YNL151c YNR003c YDL150w YPR190c YLR039c YKL125w YBL025w	RPA43 RPA49 RPA14 RPB8 RPO26 RPB5 RPC10 RPB10 RPC40 RPC19 RPC25 RPC31 RPC25 RPC31 RPC34 RPC53 RPC63 RPC82 RIC1 RRN3 RRN10	DNA-directed RNA polymerase I, 190K α subunit DNA-directed RNA polymerase I, 36K subunit DNA-directed RNA polymerase I, 49K α subunit DNA-directed RNA polymerase I, 49K α subunit DNA-directed RNA polymerase I, II, III 16K subunit DNA-directed RNA polymerase I, II, III 16K subunit DNA-directed RNA polymerase I, II, III 18K subunit DNA-directed RNA polymerase I, II, III 125K subunit DNA-directed RNA polymerase I, II, III 25K subunit DNA-directed RNA polymerase I, II, III 77K subunit DNA-directed RNA polymerase I, II, III 8.3K subunit DNA-directed RNA polymerase I, III, 16K subunit DNA-directed RNA polymerase III, 25K subunit DNA-directed RNA polymerase III, 31K subunit DNA-directed RNA polymerase III, 31K subunit DNA-directed RNA polymerase III, 34K subunit DNA-directed RNA polymerase III, 47K subunit DNA-directed RNA polymerase III, 82K subunit	YNL216W YMR302c tRNA sy YGL019W YOR224c YPR187W YBR154c YHR143W-4 YOR210W YPR110c YNL113W YOR207c YOR116c YKL144c YNL151c YNR003c YDL150W YPR190c YER148W YPR186c	RAP1 PRP12 Interest of the property of the pro	DNA-binding protein with repressor and activator activity involved in early maturation of pre-rRNA  S  casein kinase II, β subunit DNA-directed RNA polymerase I, II, III 16K subunit DNA-directed RNA polymerase I, II, III 18K subunit DNA-directed RNA polymerase I, II, III 25K subunit DNA-directed RNA polymerase I, II, III 25K subunit DNA-directed RNA polymerase I, II, III 7.7K subunit DNA-directed RNA polymerase I, II, III 8.3K subunit DNA-directed RNA polymerase I, III, III 6.K subunit DNA-directed RNA polymerase I, III, 16K subunit DNA-directed RNA polymerase III, 16K subunit DNA-directed RNA polymerase III, 16K subunit DNA-directed RNA polymerase III, 25K subunit DNA-directed RNA polymerase III, 25K subunit DNA-directed RNA polymerase III, 31K subunit DNA-directed RNA polymerase III, 34K subunit DNA-directed RNA polymerase III, 34K subunit DNA-directed RNA polymerase III, 47K subunit TRIID and TRIIB subunit TFIID and TRIIB subunit TFIID subunit (transcription initiation factor) TFIIIB subunit, 70K TFIIIB subunit, 190K TFIIIB subunit (transcription initiation
YKL022c YHR166c YFR036w YBL084c YOR213c YCR052w YFR037c YLR321c YIL126w YJR091c YIL031w YDR286w YPL129w YPR025c YLR043c YGR209c YOL115w YDL165w YDL165w YGL181w YMR043w YHR206w YDL0566w YOR028c YNL012w YOR361c YHR165c	CDC16 CDC23 CDC26 CDC27 RSC6 RSC8 SFH1 STH1 JSN1 SMT4 ZIP1 ANC1 CCL1 TRX1 TRX2 TRF4 CDC36 SW44 SW6 GTS1 MCM1 SKN7 MBP1 CIN5 SPO1 PRT1 PRP8	subunit of anaphase-promoting complex (cyclosome) subunit of the RSC complex suppresses the high-temperature lethality of tub2-150 suppressor of mif2 temperature-sensitive mutation synaptonemal complex protein TFIIF subunit (transcription initiation factor), 30K TFIIH subunit (transcription initiation factor), 30K TFIIH subunit (transcription initiation factor), cyclin C component thioredoxin I thioredoxin I thopoisomerase I-related protein transcription factor the MADS box family transcription factor with similarity to Hsf1p transcriptional regulator involved in sporulation translation initiation factor eIF3 subunit U5 snRNP protein, pre-mRNA splicing factor	YOR340c YNL248c YDR156w YOR224c YPR187w YBR154c YHR143w-a YOR210w YPR110c YNL113w YOR207c YOR116c YKL144c YNL151c YNR003c YDL150w YPR190c YLR039c YKL125w YBL025w	RPA43 RPA49 RPA14 RPB8 RPO26 RPB5 RPC10 RPB10 RPC40 RPC19 RPC28 RPO31 RPC25 RPC31 RPC34 RPC34 RPC53 RPC82 RIC1 RRN3	DNA-directed RNA polymerase I, 190K α subunit DNA-directed RNA polymerase I, 36K subunit DNA-directed RNA polymerase I, 49K α subunit DNA-directed RNA polymerase I, 414 subunit DNA-directed RNA polymerase I, II, III 16K subunit DNA-directed RNA polymerase I, II, III 16K subunit DNA-directed RNA polymerase I, II, III 18K subunit DNA-directed RNA polymerase I, II, III 25K subunit DNA-directed RNA polymerase I, II, III 7.7K subunit DNA-directed RNA polymerase I, II, III 8.3K subunit DNA-directed RNA polymerase I, II, III 8.3K subunit DNA-directed RNA polymerase I, III, 16K subunit DNA-directed RNA polymerase II, II, 16K subunit DNA-directed RNA polymerase III, 31K subunit DNA-directed RNA polymerase III, 34K subunit DNA-directed RNA polymerase III, 34K subunit DNA-directed RNA polymerase III, 34K subunit DNA-directed RNA polymerase III, 82K subunit	YNL216W YMR302c  tRNA sy YGL019W YOR224c  YPR187W YBR154c  YHR143W-4 YOR210W YPR110c  YNL113W YOR207c YOR116c  YKL144c YNL151c  YNR003c  YPR190c  YER148W YPR190c  YER148W YPR186c  YGR246c YNL039W YGR047c	RAP1 PRP12 //nthesis CKB1 RPB8 RPO26 RPB5 A RPC10 RPB10 RPC40 RPC19 RPC128 RPO31 RPC25 RPC31 RPC34 RPC53 RPC34 RPC53 RPC63 RPC82 SPT16 TFC2 BRF1 TFC6 TFC4	DNA-binding protein with repressor and activator activity involved in early maturation of pre-rRNA  S  casein kinase II, β subunit DNA-directed RNA polymerase I, II, III 16K subunit DNA-directed RNA polymerase I, II, III 18K subunit DNA-directed RNA polymerase I, II, III 25K subunit DNA-directed RNA polymerase I, II, III 77K subunit DNA-directed RNA polymerase I, II, III 77K subunit DNA-directed RNA polymerase I, II, III 8.3K subunit DNA-directed RNA polymerase I, III, 16K subunit DNA-directed RNA polymerase I, III, 16K subunit DNA-directed RNA polymerase III, 130K subunit DNA-directed RNA polymerase III, 150K subunit DNA-directed RNA polymerase III, 150K subunit DNA-directed RNA polymerase III, 25K subunit DNA-directed RNA polymerase III, 31K subunit DNA-directed RNA polymerase III, 34K subunit DNA-directed RNA polymerase III, 47K subunit DNA-directed RNA polymerase III, 82K subunit TFIID and TFIIIB subunit TFIIIB subunit (transcription initiation factor) TFIIIB subunit (transcription initiation factor) TFIIIB subunit (transcription initiation factor), 131K
YKL022c YHR166c YFR036w YBL084c YOR213c YCR052w YFR037c YLR321c YIL126w YJR091c YIL031w YDR285w YPL129w YPR025c YLR043c YGR209c YOL115w YDL165w YDL165w YGL181w YMR043w YHR206w YOL056w YOR028c YNL012w YOR028c YNL012w YOR028c YNL012w YOR0361c YHR165c YDR054c YDR054c	CDC16 CDC23 CDC26 CDC27  RSC6 RSC8 SFH1 JSN1 SMT4 ZJP1 ANC1 CCL1 TRX1 TRX2 TRF4 CDC36 SWI6 GTS1 MCM1 SKN7 MBP1 CIN5 SPO1 PRT1 PRP8 CDC34 UBC9	subunit of anaphase-promoting complex (cyclosome) subunit of the RSC complex subunit (transcriptor suppressor of mif2 temperature-sensitive mutation synaptonemal complex protein TFIIF subunit (transcription initiation factor), 30K TFIIH subunit (transcription initiation factor), 30K TFIIH subunit (transcription initiation factor), 30K TFIIH subunit (transcription initiation factor) transcription factor transcription factor transcription factor transcription factor the MADS box family transcription factor of the MADS box family transcription factor with similarity to Hsf1p transcriptional activator transcriptional activator transcriptional activator transcriptional regulator involved in sporulation translation initiation factor elF3 subunit US snRNP protein, pre-mRNA splicing factor ubiquitin-conjugating enzyme	YOR340c YNL248c YDR156W YOR224c YPR187W YBR154c YHR143W-a YOR210W YPR110c YNL113W YOR207c YOR116c YKL144c YNL151c YNR003c YDL150W YPR190c YLR039c YKL125W YBL025W YML043c	RPA43 RPA49 RPA14 RPB8 RPO26 RPB5 RPC10 RPB10 RPC40 RPC19 RPC25 RPC31 RPC25 RPC31 RPC34 RPC53 RPC63 RPC82 RIC1 RRN3 RRN10	DNA-directed RNA polymerase I, 190K α subunit DNA-directed RNA polymerase I, 36K subunit DNA-directed RNA polymerase I, 49K α subunit DNA-directed RNA polymerase I, 49K α subunit DNA-directed RNA polymerase I, 414 subunit DNA-directed RNA polymerase I, II, III 16K subunit DNA-directed RNA polymerase I, II, III 18K subunit DNA-directed RNA polymerase I, II, III 18K subunit DNA-directed RNA polymerase I, II, III 25K subunit DNA-directed RNA polymerase I, II, III 7.7K subunit DNA-directed RNA polymerase I, III, III 8.3K subunit DNA-directed RNA polymerase I, III, III 6K subunit DNA-directed RNA polymerase II, III, 16K subunit DNA-directed RNA polymerase III, 31K subunit DNA-directed RNA polymerase III, 31K subunit DNA-directed RNA polymerase III, 34K subunit DNA-directed RNA polymerase III, 34K subunit DNA-directed RNA polymerase III, 34K subunit DNA-directed RNA polymerase III, 32K subunit	YNL216W YMR302c tRNA sy YGL019W YOR224c YPR187W YBR154c YHR143W-4 YOR210W YPR110C YNL113W YOR207c YNL1151c YNL151c YNL151c YNL151c YNL156W YPR190C YER148W YPR186C YGR246C YNL039W YGR047c YAL001c	RAP1 PRP12 (Inthesis CKB1 RPB8 RP026 RPB5 A RPC10 RPB10 RPC128 RPC31 RPC34 RPC34 RPC34 RPC53 RPC82 SPT15 TFC2 BRF1 TFC5 TFC4 TFC5	DNA-binding protein with repressor and activator activity involved in early maturation of pre-rRNA  S  casein kinase II, β subunit DNA-directed RNA polymerase I, II, III 16K subunit DNA-directed RNA polymerase I, II, III 18K subunit DNA-directed RNA polymerase I, II, III 25K subunit DNA-directed RNA polymerase I, II, III 7.7K subunit DNA-directed RNA polymerase I, II, III 7.7K subunit DNA-directed RNA polymerase I, II, III 8.3K subunit DNA-directed RNA polymerase I, III, 16K subunit DNA-directed RNA polymerase II, 16K subunit DNA-directed RNA polymerase III, 18K subunit DNA-directed RNA polymerase III, 31K subunit DNA-directed RNA polymerase III, 34K subunit DNA-directed RNA polymerase III, 47K subunit DNA-directed RNA polymerase III, 47K subunit TRIII Subunit (transcription initiation factor) TFIIIB subunit, 70K TFIIIC subunit (transcription initiation factor), 131K TFIIIC subunit (transcription initiation factor), 131K
YKL022c YHR166c YFR036w YBL084c YOR213c YCR052w YFR037c YLR321c YIL126w YJR091c YIL031w YDR285w YPL129w YPR025c YLR043c YGR209c YOL115w YDL165w YER111c YLR182w YGL181w YMR043w YHR206w YOL056w YOR028c YNL012w YOR361c YHR165c	CDC16 CDC23 CDC26 CDC27  RSC6 RSC8 SFH1 JSN1 SMT4 ZJP1 ANC1 CCL1 TRX1 TRX2 TRF4 CDC36 SWI6 GTS1 MCM1 SKN7 MBP1 CIN5 SPO1 PRT1 PRP8 CDC34 UBC9	subunit of anaphase-promoting complex (cyclosome) subunit of the RSC complex suppresses the high-temperature lethality of tub2-150 suppressor of mil/2 temperature-sensitive mutation synaptonemal complex protein TFIIF subunit (transcription initiation factor), cyclin C component thioredoxin I transcription factor transcription factor transcription factor transcription factor of the Gcs1p/Glo3p/Sps18p family transcription factor of the MADS box family transcription factor with similarity to Hsf1p transcriptional regulator involved in sporulation translation initiation factor eIF3 subunit U5 snRNP protein, pre-mRNA splicing factor ubiquitin-conjugating enzyme	YOR340c YNL248c YDR156w YOR224c YPR187w YBR154c YHR143w-a YOR210w YPR110c YNL113w YOR207c YOR116c YKL144c YNL151c YNR003c YDL150w YPR190c YLR039c YKL125w YBL025w YML043c YLR141w	RPA43 RPA49 RPA14 RPB8 RPO26 RPB5 RPC10 RPC40 RPC40 RPC25 RPC31 RPC25 RPC31 RPC25 RPC31 RPC82 RIC1 RRN3 RRN10 RRN11	DNA-directed RNA polymerase I, 190K α subunit DNA-directed RNA polymerase I, 36K subunit DNA-directed RNA polymerase I, 49K α subunit DNA-directed RNA polymerase I, 49K α subunit DNA-directed RNA polymerase I, 414 subunit DNA-directed RNA polymerase I, II, III 16K subunit DNA-directed RNA polymerase I, II, III 18K subunit DNA-directed RNA polymerase I, II, III 25K subunit DNA-directed RNA polymerase I, II, III 25K subunit DNA-directed RNA polymerase I, II, III 7.7K subunit DNA-directed RNA polymerase I, III, III 8.3K subunit DNA-directed RNA polymerase I, III, III 8.0K subunit DNA-directed RNA polymerase II, III 16K subunit DNA-directed RNA polymerase III, 16K subunit DNA-directed RNA polymerase III, 16K subunit DNA-directed RNA polymerase III, 16NK subunit DNA-directed RNA polymerase III, 31K subunit DNA-directed RNA polymerase III, 31K subunit DNA-directed RNA polymerase III, 34K subunit DNA-directed RNA polymerase III, 47K subunit DNA-directed RNA polymerase III, 82K subunit	YNL216W YMR302c  tRNA sy YGL019W YOR224c  YPR187W YBR154c  YHR143W-4 YOR210W YPR110c  YNL113W YOR207c YOR116c  YKL144c YNL151c  YNR003c  YPR190c  YER148W YPR190c  YER148W YPR186c  YGR246c YNL039W YGR047c	RAP1 PRP12 //nthesis CKB1 RPB8 RPO26 RPB5 A RPC10 RPB10 RPC40 RPC19 RPC128 RPO31 RPC25 RPC31 RPC34 RPC53 RPC34 RPC53 RPC63 RPC82 SPT16 TFC2 BRF1 TFC6 TFC4	DNA-binding protein with repressor and activator activity involved in early maturation of pre-rRNA  S  casein kinase II, β subunit DNA-directed RNA polymerase I, II, III 16K subunit DNA-directed RNA polymerase I, II, III 18K subunit DNA-directed RNA polymerase I, II, III 25K subunit DNA-directed RNA polymerase I, II, III 77K subunit DNA-directed RNA polymerase I, II, III 77K subunit DNA-directed RNA polymerase I, III, III 8.3K subunit DNA-directed RNA polymerase I, III, 16K subunit DNA-directed RNA polymerase II, II 6K subunit DNA-directed RNA polymerase III, 16K subunit DNA-directed RNA polymerase III, 16K subunit DNA-directed RNA polymerase III, 180K subunit DNA-directed RNA polymerase III, 181K subunit DNA-directed RNA polymerase III, 31K subunit DNA-directed RNA polymerase III, 34K subunit DNA-directed RNA polymerase III, 34K subunit DNA-directed RNA polymerase III, 47K subunit DNA-directed RNA polymerase III, 82K subunit TFIID and TFIIIB subunit TFIIIB subunit (transcription initiation factor) TFIIIB subunit (transcription initiation factor), 138K TFIIIC subunit (transcription initiation factor), 138K TFIIIC subunit (transcription initiation factor), 138K TFIIIC subunit (transcription initiation factor), 138K
YKL022c YHR166c YFR036w YBL084c YOR213c YCR052w YFR037c YLR321c YIL126w YJR091c YIL031w YDR285w YPL129w YPR025c YLR043c YGR209c YLR043c YGR209c YLR116bw YDL165w YER111c YLR182w YGL181w YMR043w YHR206w YDL056w YOR028c YNL012w YOR361c YHR165c YDR064c YDR064c YDR064c YDR064c	CDC16 CDC23 CDC26 CDC27  RSC6 RSC6 RSC8 RSC8 RSC8 RSC8 RSC8 RSC8 RSC8 RSC8	subunit of anaphase-promoting complex (cyclosome) subunit of the RSC complex suppresses the high-temperature lethality of tub2-150 suppressor of mif2 temperature-sensitive mutation synaptonemal complex protein TFIIF subunit (transcription initiation factor), 30K TFIIH subunit (transcription initiation factor), 30K TFIIH subunit (transcription initiation factor), cyclin C component thioredoxin I thioredoxin I thioredoxin I thopoisomerase I-related protein transcription factor the MADS box family transcription factor with similarity to Hsf1p transcriptional regulator involved in sporulation translation initiation factor eIF3 subunit US snRNP protein, pre-mRNA splicing factor ubiquitin-conjugating enzyme ubiquitin-conjugating enzyme ubiquitin-like protein vanadate resistance protein weak similarity to cyclin G1 homolog	YOR340c YNL248c YDR156w YOR224c YPR187w YBR154c YHR143w-a YOR210w YPR110c YNL113w YOR207c YOR116c YNL151c YNR003c YDL150w YPR190c YLR039c YLR039c YKL125w YML043c YLR141w YBL014c	RPA43 RPA49 RPA14 RPB8 RPO26 RPB5 RPC10 RPB10 RPC40 RPC19 RPC28 RPC31 RPC25 RPC31 RPC34 RPC53 RPC82 RIC1 RRN3 RRN10 RRN11 RRN5 RRN16	DNA-directed RNA polymerase I, 190K α subunit DNA-directed RNA polymerase I, 36K subunit DNA-directed RNA polymerase I, 49K α subunit DNA-directed RNA polymerase I, 49K α subunit DNA-directed RNA polymerase I, 414 subunit DNA-directed RNA polymerase I, II, III 16K subunit DNA-directed RNA polymerase I, II, III 18K subunit DNA-directed RNA polymerase I, II, III 25K subunit DNA-directed RNA polymerase I, II, III 25K subunit DNA-directed RNA polymerase I, II, III 7.7K subunit DNA-directed RNA polymerase I, III, III 8.3K subunit DNA-directed RNA polymerase I, III, III 8.0K subunit DNA-directed RNA polymerase II, III, 16K subunit DNA-directed RNA polymerase III, 31K subunit DNA-directed RNA polymerase III, 31K subunit DNA-directed RNA polymerase III, 34K subunit DNA-directed RNA polymerase III, 34K subunit DNA-directed RNA polymerase III, 82K subunit	YNL216W YMR302c tRNA sy YGL019W YOR224c YPR187W YBR164c YHR143W-4 YOR210W YPR110c YNL113W YOR207c YOR116c YNL151c YNL161c YNL03c YPR190c YER148W YPR190c YER148W YPR186c YGR246c YNL039W YGR047c YAL001c YBR123c	RAP1 PRP12 (Inthesis CKB1 RPB8 RP026 RPB5 RPC10 RPB10 RPC40 RPC19 RPC128 RPC31 RPC34 RPC34 RPC34 RPC53 RPC25 RPC31 RPC63 RPC63 RPC63 RPC74 TFC2 BRF1 TFC6 TFC4 TFC3 TFC1	DNA-binding protein with repressor and activator activity involved in early maturation of pre-rRNA  S  casein kinase II, β subunit DNA-directed RNA polymerase I, II, III 16K subunit DNA-directed RNA polymerase I, II, III 18K subunit DNA-directed RNA polymerase I, II, III 25K subunit DNA-directed RNA polymerase I, II, III 7.7K subunit DNA-directed RNA polymerase I, II, III 7.7K subunit DNA-directed RNA polymerase I, II, III 8.3K subunit DNA-directed RNA polymerase I, III, 16K subunit DNA-directed RNA polymerase II, 16K subunit DNA-directed RNA polymerase III, 16K subunit DNA-directed RNA polymerase III, 16K subunit DNA-directed RNA polymerase III, 15K subunit DNA-directed RNA polymerase III, 25K subunit DNA-directed RNA polymerase III, 34K subunit DNA-directed RNA polymerase III, 34K subunit DNA-directed RNA polymerase III, 47K subunit DNA-directed RNA polymerase III, 82K subunit TFIID and TFIIIB subunit TFIIIB subunit, 70K TFIIIB subunit, 70K TFIIIB subunit (transcription initiation factor), 131K TFIIIC subunit (transcription initiation factor), 131K TFIIIC subunit (transcription initiation factor), 138K TFIIIC subunit (transcription initiation factor), 95K
YKL022c YHR166c YFR036w YBL084c YOR213c YCR052w YFR037c YLR321c YIL126w YJR091c YIL031w YDR285w YPL129w YPR025c YLR043c YGR209c YOL115w YDL165w YER111c YLR182w YGL181w YMR043w YHR206w YOL056w YOR028c YNL012w YOR361c YDR054c YDL064w YML115c	CDC16 CDC23 CDC26 CDC27  RSC6 RSC6 RSC8 RSC8 RSC8 RSC8 RSC8 RSC8 RSC8 RSC8	subunit of anaphase-promoting complex (cyclosome) subunit of the RSC complex subunit (fransecription suppressor of mil2 temperature lethality of tub2-150 suppressor of mil2 temperature-sensitive mutation synaptonemal complex protein TFIIF subunit (transcription initiation factor), cyclin C component thioredoxin I thioredoxin I thioredoxin I thioredoxin I thoredoxin I thoredoxin I thoredoxin I thoredoxin I transcription factor transcription factor transcription factor transcription factor of the Cast Ip/Glo3p/Sps18p family transcription factor of the MADS box family transcription factor, subunit of the MBF factor transcriptional activator transcriptional regulator involved in sporulation translation initiation factor eIF3 subunit U5 snRNP protein, pre-mRNA splicing factor ubiquitin-conjugating enzyme ubiquitin-conjugating enzyme ubiquitin-like protein vanadate resistance protein	YOR340c YNL248c YDR156w YOR224c YPR187w YBR154c YHR143w-a YOR210w YPR110c YNL113w YOR207c YOR116c YNL151c YNR003c YDL150w YPR190c YLR039c YLR039c YKL125w YML043c YLR141w YBL014c	RPA43 RPA49 RPA14 RPB8 RPO26 RPB5 RPC10 RPB10 RPC40 RPC19 RPC25 RPC31 RPC34 RPC34 RPC53 RPC82 RIC1 RRN3 RRN10 RRN11 RRN11 RRN5	DNA-directed RNA polymerase I, 190K α subunit DNA-directed RNA polymerase I, 36K subunit DNA-directed RNA polymerase I, 49K α subunit DNA-directed RNA polymerase I, 49K α subunit DNA-directed RNA polymerase I, A14 subunit DNA-directed RNA polymerase I, II, III 16K subunit DNA-directed RNA polymerase I, II, III 18K subunit DNA-directed RNA polymerase I, II, III 125K subunit DNA-directed RNA polymerase I, II, III 25K subunit DNA-directed RNA polymerase I, II, III 25K subunit DNA-directed RNA polymerase I, II, III 8.3K subunit DNA-directed RNA polymerase I, III, 16K subunit DNA-directed RNA polymerase III, 25K subunit DNA-directed RNA polymerase III, 31K subunit DNA-directed RNA polymerase III, 34K subunit DNA-directed RNA polymerase III, 34K subunit DNA-directed RNA polymerase III, 82K subunit	YNL216W YMR302c tRNA sy YGL019W YOR224c YPR187W YBR154c YHR143W-4 YOR210W YPR110C YNL113W YOR207c YNL1151c YNL151c YNL151c YNL151c YNL156W YPR190C YER148W YPR186C YGR246C YNL039W YGR047c YAL001c	RAP1 PRP12 (Inthesis CKB1 RPB8 RP026 RPB5 RPC10 RPB10 RPC40 RPC19 RPC128 RPC31 RPC34 RPC34 RPC34 RPC53 RPC25 RPC31 RPC63 RPC63 RPC63 RPC74 TFC2 BRF1 TFC6 TFC4 TFC3 TFC1	DNA-binding protein with repressor and activator activity involved in early maturation of pre-rRNA  S  casein kinase II, β subunit DNA-directed RNA polymerase I, II, III 16K subunit DNA-directed RNA polymerase I, II, III 18K subunit DNA-directed RNA polymerase I, II, III 25K subunit DNA-directed RNA polymerase I, II, III 7.7K subunit DNA-directed RNA polymerase I, II, III 7.7K subunit DNA-directed RNA polymerase I, II, III 8.3K subunit DNA-directed RNA polymerase I, III, 16K subunit DNA-directed RNA polymerase II, 16K subunit DNA-directed RNA polymerase III, 16K subunit DNA-directed RNA polymerase III, 16K subunit DNA-directed RNA polymerase III, 15K subunit DNA-directed RNA polymerase III, 25K subunit DNA-directed RNA polymerase III, 34K subunit DNA-directed RNA polymerase III, 34K subunit DNA-directed RNA polymerase III, 47K subunit DNA-directed RNA polymerase III, 82K subunit TFIID and TFIIIB subunit TFIIIB subunit, 70K TFIIIB subunit, 70K TFIIIB subunit (transcription initiation factor), 131K TFIIIC subunit (transcription initiation factor), 131K TFIIIC subunit (transcription initiation factor), 138K TFIIIC subunit (transcription initiation factor), 95K
YKL022c  YHR166c  YFR036w  YBL084c  YOR213c  YCR052w  YFR037c  YLR321c  YIL126w  YJR091c  YIL031w  YDR285w  YPL129w  YPR025c  YLR043c  YGR209c  YOL115w  YDL165w  YGL181w  YMR043w  YHR206w  YOL056w  YOR028c  YNL012w  YOR361c  YHR165c  YDR054c  YDR054c  YMR276w  YML115c  YMR276w  YML115c  YDR054c  YMR176c  YDR054c  YML115c  YDR054c  YML115c  YHR107iw  YER122c  YLR403w	CDC16  CDC23  CDC26  CDC27  RSC6 RSC8 SFH1 JSN1  SMT4  ZIP1 ANC1  CCL1  TRX1 TRX2 TRF4 CVM6 GTS1  MCM1  SKN7 MBP1  CIN5 SPO1 PRT1 PRP8  CDC34 UBC9 DSK2 VAN1  GLO3 SFP1	subunit of anaphase-promoting complex (cyclosome) subunit of the RSC complex suppresses the high-temperature lethality of tub2-150 suppressor of mif2 temperature-sensitive mutation synaptonemal complex protein TFIIF subunit (transcription initiation factor), 30K TFIIH subunit (transcription initiation factor), cyclin C component thioredoxin I thioredoxin I thoredoxin I thoredoxin I thoredoxin I thoredoxin factor transcription factor transcription factor transcription factor transcription factor the MADS box family transcription factor with similarity to Hsf1p transcriptional regulator involved in sporulation translation initiation factor eIR3 subunit U5 snRNP protein, pre-mRNA splicing factor ubiquitin-conjugating enzyme ubiquitin-conjugating enzyme ubiquitin-conjugating enzyme ubiquitin-like protein vanadate resistance protein vanadate resistance protein zinc-finger protein zinc-finger protein	YOR340c YNL248c YDR156W YOR224c YPR187W YBR154c YHR143W-a YOR210W YPR110c YNL113W YOR207c YOR116c YKL144c YNL151c YNR003c YDL150W YPR190c YLR039c YKL125W YBL025W YML043c YLR141W YBL014c YJL025W	RPA43 RPA49 RPA14 RPB8 RPO26 RPB5 RPC10 RPB10 RPC40 RPC19 RPC28 RPC31 RPC25 RPC31 RPC34 RPC53 RPC82 RIC1 RRN3 RRN10 RRN11 RRN5 RRN16	DNA-directed RNA polymerase I, 190K α subunit DNA-directed RNA polymerase I, 36K subunit DNA-directed RNA polymerase I, 49K α subunit DNA-directed RNA polymerase I, 49K α subunit DNA-directed RNA polymerase I, 11, 111 16K subunit DNA-directed RNA polymerase I, II, III 16K subunit DNA-directed RNA polymerase I, II, III 18K subunit DNA-directed RNA polymerase I, II, III 25K subunit DNA-directed RNA polymerase I, II, III 25K subunit DNA-directed RNA polymerase I, II, III 7.7K subunit DNA-directed RNA polymerase I, II, III 8.3K subunit DNA-directed RNA polymerase I, III, III 8.3K subunit DNA-directed RNA polymerase II, III, 16K subunit DNA-directed RNA polymerase III, 16K subunit DNA-directed RNA polymerase III, 16K subunit DNA-directed RNA polymerase III, 16NK subunit DNA-directed RNA polymerase III, 31K subunit DNA-directed RNA polymerase III, 34K subunit DNA-directed RNA polymerase III, 34K subunit DNA-directed RNA polymerase III, 34K subunit DNA-directed RNA polymerase III, 82K subunit DNA-directed RNA polymerase II specific transcription initiation factor RNA polymerase I specific transcription initiation factor	YNL216W YMR302c tRNA sy YGL019W YOR224c YPR187W YBR154c YHR143W-4 YOR210W YPR110c YNL113W YOR207c YOR116c YKL144c YNL151c YNR003c YDL150W YPR190c YER148W YPR186c YGR246c YNL039W YGR047c YAL001c YBR123c tRNA pi YIL075c	RAP1 PRP12 Inthesis CKB1 RPB8 RPO26 RPB5 RPC10 RPB10 RPC40 RPC19 RPC128 RPC31 RPC34 RPC34 RPC53 RPC34 RPC53 RPC34 RPC53 RPC34 RPC53 RPC34 RPC53 RPC34 RPC53 RPC63 RPC76 TFC2 BRF1 TFC6 TFC4 TFC5 TFC1 TFC9 SEN3	DNA-binding protein with repressor and activator activity involved in early maturation of pre-rRNA  S  casein kinase II, β subunit DNA-directed RNA polymerase I, II, III 16K subunit DNA-directed RNA polymerase I, II, III 18K subunit DNA-directed RNA polymerase I, II, III 25K subunit DNA-directed RNA polymerase I, II, III 77K subunit DNA-directed RNA polymerase I, II, III 77K subunit DNA-directed RNA polymerase I, II, III 8.3K subunit DNA-directed RNA polymerase I, III, 16K subunit DNA-directed RNA polymerase I, III, 16K subunit DNA-directed RNA polymerase III, 130K subunit DNA-directed RNA polymerase III, 150K subunit DNA-directed RNA polymerase III, 150K subunit DNA-directed RNA polymerase III, 25K subunit DNA-directed RNA polymerase III, 34K subunit DNA-directed RNA polymerase III, 34K subunit DNA-directed RNA polymerase III, 47K subunit DNA-directed RNA polymerase III, 82K subunit TFIID and TFIIIB subunit TFIID and TFIIIB subunit TFIIIB subunit (transcription initiation factor), 131K TFIIIC subunit (transcription initiation factor), 131K TFIIIC subunit (transcription initiation factor), 95K
YKL022c  YHR166c  YFR036w  YBL084c  YOR213c  YCR052w  YFR037c  YLR321c  YIL126w  YJR091c  YIL031w  YDR285w  YPL129w  YPR025c  YLR043c  YGR209c  YOL115w  YDL165w  YDL165w  YDL165w  YDL165w  YDL181w  YMR043w  YHR206w  YOR028c  YNL012w  YOR028c  YNL012w  YOR361c  YDR064c  YDR064c  YDR064c  YDR064c  YDR064c  YDR064c  YDR064c  YDR064c  YHR165c  HR071w  YER122c	CDC16 CDC23 CDC26 CDC27  RSC6 RSC8 RSC8 RSC8 RSC8 RSC9 RSC1 ITRA1 ITRX2 ITRX1 ITRX1 ITRX2 ITRX1 ITRX1 ITRX2 ITRX1	subunit of anaphase-promoting complex (cyclosome) subunit of the RSC complex subunit (fransecription suppresses the high-temperature lethality of tub2-150 suppressor of mi/2 temperature-sensitive mutation synaptonemal complex protein TFIIF subunit (transcription initiation factor), cyclin C component thioredoxin I thioredoxin I thioredoxin I thoredoxin I thoredoxin I thoredoxin I thoredoxin I thoredoxin I thoredoxin factor transcription factor transcription factor transcription factor transcription factor with similarity to Hsf1p transcription factor of the Gcs Ip/Glo3p/Sps18p family transcription factor with similarity to Hsf1p transcription factor with similarity to Hsf1p transcriptional regulator involved in sporulation resolution factor lef3 subunit U5 snRNP protein, pre-mRNA splicing factor ubiquitin-conjugating enzyme ubiquitin-conjugating enzyme ubiquitin-conjugating enzyme ubiquitin-like protein vanadate resistance protein veak similarity to cyclin G1 homolog HCS26 protein	YOR340c YNL248c YDR156W YOR224c YPR187W YBR154c YHR143W-a YOR210W YPR110c YNL113W YOR207c YOR116c YKL144c YNL151c YNR003c YDL150W YPR190c YLR039c YKL125W YBL025W YML043c YLR141W YBL014c YJL025W YMR270c	RPA43 RPA49 RPA14 RPB8 RPO26 RPB5 RPC10 RPB10 RPC40 RPC19 RPC128 RPO31 RPC25 RPC31 RPC34 RPC34 RPC63 RPC82 RIC1 RRN3 RRN10 RRN11 RRN5 RRN16 RRN7	DNA-directed RNA polymerase I, 190K α subunit DNA-directed RNA polymerase I, 36K subunit DNA-directed RNA polymerase I, 49K α subunit DNA-directed RNA polymerase I, 49K α subunit DNA-directed RNA polymerase I, II, III 16K subunit DNA-directed RNA polymerase I, II, III 16K subunit DNA-directed RNA polymerase I, II, III 18K subunit DNA-directed RNA polymerase I, II, III 25K subunit DNA-directed RNA polymerase I, II, III 25K subunit DNA-directed RNA polymerase I, II, III 77K subunit DNA-directed RNA polymerase I, II, III 8.3K subunit DNA-directed RNA polymerase I, III, 16K subunit DNA-directed RNA polymerase III, 25K subunit DNA-directed RNA polymerase III, 25K subunit DNA-directed RNA polymerase III, 31K subunit DNA-directed RNA polymerase III, 34K subunit DNA-directed RNA polymerase III, 34K subunit DNA-directed RNA polymerase III, 47K subunit DNA-directed RNA polymerase III, 82K subunit	YNL216W YMR302c tRNA sy YGL019W YOR224c YPR187W YBR164c YHR143W-4 YOR210W YPR110C YNL113W YOR207c YNL151c YNL151c YNL03C YNL150W YPR190C YER148W YPR186C YGR246C YNL039W YGR047c YAL001c YBR123C tRNA pt YIL075C YGL097W	RAP1 PRP12 (Inthesis CKB1 RPB8 RP026 RPB5 RPC10 RPB10 RPC128 RPC128 RPC31 RPC34 RPC34 RPC34 RPC34 RPC53 RPC82 SPT15 TFC2 BRF1 TFC5 TFC4 TFC3 TFC1 COCCSSIN	DNA-binding protein with repressor and activator activity involved in early maturation of pre-rRNA  S  casein kinase II, β subunit DNA-directed RNA polymerase I, II, III 16K subunit DNA-directed RNA polymerase I, II, III 18K subunit DNA-directed RNA polymerase I, II, III 25K subunit DNA-directed RNA polymerase I, II, III 25K subunit DNA-directed RNA polymerase I, II, III 7.7K subunit DNA-directed RNA polymerase I, II, III 8.3K subunit DNA-directed RNA polymerase I, III, 16K subunit DNA-directed RNA polymerase II, 16K subunit DNA-directed RNA polymerase III, 16K subunit DNA-directed RNA polymerase III, 16K subunit DNA-directed RNA polymerase III, 180K subunit DNA-directed RNA polymerase III, 180K subunit DNA-directed RNA polymerase III, 25K subunit DNA-directed RNA polymerase III, 31K subunit DNA-directed RNA polymerase III, 34K subunit DNA-directed RNA polymerase III, 47K subunit DNA-directed RNA polymerase III, 82K subunit TFIID and TFIIIB subunit TFIIIB subunit (transcription initiation factor) TFIIIB subunit (transcription initiation factor), 131K TFIIIC subunit (transcription initiation factor), 138K TFIIIC subunit (transcription initiation factor), 138K TFIIIC subunit (transcription initiation factor), 95K  ng  26S proteasome regulatory subunit GDP/GTP exchange factor for Gap1p/Gsp2p
YKL022c YHR166c YFR036w YBL084c YOR213c YOR052w YFR037c YLL321c YIL126w YJR091c YIL031w YDR285w YPL129w YPR025c YLR043c YGR209c YOL115w YDL165w YER111c YLR182w YGL181w YMR043w YHR206w YOR028c YNL012w YOR056c YDR056c YDR056c YDR056c YDR066c YRR0110c YR	CDC16  CDC23  CDC26  CDC27  RSC6 RSC8 SFH1 JSN1  SMT4  ZIP1 ANC1  CCL1  TRX1 TRX2 TRF4 CVM6 GTS1  MCM1  SKN7 MBP1  CIN5 SPO1 PRT1 PRP8  CDC34 UBC9 DSK2 VAN1  GLO3 SFP1	subunit of anaphase-promoting complex (cyclosome) subunit of the RSC complex suppresses the high-temperature lethality of tub2-150 suppressor of mif2 temperature-sensitive mutation synaptonemal complex protein TFIIF subunit (transcription initiation factor), 30K TFIIH subunit (transcription initiation factor), cyclin C component thioredoxin I thioredoxin I thoredoxin I thoredoxin I thoredoxin I thoredoxin factor transcription factor transcription factor transcription factor transcription factor the MADS box family transcription factor with similarity to Hsf1p transcriptional regulator involved in sporulation translation initiation factor eIR3 subunit U5 snRNP protein, pre-mRNA splicing factor ubiquitin-conjugating enzyme ubiquitin-conjugating enzyme ubiquitin-conjugating enzyme ubiquitin-like protein vanadate resistance protein vanadate resistance protein zinc-finger protein zinc-finger protein	YOR340c YNL248c YDR156W YOR224c YPR187W YBR154c YHR143W-a YOR210W YPR110c YNL113W YOR207c YOR116c YKL144c YNL151c YNR003c YDL150W YPR190c YLR039c YKL125W YBL025W YML043c YLR141W YBL014c YJL025W YMR270c	RPA43 RPA49 RPA14 RPB8 RPO26 RPB5 RPC10 RPC40 RPC40 RPC25 RPC31 RPC25 RPC31 RPC82 RIC1 RRN3 RRN10 RRN11 RRN5 RRN16 RRN7 RRN9	DNA-directed RNA polymerase I, 190K α subunit DNA-directed RNA polymerase I, 36K subunit DNA-directed RNA polymerase I, 49K α subunit DNA-directed RNA polymerase I, 49K α subunit DNA-directed RNA polymerase I, A14 subunit DNA-directed RNA polymerase I, II, III 16K subunit DNA-directed RNA polymerase I, II, III 18K subunit DNA-directed RNA polymerase I, II, III 125K subunit DNA-directed RNA polymerase I, II, III 25K subunit DNA-directed RNA polymerase I, II, III 25K subunit DNA-directed RNA polymerase I, II, III 8.3K subunit DNA-directed RNA polymerase I, III, III 8.3K subunit DNA-directed RNA polymerase II, III 6K subunit DNA-directed RNA polymerase III, 16K subunit DNA-directed RNA polymerase III, 16K subunit DNA-directed RNA polymerase III, 16K subunit DNA-directed RNA polymerase III, 18K subunit DNA-directed RNA polymerase III, 31K subunit DNA-directed RNA polymerase III, 31K subunit DNA-directed RNA polymerase III, 34K subunit DNA-directed RNA polymerase III, 82K subunit	YNL216W YMR302c tRNA sy YGL019W YOR224c YPR187W YBR154c YHR143W-4 YOR210W YPR110c YNL113W YOR207c YOR116c YKL144c YNL151c YNR003c YDL150W YPR190c YER148W YPR186c YGR246c YNL039W YGR047c YAL001c YBR123c tRNA pi YIL075c	RAP1 PRP12 (Inthesis CKB1 RPB8 RP026 RPB5 RPC10 RPB10 RPC128 RPC128 RPC31 RPC34 RPC34 RPC34 RPC34 RPC53 RPC82 SPT15 TFC2 BRF1 TFC5 TFC4 TFC3 TFC1 COCCSSIN	DNA-binding protein with repressor and activator activity involved in early maturation of pre-rRNA  S  casein kinase II, β subunit DNA-directed RNA polymerase I, II, III 16K subunit DNA-directed RNA polymerase I, II, III 18K subunit DNA-directed RNA polymerase I, II, III 25K subunit DNA-directed RNA polymerase I, II, III 25K subunit DNA-directed RNA polymerase I, II, III 27K subunit DNA-directed RNA polymerase I, II, III 8.3K subunit DNA-directed RNA polymerase I, III, 16K subunit DNA-directed RNA polymerase I, III, 16K subunit DNA-directed RNA polymerase III, 31K subunit DNA-directed RNA polymerase III, 31K subunit DNA-directed RNA polymerase III, 34K subunit DNA-directed RNA polymerase III, 34K subunit DNA-directed RNA polymerase III, 82K subunit TFIID and TFIIIB subunit TFIIIC subunit (transcription initiation factor), 131K TFIIIC subunit (transcription initiation factor), 138K TFIIIC subunit (transcription initiation factor), 138K TFIIIC subunit (transcription initiation factor), 138K TFIIIC subunit (transcription initiation factor), 95K

YHR006w		involved in pre-tRNA splicing	YIL021w	RPB3	DNA-directed RNA-polymerase II, 45K	YOR047c	STD1	dosage-dependent modulator of glucose
YLR375w	STP3	involved in pre-tRNA splicing and in uptake of branched-chain amino acids	YIL128W	MMS19	involved in repair and RNA polymerase transcription	YER159c	NCB1	repression functional homologue of human NC2α
YDL048c	STP4	involved in pre-tRNA splicing and in uptake of branched-chain amino acids	YMR228w	MIF1	RNA polymerase specific factor, mitochondrial	YDR397c	YNC2β	functional homologue of human NC2B/Dr1
YCL017c	NFS1	involved in tRNA processing and mitochondrial metabolsim	YPR056w		similarity to human transcription factor BTF2/TFIIH subunit p34	YPL037c YJL110c	EGD1 GZF3	GAL4 DNA-binding enhancer protein GATA zinc-finger protein 3
YNR034w YCR073w-a		multicopy suppressor of los1-1 multicopy suppressor of los1-1	YPL046c		strong similarity to human DNA-directed RNA polymerase II elongation factor SIII,	YIL038c	NOT3	general negative regulator of transcription, subunit 3
YMR047c YGL092w	NUP116	nuclear pore protein	YDR045c		p15 strong similarity to <i>S. acidocaldarius</i>	YBR112c YCR084c	CYC8 TUP1	general repressor of transcription
YJR042w	NUP85	nuclear pore protein nuclear pore protein			transcription elongation factor tfs	YDR176w	NGG1	general transcription repressor general transcriptional adaptor or co-
YLR430w		positive effector of tRNA-splicing endonuclease	YKL058w	TOA2	TFIIA subunit (transcription initiation factor), 13.5K	YBR045c	GIP1	activator Glc7p-interacting protein
YAL043c YKL205w	PTA1 LOS1	pre-tRNA processing protein pre-tRNA splicing protein	YOR194c	TOA1	TFIIA subunit (transcription initiation factor), 32K	YNL236w YHL025w	SIN4 SNF6	global regulator protein global transcription activator
YDR463w YNL221c	STP1 POP1	pre-tRNA splicing protein protein component of ribonuclease P and	YPR086w	SUA7	TFIIB subunit (transcription initiation factor), factor E	YER027c YNL199c	GAL83 GCR2	glucose repression protein glycolytic genes transcriptional activator
YML091c		ribonuclease MRP	YER148w YGR274c	SPT15 TAF145	TFIID and TFIIIB subunit TFIID subunit (TBP-associated factor),	YGL073w YPR065w	HSF1 ROX1	heat shock transcription factor
YFR004w	MPR1	ribonuclease P, mitochondrial strong similarity to S. pombe pad1 protein			145K			heme-dependent transcriptional repressor of hypoxic genes
YGR248w YJL087c	TRL1	strong similarity to Sol3p tRNA ligase	YMR236w YML098w	TAF19	TFIID subunit (TBP-associated factor), 17K TFIID subunit (TBP-associated factor), 19K	YDR006c	SOK1	high copy suppressor of a cyclic AMP- dependent protein kinase mutant
YLR105c YHR163w	SEN2 SOL3	tRNA splicing endonuclease β subunit weak multicopy suppressor of <i>los1-1</i>	YDR167w YML015c	TAF23 TAF40	TFIID subunit (TBP-associated factor), 23K TFIID subunit (TBP-associated factor), 40K	YMR070w	HMS1	high-copy suppressor of mot1 spt3 synthetic lethality
tRNA m	odificat	tion	YGL112c YDR145w	TAF60 TAF61	TFIID subunit (TBP-associated factor), 60K TFIID subunit (TBP-associated factor), 61K	YGR252w YDR225w	GCN5 HTA1	histone acetyltransferase histone H2A
YGR204w		C1-tetrahydrofolate synthase, cytoplasmic	YMR227c YBR198c	TAF67 TAF90	TFIID subunit (TBP-associated factor), 67K TFIID subunit (TBP-associated factor), 90K	YBL003c YDR224c	HTA2 HTB1	histone H2A.2 histone H2B
YMR283c	RIT1	initiator tRNA phosphoribosyl-transferase	YKR062w	TFA2	TFIIE subunit (transcription initiation	YBL002w	HTB2	histone H2B.2
YDR120c	TRM1	N2,N2-dimethylguanine tRNA methyltransferase	YKL028w	TFA1	factor), 43K TFIIE subunit (transcription initiation	YBR010w YNL031c	HHT1 HHT2	histone H3 histone H3
YGL105w	G4P1	protein with specific affinity for G4 quadruplex nucleic acids	YGR186w	TFG1	factor), 66K TFIIF subunit (transcription initiation	YBR009c YNL030w	HHF1 HHF2	histone H4 histone H4
YPL212c YGL063w	PUS1 PUS2	pseudouridine synthase 1 pseudouridine synthase 2	YPL129w	ANC1	factor), 105K TFIIF subunit (transcription initiation	YBL008w YOR038c	HIR1 HIR2	histone transcription regulator histone transcription regulator
YFR010w		similarity to <i>C. elegans</i> tRNA-guanine transglycosylase	YGR005c	TFG2	factor), 30K TFIIF subunit (transcription initiation	YER161c YDL106c	SPT2 GRF10	HMG-like chromatin protein homeodomain protein
YBL013w		similarity to methionyl-tRNA	YDR311w	TFB1	factor), 54K TFIIH subunit (transcription initiation	YDR138w	HPR1	hyperrecombination protein related to
YOR274w	MOD5	formyltransferase tRNA isopentenyltransferase			factor), 75K	YJL089w	SIP4	Top1p interacts with SNF1 protein kinase
YER168c	CCA1	tRNA nucleotidyltransferase	YPR025c	CCL1	TFIIH subunit (transcription initiation factor), cyclin C component	YKL032c	IXR1	intrastrand crosslink recognition protein and transcription factor
other th	RNA-tra	nscription activities	YLR005w	SSL1	TFIIH subunit (transcription initiation factor), factor B	YBR081c	SPT7	involved in alteration of transcription start site selection
YOR061w YOR039w		casein kinase II α' subunit casein kinase II β' subunit	YPL122c YDR460w	TFB2 TFB3	TFIIH subunit (transcription/repair factor) TFIIH subunit (transcription/repair factor)	YKR072c	SIS2	involved in cell cycle-specific gene expression
YJL041w	NSP1	nuclear pore protein	YGL043w YGR063c	DST1 SPT4	TFIIS (transcription elongation factor) transcription initiation protein	YNL251c	NRD1	involved in regulation of nuclear pre- mRNA abundance
mRNA s	ynthes	is	YML010w	SPT5	transcription initiation protein	YIL046w	MET30	involved in regulation of sulphur
		on activities	YGR116w		transcription initiation protein	YDL153c	SAS10	assimilation genes involved in silencing
YDL108w YIL143c	SSL2	cyclin-dependent ser/thr protein kinase DNA helicase	transcripti YOR259c	CRL13	26S proteasome subunit	YMR127c YGR097w	SAS2 ASK10	involved in silencing at HMR involved in Skn7p-dependent transcription
YER171w YOR224c	RAD3 RPB8	DNA helicase/ATPase DNA-directed RNA polymerase I, II, III 16K	YJL115w YDL197c	ASF1 ASF2	anti-silencing protein anti-silencing protein	YLR039c	RIC1	involved in transcription of ribosomal proteins and ribosomal RNA
YPR187w	RPO26	subunit DNA-directed RNA polymerase I, II, III 18K	YDR173c YKL112w	ARG82 ABF1	arginine metabolism transcription factor ARS-binding factor	YGL071w YJR060w	RCS1 CBF1	iron-regulated transcriptional repressor kinetochore protein
YBR154c	RPB5	subunit DNA-directed RNA polymerase I, II, III 25K	YDR123c	INO2	basic helix-loop-helix (BHLH) transcription factor	YDR159w YGR100w	SAC3 MIC1	leucine permease transcriptional regulator Mac1p interacting protein
		subunit	YOL108c	INO4	basic helix-loop-helix transcription factor	YBR297w	MAL33	maltose fermentation regulatory protein
YHR143w-a		DNA-directed RNA polymerase I, II, III 7.7K subunit	YOL067c YOR344c	RTG1 TYE7	basic helix-loop-helix transcription factor basic helix-loop-helix transcription factor	YGR288w YCR040w	MAL13 MATα1	maltose pathway regulatory protein mating type regulatory protein (expressed
YOR210w		DNA-directed RNA polymerase I, II, III 8.3K subunit	YBL103c YHL009c	RTG3	bHLH/zip transcription factor bZip DNA binding protein	YCR039c	ΜΑΤα2	copy at MAT locus) mating type regulatory protein (expressed
YOL051w	GAL11	DNA-directed RNA polymerase II holoenzyme and Kornberg's mediator	YGL209w YKL190w	MIG2 CNB1	C2H2 zinc-finger protein calcineurin B, regulatory subunit	YCL067c	α2	copy at MAT locus) mating type regulatory protein (silenced
YDR443c	SCA1	(SRB) subcomplex subunit DNA-directed RNA polymerase II	YML112w	CTK3	carboxy terminal domain (CTD) kinase, γ subunit	YHL027w	RIM101	copy at HML locus) meiotic regulatory protein
15111100	00, 11	holoenzyme and Kornberg's mediator (SRB) subcomplex subunit	YJL006c	CTK2	carboxy-terminal domain (CTD) kinase , β subunit	YLR216c YJR032w	CPR6 CPR7	member of the cyclophilin family member of the cyclophilin family
YHR041c	SRB2	DNA-directed RNA polymerase II	YKL139w	CTK1	carboxy-terminal domain (CTD) kinase,	YLR136c	TIS11	member of the inducible ccch zinc-finger
		holoenzyme and Kornberg's mediator (SRB) subcomplex subunit	YIL035c	CKA1	α subunit casein kinase II, catalytic α subunit	YOL148c	SPT20	family member of the TBP class of SPT proteins
YER022w	SRB4	DNA-directed RNA polymerase II holoenzyme and Kornberg's mediator	YGL237c YBL021c	HAP2 HAP3	CCAAT-binding factor subunit CCAAT-binding factor subunit	YMR021c	MAC1	that alter transcription site selection metal binding activator
YGR104c	SRB5	(SRB) subcomplex subunit DNA-directed RNA polymerase II	YKL109w YOR358w	HAP4 HAP5	CCAAT-binding factor subunit CCAAT-binding factor subunit	YLR131c YBR026c	ACE2 (MRF1)	metallothionein expression activator mitochondrial respiratory function protein
		holoenzyme and Kornberg's mediator (SRB) subcomplex subunit	YJR122w YKR036c	CAF17 CAF4	CCR4-associated factor CCR4-associated factor	YML051w	GAL80	negative regulator for expression of galactose-induced genes
				HPC2	cell-cycle regulatory protein	YGL151w	NUT1	negative regulator of HO endonuclease
YDR308c	SRB7	DNA-directed RNA polymerase II	YBR215w YDL220c	CDC13	cell division control protein	YPR168w	NI IT2	negative regulator of HO endonuclease
		holoenzyme and Kornberg's mediator (SRB) subcomplex subunit	YDL220c YDR073w	CDC13 SNF11	cell division control protein component of SWI/SNF transcription	YPR168w YKL185w	NUT2 ASH1	negative regulator of HO endonuclease negative regulator of HO expression
YDR308c YCR081w	SRB7 SRB8	holoenzyme and Kornberg's mediator (SRB) subcomplex subunit DNA-directed RNA polymerase II holoenzyme and Kornberg's mediator	YDL220c	CDC13 SNF11 SNF12	component of SWI/SNF transcription activator complex component of SWI/SNF transcription	YKL185w YHL020c	ASH1 OPI1	negative regulator of HO expression negative regulator of phospholipid biosynthesis pathway
		holoenzyme and Kornberg's mediator (SRB) subcomplex subunit DNA-directed RNA polymerase II holoenzyme and Kornberg's mediator (SRB) subcomplex subunit DNA-directed RNA polymerase II	YDL220c YDR073w	SNF11	component of SWI/SNF transcription activator complex component of SWI/SNF transcription activator complex component of SWI/SNF transcription	YKL185w YHL020c YDR464w	ASH1 OPI1 SPP41	negative regulator of HO expression negative regulator of phospholipid biosynthesis pathway negative regulator of PRP3 and PRP4 gene expression
YCR081w	SRB8	holoenzyme and Kornberg's mediator (SRB) subcomplex subunit DNA-directed RNA polymerase II holoenzyme and Kornberg's mediator (SRB) subcomplex subunit	YDL220c YDR073w YNR023w	SNF11 SNF12	component of SWI/SNF transcription activator complex component of SWI/SNF transcription activator complex	YKL185w YHL020c YDR464w YNL076w YDR207c	ASH1 OPI1	negative regulator of HO expression negative regulator of phospholipid biosynthesis pathway negative regulator of PRP3 and PRP4
YCR081w	SRB8	holoenzyme and Kornberg's mediator (SRB) subcomplex subunit DNA-directed RNA polymerase II holoenzyme and Kornberg's mediator (SRB) subcomplex subunit DNA-directed RNA polymerase II holoenzyme and Kornberg's mediator	YDL220c YDR073w YNR023w YOR290c	SNF11 SNF12 SNF2	component of SWI/SNF transcription activator complex	YKL185w YHL020c YDR464w YNL076w	ASH1 OPI1 SPP41 MKS1	negative regulator of HO expression negative regulator of phospholipid biosynthesis pathway negative regulator of PRP3 and PRP4 gene expression negative regulator of RAS-cAMP pathway
YCR081w YNL025c YLR071c	SRB8 SSN8 RGR1	holoenzyme and Kornberg's mediator (SRB) subcomplex subunit DNA-directed RNA polymerase II holoenzyme and Kornberg's mediator (SRB) subcomplex subunit DNA-directed RNA polymerase II holoenzyme and Kornberg's mediator (SRB) subcomplex subunit, cyclin C homologue DNA-directed RNA polymerase II holoenzyme subunit	YDL220c YDR073w YNR023w YOR290c YBR289w YPL016w	SNF11 SNF12 SNF2 SNF5 SWI1	component of SWI/SNF transcription activator complex	YKL185w YHL020c YDR464w YNL076w YDR207c YGL221c YGL115w YCR093w	ASH1 OPI1 SPP41 MKS1 UME6 NIF3 SNF4 CDC39	negative regulator of HO expression negative regulator of phospholipid biosynthesis pathway negative regulator of PRP3 and PRP4 gene expression negative regulator of RAS-cAMP pathway negative transcriptional regulator Ngg1p-interacting factor 3 nuclear regulatory protein nuclear transmembrane protein
YCR081w YNL025c YLR071c YBR253w	SRB8 SSN8 RGR1 SRB6	holoenzyme and Kornberg's mediator (SRB) subcomplex subunit DNA-directed RNA polymerase II holoenzyme and Kornberg's mediator (SRB) subcomplex subunit DNA-directed RNA polymerase II holoenzyme and Kornberg's mediator (SRB) subcomplex subunit, cyclin C homologue DNA-directed RNA polymerase II holoenzyme subunit DNA-directed RNA polymerase II holoenzyme subunit DNA-directed RNA polymerase II suppressor protein	YDL220c YDR073w YNR023w YOR290c YBR289w YPL016w YCR042c YPL177c	SNF11 SNF12 SNF2 SNF5 SWI1 TSM1 CUP9	component of SWI/SNF transcription activator complex component of TAF(II) complex copper homeostasis protein	YKL185W YHL020c YDR464W YNL076W YDR207c YGL221c YGL115W YCR093W YML065W YNL261W	ASH1 OPI1 SPP41 MKS1 UME6 NIF3 SNF4 CDC39 ORC1 ORC5	negative regulator of HO expression negative regulator of phospholipid biosynthesis pathway negative regulator of PRP3 and PRP4 gene expression negative regulator of RAS-cAMP pathway negative transcriptional regulator Ngg1p-interacting factor 3 nuclear regulatory protein nuclear transmembrane protein origin recognition complex, 104K subunit origin recognition complex, 50K subunit
YCR081w YNL025c YLR071c YBR253w YOL005c	SRB8 SSN8 RGR1 SRB6 RPB11	holoenzyme and Kornberg's mediator (SRB) subcomplex subunit DNA-directed RNA polymerase II holoenzyme and Kornberg's mediator (SRB) subcomplex subunit DNA-directed RNA polymerase II holoenzyme and Kornberg's mediator (SRB) subcomplex subunit, cyclin C homologue DNA-directed RNA polymerase II holoenzyme subunit DNA-directed RNA polymerase II suppressor protein DNA-directed RNA polymerase II, 13.6K subunit	YDL220c YDR073w YNR023w YOR290c YBR289w YPL016w YCR042c YPL177c YGL166w YNL167c	SNF11 SNF12 SNF2 SNF5 SWI1 TSM1 CUP9 CUP2 SKO1	component of SWI/SNF transcription activator complex component of TAF(II) complex copper homeostasis protein copper-dependent transcription factor cre-binding bzip protein	YKL185W YHL020c YDR464W YNL076W YDR207c YGL21c YGL115W YCR093W YML065W YNL261W YHR118c YPR162c	ASH1 OPI1 SPP41 MKS1 UME6 NIF3 SNF4 CDC39 ORC1 ORC5 ORC6 ORC6	negative regulator of HO expression negative regulator of phospholipid biosynthesis pathway negative regulator of PRP3 and PRP4 gene expression negative regulator of RAS-cAMP pathway negative regulator of RAS-cAMP pathway negative transcriptional regulator Ngg 1p-interacting factor 3 nuclear regulatory protein nuclear transmembrane protein origin recognition complex, 50K subunit origin recognition complex, 50K subunit origin recognition complex, 50K subunit origin recognition complex, 56K subunit
YCR081w YNL025c YLR071c YBR253w YOL005c YGL070c	SRB8 SSN8 RGR1 SRB6 RPB11 RPB9	holoenzyme and Kornberg's mediator (SRB) subcomplex subunit DNA-directed RNA polymerase II holoenzyme and Kornberg's mediator (SRB) subcomplex subunit DNA-directed RNA polymerase II holoenzyme and Kornberg's mediator (SRB) subcomplex subunit, cyclin C homologue DNA-directed RNA polymerase II holoenzyme subunit DNA-directed RNA polymerase II suppressor protein DNA-directed RNA polymerase II, 13.6K subunit DNA-directed RNA polymerase II, 14.2K subunit	YDL220c YDR073w YNR023w YOR290c YBR289w YPL016w YCR042c YPL177c YGL166w YNL167c YPL042c YLR176c	SNF11 SNF12 SNF2 SNF5 SWI1 TSM1 CUP9 CUP9 CUP9 SSN3 RFX1	component of SWI/SNF transcription activator complex component of TAF(II) complex component of TAF(III) complex copper-dependent transcription factor cre-binding bzip protein cyclin-dependent ser/thr protein kinase DNA binding protein	YKL185W YHL020c YDR464W YNL076W YDR207c YGL221c YGL115W YCR093W YML065W YNL261W YHR118c YPR162c YLL004W YBR060c	ASH1 OPI1 SPP41 MKS1 UME6 NIF3 SNF4 CDC39 ORC1 ORC5 ORC6 ORC4 ORC3 RRR1	negative regulator of HO expression negative regulator of phospholipid biosynthesis pathway negative regulator of PRP3 and PRP4 gene expression negative regulator of RAS-cAMP pathway negative transcriptional regulator Ngg1p-interacting factor 3 nuclear regulatory protein nuclear transmembrane protein origin recognition complex, 104K subunit origin recognition complex, 50K subunit origin recognition complex, 56K subunit origin recognition complex, 68K subunit origin recognition complex, 68K subunit origin recognition complex, 68K subunit origin recognition complex, 72K subunit origin recognition complex, 72K subunit
YCR081w YNL025c YLR071c YBR253w YOL005c YGL070c YOR151c	SRB8 SSN8 RGR1 SRB6 RPB11 RPB9 RPB2	holoenzyme and Kornberg's mediator (SRB) subcomplex subunit DNA-directed RNA polymerase II holoenzyme and Kornberg's mediator (SRB) subcomplex subunit DNA-directed RNA polymerase II holoenzyme and Kornberg's mediator (SRB) subcomplex subunit, cyclin C homologue DNA-directed RNA polymerase II holoenzyme subunit DNA-directed RNA polymerase II suppressor protein DNA-directed RNA polymerase II, 13.6K subunit DNA-directed RNA polymerase II, 13.6K subunit DNA-directed RNA polymerase II, 14.2K	YDL220c YDR073w YNR023w YOR290c YBR289w YPL016w YCR042c YPL177c YGL166w YNL167c YPL042c	SNF11 SNF12 SNF2 SNF5 SWI1 TSM1 CUP9 CUP2 SK01 SSN3	component of SWI/SNF transcription activator complex component of TAF(II) complex copper homeostasis protein copper-dependent transcription factor cre-binding bzip protein cyclin-dependent ser/thr protein kinase	YKL185W YHL020c YDR464W YNL076W YDR207c YGL21c YGL115W YCR093W YML065W YNL261W YHR118c YPR162c YLL004W YBR060c YAL051W	ASH1 OPI1 SPP41 MKS1 UME6 NIF3 SNF4 CDC39 ORC1 ORC5 ORC6 ORC4 ORC3 RRR1 OAF1	negative regulator of HO expression negative regulator of phospholipid biosynthesis pathway negative regulator of PRP3 and PRP4 gene expression negative regulator of RAS-cAMP pathway negative regulator of RAS-cAMP pathway negative transcriptional regulator Ngg1p-interacting factor 3 nuclear regulatory protein nuclear transmembrane protein origin recognition complex, 104K subunit origin recognition complex, 50K subunit origin recognition complex, 50K subunit origin recognition complex, 56K subunit
YCR081w YNL025c YLR071c YBR253w YOL005c YGL070c	SRB8 SSN8 RGR1 SRB6 RPB11 RPB9	holoenzyme and Komberg's mediator (SRB) subcomplex subunit DNA-directed RNA polymerase II holoenzyme and Kornberg's mediator (SRB) subcomplex subunit DNA-directed RNA polymerase II holoenzyme and Kornberg's mediator (SRB) subcomplex subunit, cyclin C homologue DNA-directed RNA polymerase II holoenzyme subunit DNA-directed RNA polymerase II suppressor protein DNA-directed RNA polymerase II, 13.6K subunit DNA-directed RNA polymerase II, 14.2K subunit DNA-directed RNA polymerase II, 14.2K subunit	YDL220c YDR073w YNR023w YOR290c YBR289w YPL016w YCR042c YPL177c YGL166w YNL167c YPL042c YDR217c YNL042c YNR176c YDR217c YNL216w	SNF11 SNF12 SNF2 SNF5 SWI1 TSM1 CUP9 CUP2 SKO1 SSN3 REX1 RAD9 RAP1	component of SWI/SNF transcription activator complex component of TAF(II) complex component of TAF(II) complex copper homeostasis protein copper-dependent transcription factor cre-binding bzip protein cyclin-dependent ser/thr protein kinase DNA binding protein DNA repair checkpoint protein DNA repair checkpoint protein DNA-binding protein with repressor and activator activity	YKL185W YHL020c YDR464W YNL076W YDR207c YGL221c YGL115W YCR093W YML065W YNL261W YHR118c YPR162c YLL004W YBR060c	ASH1 OPI1 SPP41 MKS1 UME6 NIF3 SNF4 CDC39 ORC1 ORC5 ORC6 ORC4 ORC3 RRR1	negative regulator of HO expression negative regulator of phospholipid biosynthesis pathway negative regulator of PRP3 and PRP4 gene expression negative regulator of RAS-cAMP pathway negative regulator of RAS-cAMP pathway negative transcriptional regulator Ngg1p-interacting factor 3 nuclear regulatory protein nuclear regulatory protein nuclear transmembrane protein origin recognition complex, 50K subunit origin recognition complex, 50K subunit origin recognition complex, 56K subunit origin recognition complex, 62K subunit origin recognition complex, 72K subunit origin recognition complex, 72K subunit peroxisome proliferating transcription
YCR081w YNL025c YLR071c YBR253w YOL005c YGL070c YOR151c	SRB8 SSN8 RGR1 SRB6 RPB11 RPB9 RPB2	holoenzyme and Kornberg's mediator (SRB) subcomplex subunit DNA-directed RNA polymerase II holoenzyme and Kornberg's mediator (SRB) subcomplex subunit DNA-directed RNA polymerase II holoenzyme and Kornberg's mediator (SRB) subcomplex subunit, cyclin C homologue DNA-directed RNA polymerase II holoenzyme subunit DNA-directed RNA polymerase II suppressor protein DNA-directed RNA polymerase II, 13.6K subunit DNA-directed RNA polymerase II, 14.2K subunit DNA-directed RNA polymerase II, 140K subunit DNA-directed RNA polymerase II, 140K subunit DNA-directed RNA polymerase II, 18K subunit DNA-directed RNA polymerase II, 19K subunit DNA-directed RNA polymerase II, 19K subunit DNA-directed RNA polymerase II, 215K	YDL220c YDR073W YNR023W YOR290c YBR289W YPL016W YCR042c YPL177c YGL166W YNL167c YPL042c YLR176c YDR217c YNL216W YLR418c	SNF11 SNF12 SNF2 SNF5 SWI1 TSM1 CUP9 CUP9 SKO1 SSN3 RFX1 RAD9 RAP1 CDC73	component of SWI/SNF transcription activator complex component of TAF(II) complex component of TAF(II) complex component of TAF(II) complex copper homeostasis protein copper-dependent transcription factor cre-binding bzip protein copper-dependent ser/thr protein kinase DNA binding protein DNA repair checkpoint protein DNA-binding protein with repressor and activator activity DNA-directed RNA polymerase II accessory protein	YKL185W YHL020c YDR464W YNL076W YDR207c YGL21c YGL115W YCR093W YML065W YNL261W YHR118c YPR162c YLL004W YBR060c YAL051W	ASH1 OPI1 SPP41 MKS1 UME6 NIF3 SNF4 CDC39 ORC1 ORC5 ORC6 ORC4 ORC3 RRR1 OAF1	negative regulator of HO expression negative regulator of phospholipid biosynthesis pathway negative regulator of PRP3 and PRP4 gene expression negative regulator of RAS-cAMP pathway negative regulator of RAS-cAMP pathway negative transcriptional regulator Ngg1p-interacting factor 3 nuclear regulatory protein nuclear transmembrane protein origin recognition complex, 104K subunit origin recognition complex, 50K subunit origin recognition complex, 50K subunit origin recognition complex, 56K subunit origin recognition complex, 50K subunit origin recognition compl
YCR081w YNL025c YLR071c YBR253w YOL005c YGL070c YOR151c YDR404c	SRB8 SSN8 RGR1 SRB6 RPB11 RPB9 RPB2 RPB7	holoenzyme and Kornberg's mediator (SRB) subcomplex subunit DNA-directed RNA polymerase II holoenzyme and Kornberg's mediator (SRB) subcomplex subunit DNA-directed RNA polymerase II holoenzyme and Kornberg's mediator (SRB) subcomplex subunit, cyclin C homologue DNA-directed RNA polymerase II holoenzyme subunit DNA-directed RNA polymerase II suppressor protein DNA-directed RNA polymerase II, 13.6K subunit DNA-directed RNA polymerase II, 14.2K subunit DNA-directed RNA polymerase II, 140K subunit DNA-directed RNA polymerase II, 19K subunit DNA-directed RNA polymerase II, 19K subunit DNA-directed RNA polymerase II, 19K subunit DNA-directed RNA polymerase II, 215K subunit DNA-directed RNA polymerase II, 215K subunit DNA-directed RNA polymerase II, 32K	YDL220c YDR073w YNR023w YOR290c YBR289w YPL016w YCR042c YPL177c YGL166w YNL167c YPL042c VLR176c YDR217c YNL216w YLR216w YLR216w YLR216w YLR216w YLR216w YLR216w YLR216w YLR216w YLR216w YLR216w YLR216w YLR216w YLR216w YLR216w	SNF11  SNF12  SNF2  SNF5  SWI1  TSM1  CUP9  CUP2  SKO1  SSN3  REX1  RAD9  RAP1  CDC73  PAF1	component of SWI/SNF transcription activator complex component of TAF(II) complex copper homeostasis protein copper-dependent transcription factor cre-binding bzip protein cyclin-dependent ser/thr protein kinase DNA binding protein bNA repair checkpoint protein DNA-binding protein with repressor and activator activity DNA-directed RNA polymerase II accessory protein DNA-directed RNA polymerase II regulator	YKL185w YHL020c YDR464w YNL076w YDR207c YGL211c YGL115w YCR093w YML065w YML066tw YHL261w YHR118c YPR162c YLL004w YBR060c YAL051w YOR363c	ASH1 OPI1 SPP41 MKS1 UME6 NIF3 SNF4 CDC39 ORC1 ORC5 ORC4 ORC3 RRR1 OAF1	negative regulator of HO expression negative regulator of phospholipid biosynthesis pathway negative regulator of PRP3 and PRP4 gene expression negative regulator of RAS-cAMP pathway negative regulator of RAS-cAMP pathway negative transcriptional regulator Ngg1p-interacting factor 3 nuclear regulatory protein nuclear transmembrane protein origin recognition complex, 50K subunit origin recognition complex, 50K subunit origin recognition complex, 62K subunit origin recognition recognition complex, 62K subunit origin recogn
YCR081w YNL025c YLR071c YBR253w YOL005c YGL070c YOR151c YDR404c YDL140c	SRB8 SSN8 RGR1 SRB6 RPB11 RPB9 RPB2 RPB7 RPO21	holoenzyme and Kornberg's mediator (SRB) subcomplex subunit DNA-directed RNA polymerase II holoenzyme and Kornberg's mediator (SRB) subcomplex subunit DNA-directed RNA polymerase II holoenzyme and Kornberg's mediator (SRB) subcomplex subunit, cyclin C homologue DNA-directed RNA polymerase II holoenzyme subunit DNA-directed RNA polymerase II suppressor protein DNA-directed RNA polymerase II, 13.6K subunit DNA-directed RNA polymerase II, 14.2K subunit DNA-directed RNA polymerase II, 140K subunit DNA-directed RNA polymerase II, 19K subunit DNA-directed RNA polymerase II, 19K subunit DNA-directed RNA polymerase II, 19K subunit DNA-directed RNA polymerase II, 215K subunit	YDL220c YDR073W YNR023W YOR290c YBR289W YPL016W YCR042c YPL177c YGL166W YNL167c YPL042c YLR176c YDR217c YNL216W YLR418c	SNF11 SNF12 SNF2 SNF5 SWI1 TSM1 CUP9 CUP9 SKO1 SSN3 RFX1 RAD9 RAP1 CDC73	component of SWI/SNF transcription activator complex component of TAF(II) complex copper homeostasis protein copper-dependent transcription factor cre-binding bzip protein cyclin-dependent ser/thr protein kinase DNA binding protein DNA repair checkpoint protein DNA repair checkpoint protein DNA-directed RNA polymerase II accessory protein DNA-directed RNA polymerase II	YKL185w YHL020c YDR464w YNL076w YDR207c YGL211c YGL115w YCR093w YML065w YML065w YHR1162c YLL004w YBR060c YAL051w YDR363c YBL005w	ASH1 OPI1 SPP41 MKS1 UME6 NIF3 SNF4 CDC39 ORC1 ORC5 ORC6 ORC4 ORC3 RRR1 OAF1 PIP2 PDR3	negative regulator of HO expression negative regulator of phospholipid biosynthesis pathway negative regulator of PRP3 and PRP4 gene expression negative regulator of RAS-cAMP pathway negative regulator of RAS-cAMP pathway negative transcriptional regulator Ngq1 p-interacting factor 3 nuclear regulatory protein nuclear transmembrane protein origin recognition complex, 50K subunit origin recognition complex, 50K subunit origin recognition complex, 56K subunit peroxisome proliferating transcription factor peroxisome proliferating transcription factor pleiotropic drug resistance regulatory protein

YDR017c	KCS1	potential transcription factor of the BZIP	YFR037c	RSC8	subunit of the RSC complex	chromatin	modifica	tion
		type	YLR321c	SFH1	subunit of the RSC complex		MSI1	chromatin assembly complex, subunit
YGL025c YER108c	PGD1 FLO8	probable transcription factor probable transcriptional activator of Flo1p	YIL126w YGL254w	STH1 FZF1	subunit of the RSC complex sulphite resistance protein	YML102w	CAC2	p50 chromatin assembly complex, subunit
YGL194c YJL103c	RTL1	putative deacetylase putative regulatory protein	YNL222w YDR310c		suppressor of cs mutant sua7 suppressor of mar1-1	YPR018w	RLF2	p60 chromatin assembly complex, subunit
YBL066c	SEF1	putative transcription factor	YKR099w	BAS1	transcription factor			p90
YHR056c YBR275c	RIF1	putative transcription regulator Rap1p-interacting factor 1	YDL165w YLR098c	CDC36 CHA4	transcription factor transcription factor	YGL207w YGR252w		general chromatin factor histone acetyltransferase
YKL038w	RGT1	regulator of glucose induced genes	YPL248c	GAL4	transcription factor	YGL194c	RTL1	putative deacetylase
YDR257c YDR392w	RMS1 SPT3	regulatory protein regulatory protein	YFL031w YLR256w		transcription factor transcription factor	YHR119w YBR238c	YTX1	regulatory protein strong similarity to general chromatin
YMR016c	SOK2	regulatory protein in the PKA signal transduction pathway	YCR065w YLR451w	HCM1 LEU3	transcription factor transcription factor	YFR004w	MPR1	factor Spt16p strong similarity to <i>S. pombe</i> pad1 protein
YCL055w	KAR4	regulatory protein required for pheromone	YGL013c	PDR1	transcription factor	YOR213c		subunit of the RSC complex
YNR052c	POP2	induction of karyogamy genes required for glucose derepression	YKL043w YFR034c	PHD1 PHO4	transcription factor transcription factor	YCR052w YFR037c	RSC6 RSC8	subunit of the RSC complex subunit of the RSC complex
YMR179w		required for normal transcription at a	YBR049c	REB1	transcription factor	YLR321c	SFH1	subunit of the RSC complex
YKL093w	MBR1	number of loci required for optimal growth on glycerol	YBL093c YOR140w	ROX3 SFL1	transcription factor transcription factor	YIL126w YGR274c	STH1 TAF145	subunit of the RSC complex TFIID subunit (TBP-associated factor),
YOL068c YOR025w	HST1 HST3	silencing protein silencing protein	YLR055c YER111c	SPT8 SWI4	transcription factor transcription factor	YGR063c	SPT4	145K transcription initiation protein
YBL052c	SAS3	silencing protein	YDR146c	SWI5	transcription factor	YML010w	SPT5	transcription initiation protein
YKR101w YDL042c	SIR1 SIR2	silencing regulatory protein silencing regulatory protein	YLR182w YFL021w	SWI6 GAT1	transcription factor transcription factor for nitrogen regulation	YGR116w	SPT6	transcription initiation protein
YLR442c YDR227w	SIR3 SIR4	silencing regulatory protein silencing regulatory protein	YER040w	GLN3	transcription factor for positive nitrogen regulation	mRNA p	rocess	ing (splicing)
YKL070w	01114	similarity to B. subtilis transcriptional	YMR042w	ARG80	transcription factor involved in arginine	YBL074c	AAR2	A1 cistron splicing factor
YDL070w		regulatory protein similarity to bromodomain protein BDF1	YML099c	ARG81	metabolism transcription factor involved in arginine	YHL038c	CBP2	apo-cytochrome b pre-mRNA processing protein 2
YIL131c	FKH1	similarity to D. melanogaster fork head			metabolism	YPL119c	DBP1	ATP-dependent RNA helicase
YJL056c		protein similarity to developmental control	YMR280c	CAT8	transcription factor involved in gluconeogenesis	YOR204w YBR142w	DED1 MAK5	ATP-dependent RNA helicase ATP-dependent RNA helicase
YBR061c		proteins similarity to <i>E. coli</i> ftsJ protein	YGL181w	GTS1	transcription factor of the Gcs1p/Glo3p/Sps18p family	YPL029w	SUV3	ATP-dependent RNA helicase, mitochondrial
YJR147w		similarity to heat-shock transcription	YMR043w	MCM1	transcription factor of the MADS box		CUS2	cold sensitive U2 snRNA suppressor
YGR249w	MGA1	factors similarity to heat-shock transcription	YPL089c	RLM1	family transcription factor of the MADS box	YIR021w	MRS1	involved in mitochondrial RNA splicing of COB mRNA
YPL015c	HST2	factors		PPR1	family	YOR148c	SPP2 BRR1	involved in pre-mRNA processing
YPLUISC YDR191w		similarity to Hst1p and Sir2p similarity to Hst3p,Hst1p and Sir2p	YLR014c	PPRI	transcription factor regulating pyrimidine pathway	YPR057w YLR382c	NAM2	involved in snRNP biogenesis leucine-tRNA ligase, mitochondrial
YNL107w YHR193c	EGD2	similarity to human AF-9 protein similarity to human α-NAC	YJR094c	IME1	transcription factor required for sporulation	YNL210w YHR086w	MER1 NAM8	meiotic recombination protein meiotic recombination protein
YAR003w	FUN16	similarity to human RB protein binding	YHR206w	SKN7	transcription factor with similarity to Hsf1p	YMR023c	MSS1	mitochondrial GTPase involved in
YER169w		protein similarity to human retinoblastoma	YDL056w	MBP1	transcription factor, subunit of the MBF factor	YLL036c	PRP19	expression of COX1 non-snRNP sliceosome component
YJR119c		binding protein 2 similarity to human retinoblastoma	YNL330c YOL004w	RPD3 SIN3	transcription modifier protein transcription regulatory protein	YBR237w	PRP5	required for DNA repair pre-mRNA processing RNA-helicase
		binding protein 2	YJL127c	SPT10	transcription regulatory protein	YKL074c	MUD2	pre-mRNA splicing factor
YLR116w		similarity to human ZFM1 protein and mouse CW17R protein	YJL176c YPL082c	SWI3 MOT1	transcription regulatory protein transcriptional accessory protein	YDL043c YJL203w	PRP11 PRP21	pre-mRNA splicing factor pre-mRNA splicing factor
YJL206c		similarity to hypothetical protein YIL130p and Put3p	YDR423c YOR028c	CAD1 CIN5	transcriptional activator transcriptional activator	YER013w YMR268c	PRP22 PRP24	pre-mRNA splicing factor pre-mRNA splicing factor
YOL133w		similarity to Lotus RING-finger protein	YPL075w	GCR1	transcriptional activator	YGR075c	PRP38	pre-mRNA splicing factor
YER130c YER184c		similarity to Msn2p and Msn4p similarity to multidrug resistance protein	YOL116w YKL062w	MSN1 MSN4	transcriptional activator transcriptional activator	YML046w YDL030w	PRP39 PRP9	pre-mRNA splicing factor pre-mRNA splicing factor (snRNA-
YIL050w		PDR3 similarity to <i>N. crassa</i> regulatory protein	YHR084w YIR023w	STE12 DAL81	transcriptional activator transcriptional activator for allantoin and	YDR088c	SLU7	associated protein) pre-mRNA splicing factor affecting 3'
		preg(+)			GABA catabolic genes			splice site choice
YLR013w YDR334w		similarity to nitrogen regulatory proteins similarity to nuclear Sth1p, Snf2p and	YNL314w	DAL82	transcriptional activator for allantoin catabolic genes	YDR243c	PRP28	pre-mRNA splicing factor RNA helicase of DEAD box family
YPR115w		related proteins similarity to probable transcription factor	YDL170w	UGA3	transcriptional activator for GABA catabolic genes		PRP31 MTF2	pre-mRNA splicing protein protein involved in mRNA splicing and
		Ask10p, and to hypothetical proteins YNL047c and YIL105c	YML007w	YAP1	transcriptional activator involved in		MRS5	protein synthesis, mitochondrial regulator of intron splicing, mitochondrial
YIL130w		similarity to Put3p and to hypothetical	YEL009c	GCN4	oxidative stress response transcriptional activator of amino acid	YDR028c		regulatory subunit for protein
YCR020c	PET18	protein YJL206c similarity to regulatory protein	YDR034c	LYS14	biosynthetic genes transcriptional activator of lysine pathway	YDR478w	SNM1	phosphatase Glc7p RNA binding protein of RNase MRP
YBR182c YKR008w		similarity to Rlm1p,Mcm1p, and hMEF2 similarity to <i>S. pombe</i> bromodomain	YIR017c		genes			RNA helicase of the DEAD box family, mitochondrial
		protein		MET28	transcriptional activator of sulphur amino acid metabolism	YER172c	BRR2	RNA helicase-related protein
YGL150c YLR228c		similarity to Snf2p and human SNF2α similarity to transcription activator Lys14p	YNL103w	MET4	transcriptional activator of sulphur metabolism	YOR334w	MRS2	RNA splicing protein and member of the mitochondrial carrier family (MCF)
YLL054c YLR266c		similarity to transcription factor Pip2p similarity to transcription factors	YPR104c	FHL1	transcriptional activator of the forkhead/hnf3 family	YJL133w	MRS3	RNA splicing protein and member of the mitochondrial carrier family (MCF)
YLR278c		similarity to transcription factors	YDR448w	ADA2	transcriptional adaptor	YKR052c	MRS4	RNA splicing protein and member of the
YDR303c		similarity to transcriptional regulator proteins	YMR039c YAL021c	SUB1 CCR4	transcriptional coactivator transcriptional regulator	YKR086w	PRP16	mitochondrial carrier family (MCF) RNA-dependent ATPase
YMR019w YHR178w		SIN3 binding protein SIN3 binding protein	YER164w YIL084c	CHD1 SDS3	transcriptional regulator transcriptional regulator	YNR011c	PRP2	RNA-dependent ATPase of DEAH box family
YKL072w	STB6	SIN3 binding protein	YNL012w	SP01	transcriptional regulator involved in	YHR004c-a		similarity to mitochondrial splicing protein
YNL309w YMR053c		Sin3p binding protein Sin3p binding protein	YGL035c	MIG1	sporulation transcriptional repressor	YKR024c		Mrs5p similarity to pre-mRNA processing protein
YLR399c YNL204c	BDF1 SPS18	sporulation protein sporulation-specific zinc-finger protein	YER068w YKR034w	MOT2 DAL80	transcriptional repressor transcriptional repressor for allantoin and	YGR074w	SMD1	Prp5p snRNA-associated protein
YMR037c	0, 010	stress responsive regulatory protein			GABA catabolic genes	YPR182w	SMX3	snRNA-associated protein of the SM
YDR026c		strong similarity to DNA-binding protein Reb1p	YMR182c YCL054w		transcriptional repressor protein transcriptional silencing protein	YBR055c	PRP6	family snRNP(U4/U6)-associated splicing factor
YDR252w	BTT1	strong similarity to Egd1p and to human Btf3 protein	YBR083w YOR337w		Ty transcription activator TY1 enhancer activator	YKL012w YPR134w	PRP40 MSS18	splicing factor splicing protein
YHR211w	FLO5	strong similarity to Flo1p	YER151c	UBP3	ubiquitin-specific proteinase	YGR222w	PET54	splicing protein and translational activator,
YOR304w		strong similarity to human Snf2p homologue	YER088c		weak similarity human transforming proteins (B-myb)	YKL078w		mitochondrial strong similarity to ATP-dependent RNA
YOL055c		strong similarity to hypothetical proteins YPL258c, YPR121w, similarity to <i>B. subtilis</i>	YBR240c YML076c		weak similarity to regulatory proteins weak similarity to transcription factor	YOR159c	SME1	helicases strong similarity to human small nuclear
YFL052w		transcriptional activator tenA strong similarity to Mal63p, Mal23p and	YCR106w		weak similarity to transcription factor Pip2p	YLR275w		ribonucleoprotein E strong similarity to human snRNP subunit
		Mal33p	YBR033w		weak similarity to transcription factors	ILDZ/DW		D2 involved in systemic lupus
YPR196w		strong similarity to regulatory protein Mal63p	YKR064w YOL089c		weak similarity to transcription factors weak similarity to transcription factors	YPL060w		erythematosus strong similarity to Mrs2p
YBR245c		strong similarity to SNF2/SWI2 DNA	YKL222c		weak similarity to transcription factors,	YGL120c	SMD3	strong similarity to Prp22p
YDR253c		binding regulatory protein strong similarity to zinc-finger proteins			similarity to finger proteins YOR162c, YOR172w and YLR266c	YLR147c		strong similarity to small nuclear ribonucleoprotein D3
YML081w YEL056w	HAT2	strong similarity to ZMS1 protein subunit of the major yeast histone	YBL054w		weak similarity transforming protein (B- myb)	YIR009w	MSL1	strong similarity to small nuclear ribonucleoproteins
YOR213c		acetyltransferase subunit of the RSC complex	YER122c YDR216w	GLO3 ADR1	zinc-finger protein zinc-finger transcription factor	YIL061c YBR119w	SNP1 MUD1	U1 small nuclear ribonucleoprotein U1 snRNP-specific A protein
YCR052w	RSC6	subunit of the RSC complex	YGR044c	RME1	zinc-finger transcription factor	YMR240c		U2 snRNP protein
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YPR178w	PRP4	U4/U6 snRNP 52K protein	YER110c	KAP123	RAN-binding protein	YOR096w	RP30	ribosomal	protein	
YGR006w	PRP18	U5 snRNA-associated protein	YDR002w	YRB1	ran-specific GTPase-activating protein	YKL006w	RPL14A	ribosomal	protein	
YHR165c	PRP8	U5 snRNP protein, pre-mRNA splicing factor	YER107c	GLE2	required for nuclear pore complex structure and function	YHL001w YMR242c		ribosomal ribosomal		
YER112w	USS1	U6 snRNA associated protein	YIR011c	STS1	required for transport of Rna15p from the cytoplasm to the nucleus	YOR312c YDR471w		ribosomal		
		ing (5′-end, 3′-end processing	YDL207w	GLE1	RNA export mediator	YLR344w	RPL33A	ribosomal ribosomal		
and mR	NA degi	radation)	YLR119w	SRN2	suppressor of rna1-1 mutation	YMR194w YDL184c		ribosomal ribosomal		
YJL209w	CBP1	apo-cytochrome b pre-mRNA processing	other tr	anscrip	tion activities	YDL133c-a	RPL47B	ribosomal	protein	
YBR120c	CBP6	protein apo-cytochrome b pre-mRNA processing	YGL127c	SOH1	allows hpr1 null mutant to grow at 37°C	YPL198w YOL040c		ribosomal ribosomal		
		protein	YOR113w	AZF1	asparagine-rich zinc-finger protein	YLR287c-a	RPS30A	ribosomal	protein	
YPL178w YGL094c	SAE1 PAN2	cell cycle block in meiotic prophase component of Pab1p-stimulated poly(A)	YPR198w YBR212w	SGE1 NGR1	drug resistance protein glucose-repressible RNA-binding protein	YDL191w YDL136w		ribosomal ribosomal		
		ribonuclease	YML027w	YOX1	homoeodomain protein	YPL220w	SSM1A	ribosomal	protein	
YMR061w	RNA14	component of pre-mRNA 3'-end processing factor	YNL068c	FKH2	homology to <i>D. melanogaster</i> forkhead protein	YGL135w YGL123w		ribosomal ribosomal		
YGL044c	RNA15	component of pre-mRNA 3'-end	YIL030c	SSM4	involved in mRNA turnover	YIL148w	UBI1	ribosomal	protein	
YJR093c	FIP1	processing factor component of pre-mRNA polyadenylation	YNL282w YCR087c-a	(POP2)	involved in processsing RNAs nucleic acid-binding protein	YKR094c YHL015w		ribosomal ribosomal		
YKL025c	PAN3	factor component of the Pab1p-dependent poly	YDL051w YMR164c	YLA1	RNA binding protein similarity to CYC8 protein	YML073c YLR448w		ribosomal ribosomal		
		(A)	YGL014w		similarity to <i>D. melanogaster</i> pumilio	YDR500c	RPL35B	ribosomal	protein	L.37.e
YOL149w	DCP1	component of the yeast decapping enzyme	YIR001c		protein and HTR1 protein similarity to <i>D. melanogaster</i> RNA binding	YPR102c YDR418w		ribosomal ribosomal		
YGL097w	SRM1	GDP/GTP exchange factor for			protein	YEL054c	RPL15B	ribosomal	protein	L12.e
YGR158c	MTR3	Gsp1p/Gsp2p involved in mRNA transport	YNL004w YBR233w	HRB1	similarity to Gbp2p similarity to human hnRNP-E1 protein	YDL082w YKL170w		ribosomal ribosomal		L13 L14, mitochondrial
YBR236c	ABD1	methyltransferase	YPR031w		similarity to human zinc-finger protein	YLR029c	RPL13A	ribosomal	protein	L15.e.c12
YGL130w	CEG1	mRNA guanylyltransferase (mRNA capping enzyme, α subunit)	YCL033c		BR140 similarity to <i>M. capricolum</i> transcription	YMR121c YJL063c		ribosomal ribosomal		L17, mitochondrial
YER165w YLR277c	PAB1 BRR5	mRNA polyadenylate-binding protein mRNA processing protein	YIR005w		repressor	YKL180w YJL177w		ribosomal ribosomal		
YKR002w	PAP1	poly(A) polymerase	YMR213w		similarity to RNA-binding proteins similarity to <i>S. pombe</i> putative	YNL301c	RP28B	ribosomal	protein	L18.e
YGL122c YPL190c	NAB2 NAB3	poly(A)-binding protein polyadenylated RNA-binding protein	YNL175c		transcription factor cdc5 similarity to <i>S. pombe</i> Rnp24p	YBL027w YBR084c-a		ribosomal ribosomal		
YDR301w	CFT1	pre-mRNA 3'-end processing factor	YOR244w		similarity to SAS2 and SAS3 protein	YPL079w	URP1B	ribosomal	protein	L21
YJR017c YDR195w	ESS1 REF2	processing/termination factor 1 RNA 3'-end formation protein	YPR008w YPL230w		similarity to transcription factor similarity to transcription factors	YBR191w YBL087c		ribosomal ribosomal		
YOR179c		similarity to BRR5 protein	YPR013c		similarity to transcription factors	YER117w	RPL17B	ribosomal	protein	L23.e
YOR319w	HSH49	similarity to human SAP49 and RNA- binding proteins	YPR015c YNL027w		similarity to transcription factors similarity to zinc-finger proteins	YOL127w YGL031c		ribosomal ribosomal		
YHR015w YOR159c	SME1	similarity to PES4 PAB-like protein	YPL038w YDR169c	STB3	similarity to zinc-finger proteins SIN3 protein-binding protein	YGR148c YGR034w		ribosomal ribosomal		
TOMISSE	SIVIL I	strong similarity to human small nuclear ribonucleoprotein E	YPR107c	0100	strong similarity to <i>D. melanogaster</i> zinc-	YHR010w	RPL27A	ribosomal	protein	L27.e
other m	RNA-tr	anscription activities	YIL105c		finger protein strong similarity to hypothetical protein	YGL103w YBR031w		ribosomal ribosomal		
		•	1121000		YNL047c, similarity to hypothetical protein	YOR063w	TCM1	ribosomal	protein	L3.e
YGL171w YOL006c	ROK1 TOP1	ATP-dependent RNA helicase DNA topoisomerase I			YPR115w and to probable transcription factor Ask10p	YGL030w YDL075w		ribosomal ribosomal		
YGL251c	HFM1 IDH1	DNA/RNA helicase	YNL255c		strong similarity to nucleic acid-binding	YLR406c YBL092w	RPL34B	ribosomal	protein	L31.e.c12
YNL037c	IDHI	isocitrate dehydrogenase (NAD*) subunit 1, mitochondrial	YHR169w		proteins strong similarity to RNA helicase	YIL052c		ribosomal ribosomal		
YOR136w	IDH2	isocitrate dehydrogenase (NAD*) subunit 2, mitochondrial	YGL078c		strong similarity to RNA helicase DBP2 protein	YOR234c YPL143w				L35a.e.c15 L35a.e.c16
YNL016w	PUB1	major polyadenylated RNA-binding protein	YCR004c	YCP4	strong similarity to S. pombe protein obr1	YNL162w	RPL41A	ribosomal	protein	L36a.e
YHR170w	NMD3	of nucleus and cytoplasm nonsense-mediated mRNA decay protein	YFL017w-a	SNP2	strong similarity to snRNP E	YHR141c	RPL41B			1 36a e
YMR064w			I YDR451c	0.4.2				ribosomal ribosomal		
		nuclear control of ATPase messenger	YDR451c YML017w	PSP2	strong similarity to Yox1p suppressor of DNA polymerase α	YLR185w YPR043w	RPL35A	ribosomal ribosomal	protein protein	L37.e L37a.e
YOL123w		nuclear control of ATPase messenger RNA expression protein	YML017w		strong similarity to Yox1p suppressor of DNA polymerase $\alpha$ mutation	YLR185w YPR043w YJL189w	RPL35A RPL46	ribosomal	protein protein protein	L37.e L37a.e L39.e
YOL123w YLR067c	AEP1	nuclear control of ATPase messenger RNA expression protein polyadenylated RNA-binding protein required for stability and translation of	YML017w YKR092c	PSP2	strong similarity to Yox1p suppressor of DNA polymerase α mutation suppressor of mutant AC40 of RNA polymerase I and III	YLR185w YPR043w YJL189w YDR012w YPL131w	RPL35A RPL46 RPL2B RPL1	ribosomal ribosomal ribosomal ribosomal ribosomal	protein protein protein protein protein	L37.e L37a.e L39.e L4.e.B L5.e
	AEP1 HRP1	nuclear control of ATPase messenger RNA expression protein polyadenylated RNA-binding protein	YML017w	PSP2	strong similarity to Yox1p suppressor of DNA polymerase $\alpha$ mutation suppressor of mutant AC40 of RNA	YLR185w YPR043w YJL189w YDR012w	RPL35A RPL46 RPL2B RPL1 RLP7	ribosomal ribosomal ribosomal ribosomal	protein protein protein protein protein protein	L37.e L37a.e L39.e L4.e.B L5.e L7.e
YLR067c YAL016w	AEP1 HRP1 PET309	nuclear control of ATPase messenger RNA expression protein polyadenylated RNA-binding protein required for stability and translation of COX1 mRNA ser/thr phosphatase 2A, regulatory subunit A	YML017w YKR092c	PSP2	strong similarity to Yox1p suppressor of DNA polymerase α mutation suppressor of mutant AC40 of RNA polymerase I and III weak similarity to <i>D. melanogaster</i> transcription elongation factor DmS-II weak similarity to CYC1/CYP3	YLR185w YPR043w YJL189w YDR012w YPL131w YNL002c YGL076c YHL033c	RPL35A RPL46 RPL2B RPL1 RLP7 RPL6A RPL4A	ribosomal ribosomal ribosomal ribosomal ribosomal ribosomal ribosomal ribosomal	protein protein protein protein protein protein protein protein	L37.e L37.a.e L39.e L4.e.B L5.e L7.e.A L7.e.A L7a.e.A
YLR067c YAL016w YOL042w YER146w	AEP1 HRP1 PET309	nuclear control of ATPase messenger RNA expression protein polyadenylated RNA-binding protein required for stability and translation of COX1 mRNA ser/thr phosphatase 2A, regulatory subunit A similarity to CCR4 protein similarity to human snRNP E	YML017w YKR092c YKL005c YNR063w YJL124c	PSP2	strong similarity to Yox1p suppressor of DNA polymerase α mutation suppressor of mutant AC40 of RNA polymerase I and III weak similarity to <i>D. melanogaster</i> transcription elongation factor DmS-II weak similarity to CYC1/CYP3 transcription activator weak similarity to human Sm protein G	YLR185W YPR043W YJL189W YDR012W YPL131W YNL002c YGL076c YHL033c YLL045c YIL018W	RPL35A  RPL46 RPL2B RPL1 RLP7 RPL6A RPL4A RPL4B RPL4B RPL5A	ribosomal ribosomal ribosomal ribosomal ribosomal ribosomal ribosomal ribosomal ribosomal ribosomal	protein protein protein protein protein protein protein protein protein protein	L37e L37a.e L39.e L4.e.B L5.e L7e L7e.A L7a.e.A L7a.e.B L8.e
YLR067c YAL016w YOL042w	AEP1 HRP1 PET309	nuclear control of ATPase messenger RNA expression protein polyadenylated RNA-binding protein required for stability and translation of COX1 mRNA ser/thr phosphatase 2A, regulatory subunit A similarity to CCR4 protein similarity to human snRNP E similarity to human snRNP-associated	YML017w YKR092c YKL005c YNR063w	PSP2	strong similarity to Yox1p suppressor of DNA polymerase α mutation suppressor of mutant AC40 of RNA polymerase I and III weak similarity to <i>D. melanogaster</i> transcription elongation factor DmS-II weak similarity to CYC1/CYP3 transcription activator weak similarity to human Sm protein G weak similarity to human Sm protein G weak similarity to K. marxianus Mig1 and	YLR185W YPR043W YJL189W YDR012W YPL131W YNL002c YGL076c YHL033c YLL045c YIL018W YFR031c-a	RPL35A  RPL46 RPL2B RPL1 RLP7 RPL6A RPL4A RPL4A RPL4B RPL5A RPL5B	ribosomal ribosomal ribosomal ribosomal ribosomal ribosomal ribosomal ribosomal ribosomal ribosomal ribosomal ribosomal	protein protein protein protein protein protein protein protein protein protein protein protein	L37e L37a.e L39.e L4.e.B L5.e L7.e.A L7a.e.A L7a.e.B L8.e
YLR067c YAL016w YOL042w YER146w YER029c YER028c	AEP1 HRP1 PET309	nuclear control of ATPase messenger RNA expression protein polyadenylated RNA-binding protein required for stability and translation of COX1 mRNA ser/thr phosphatase 2A, regulatory subunit A similarity to CCR4 protein similarity to human snRNP E similarity to human snRNP-associated protein B similarity to hug1p	YML017w YKR092c YKL005c YNR063w YJL124c	PSP2	strong similarity to Yox1p suppressor of DNA polymerase $\alpha$ mutation suppressor of mutant AC40 of RNA polymerase I and III weak similarity to <i>D. melanogaster</i> transcription elongation factor DmS-II weak similarity to CYC1/CYP3 transcription activator weak similarity to human Sm protein G weak similarity to <i>K. marxianus</i> Mig1 and other regulatory proteins weak similarity to transcription activator	YLR185W YPR043W YJL189W YDR012W YPL131W YNL002c YGL076c YHL033c YLL045c YIL018W YFR031c-a YGL147c YNL067W	RPL35A  RPL46 RPL2B RPL1 RLP7 RPL6A RPL4A RPL4B RPL5A RPL5B RPL5B RPL9A RPL9B	ribosomal ribosomal ribosomal ribosomal ribosomal ribosomal ribosomal ribosomal ribosomal ribosomal ribosomal ribosomal ribosomal ribosomal ribosomal	protein protein protein protein protein protein protein protein protein protein protein protein protein protein protein	L37e L37a.e L39.e L4.e.B L5.e L7e L7e.A L7a.e.A L7a.e.B L8.e L8.e L9.e. L9.e.C14
YLR067c YAL016w YOL042w YER146w YER029c YER028c YDR429c	AEP1 HRP1 PET309 TPD3	nuclear control of ATPase messenger RNA expression protein polyadenylated RNA-binding protein required for stability and translation of COX1 mRNA ser/thr phosphatase 2A, regulatory subunit A similarity to CCR4 protein similarity to thuman snRNP E similarity to human snRNP-associated protein B similarity to Mig1p similarity to Mig1p similarity to nuclear RNA binding proteins	YML017w YKR092c YKL005c YNR063w YJL124c YDR043c YIR018w	PSP2	strong similarity to Yox1p suppressor of DNA polymerase α mutation suppressor of mutant AC40 of RNA polymerase I and III weak similarity to <i>D. melanogaster</i> transcription elongation factor DmS-II weak similarity to CYC1/CYP3 transcription activator weak similarity to human Sm protein G weak similarity to the Manual Smilarity to K. marxianus Mig1 and other regulatory proteins weak similarity to transcription activator Pdr4p	YLR185W YPR043W YJL189W YDR012W YPL131W YNL002c YGL076c YHL033c YLL045c YIL018W YFR031c-a YGL147c	RPL35A  RPL46 RPL2B RPL1 RLP7 RPL6A RPL4A RPL4B RPL5A RPL5B RPL9B MRPL25	ribosomal ribosomal ribosomal ribosomal ribosomal ribosomal ribosomal ribosomal ribosomal ribosomal ribosomal ribosomal ribosomal ribosomal ribosomal ribosomal	protein protein protein protein protein protein protein protein protein protein protein protein protein protein protein protein protein	L37e L37a.e L39.e L4.e.B L5.e L7e L7e.A L7a.e.A L7a.e.B L8.e L8.e
YLR067c YAL016w YOL042w YER146w YER029c YER028c YDR429c YJR127c YDL031w	AEP1 HRP1 PET309	nuclear control of ATPase messenger RNA expression protein polyadenylated RNA-binding protein required for stability and translation of COX1 mRNA ser/thr phosphatase 2A, regulatory subunit A similarity to CCR4 protein similarity to human snRNP E similarity to human snRNP-associated protein B similarity to muclear RNA binding proteins similarity to nuclear RNA binding proteins similarity to regulatory protein ADR1 similarity to RNA helicases	YML017w YKR092c YKL005c YNR063w YJL124c YDR043c YIR018w YPR199c	PSP2	strong similarity to Yox1p suppressor of DNA polymerase α mutation suppressor of mutant AC40 of RNA polymerase I and III weak similarity to D. melanogaster transcription elongation factor DmS-II weak similarity to CYC1/CYP3 transcription activator weak similarity to thuman Sm protein G weak similarity to thuman Sm protein G weak similarity to transcription activator Pdr4p weak similarity to transcription activator Pdr4p weak similarity to transcription activator Yap1p	YLR185W YPR043W YJL189W YDR012W YPL131W YNL002c YGL076c YLL045c YLL045c YLL018W YFR031c-a YGL147c YNL067W YGR076c YJR094W-a	RPL35A  RPL46 RPL2B RPL1 RLP7 RPL6A RPL4A RPL4B RPL5B RPL5B RPL9A RPL9B MRPL25	ribosomal ribosomal ribosomal ribosomal ribosomal ribosomal ribosomal ribosomal ribosomal ribosomal ribosomal ribosomal ribosomal ribosomal ribosomal ribosomal ribosomal ribosomal	protein protei	L37ae L37a.e L39.e L4e.B L5.e L7e.A L7a.e.A L7a.e.B L8.e L8.e L9.e L9.e.c14 m (YML25),
YLR067c  YAL016w  YOL042w YER146w YER029c  YER028c YDR429c YJR127c YDL031w YNL147w YNL021w	AEP1 HRP1 PET309 TPD3	nuclear control of ATPase messenger RNA expression protein polyadenylated RNA-binding protein required for stability and translation of COX1 mRNA ser/thr phosphatase 2A, regulatory subunit A similarity to CCR4 protein similarity to human snRNP E similarity to human snRNP-associated protein B similarity to Mig1p similarity to nuclear RNA binding proteins similarity to regulatory protein ADR1 similarity to RNA helicases similarity to RNA helicases similarity to transcription factor Rpd3p	YML017w YKR092c YKL005c YNR063w YJL124c YDR043c YIR018w YPR199c YBR239c	PSP2	strong similarity to Yox1p suppressor of DNA polymerase α mutation suppressor of mutant AC40 of RNA polymerase I and III weak similarity to <i>D. melanogaster</i> transcription elongation factor DmS-II weak similarity to CYC1/CYP3 transcription activator weak similarity to human Sm protein G weak similarity to human Sm protein G weak similarity to <i>K. marxianus</i> Mig1 and other regulatory proteins weak similarity to transcription activator Pdr4p weak similarity to transcription activator Yap1p weak similarity to transcription factor Put3p	YLR185W YPR043W YJL189W YDR012W YPL131W YNL002c YGL076c YHL045c YIL018W YFR031c-a YGL147c YNL067W YGR076c YJR094W-a YOR293W YDR025W	RPL35A  RPL46 RPL2B RPL1 RLP7 RPL6A RPL4A RPL4B RPL5B RPL5B RPL5B RPL9A RPL9B RRPL9E RPL9A RPL9B RPL9B RPL3A RPL9B RPL3A	ribosomal	protein protei	L37e L37a.e L39.e L4.e.B L5.e L7e L7eA L7a.e.A L7a.e.A L7a.e.B L8.e L9.e L9.e.c.14 m (YML25), of the large subunit S10.e
YLR067c  YAL016w  YOL042w YER146w YER029c  YER028c YDR429c YJR127c YDL031w YNL147w YNL021w YPR068c	AEP1 HRP1 PET309 TPD3	nuclear control of ATPase messenger RNA expression protein polyadenylated RNA-binding protein required for stability and translation of COX1 mRNA ser/thr phosphatase 2A, regulatory subunit A similarity to CCR4 protein similarity to human snRNP E similarity to human snRNP-associated protein B similarity to muclear RNA binding proteins similarity to nuclear RNA binding proteins similarity to regulatory protein ADR1 similarity to snRNP proteins similarity to snRNP proteins similarity to transcription factor Rpd3p similarity to transcription factor Rpd3p	YML017w YKR092c YKL005c YNR063w YJL124c YDR043c YIR018w YPR199c YBR239c YBR150c	PSP2	strong similarity to Yox1p suppressor of DNA polymerase α mutation suppressor of mutant AC40 of RNA polymerase I and III weak similarity to D. melanogaster transcription elongation factor DmS-II weak similarity to CYC1/CYP3 transcription activator weak similarity to thuman Sm protein G weak similarity to thuman Sm protein G weak similarity to transcription activator Pdr4p weak similarity to transcription activator Pdr4p weak similarity to transcription activator Yap1p weak similarity to transcription factor Put3p weak similarity to transcription factor Put3p weak similarity to transcription factors	YLR185w YPR043w YJL189w YDR012w YPL131w YNL002c YGL076c YHL033c YLL045c YIL045c YIL018w YFR031c-a YGL147c YNL067w YGR076c YJR094w-a YOR293w YDR025w YBR025w YBR0248w	RPL35A  RPL46 RPL2B RPL1 RLP7 RPL6A RPL4A RPL4A RPL5A RPL5B RPL5B RPL9B MRPL25  RPS18A RPS18A RPS18B	ribosomal	protein protei	L37e L37a.e L39.e L4e.B L5e L7e L7e.A L7a.e.A L7a.e.B L8e L9e L9e L9e.co14 m (YML25), of the large subunit S10.e S11.e.B
YLR067c  YAL016w  YOL042w YER146w YER029c  YER028c YDR429c YJR127c YDL031w YNL147w YNL021w YPR068c YPL213w YBL026w	AEP1 HRP1 PET309 TPD3  ZMS1	nuclear control of ATPase messenger RNA expression protein polyadenylated RNA-binding protein required for stability and translation of COX1 mRNA ser/thr phosphatase 2A, regulatory subunit A similarity to CCR4 protein similarity to human snRNP E similarity to human snRNP-associated protein B similarity to hugar snRNP-associated protein B similarity to nuclear RNA binding proteins similarity to regulatory protein ADR1 similarity to RNA helicases similarity to transcription factor Rpd3p similarity to U2 snRNP protein A' snRNP-related protein	YML017w YKR092c YKL005c YNR063w YJL124c YDR043c YIR018w YPR199c YBR239c YBR150c YGR067c YPL133c	PSP2	strong similarity to Yox1p suppressor of DNA polymerase $\alpha$ mutation suppressor of mutant AC40 of RNA polymerase I and III weak similarity to <i>D. melanogaster</i> transcription elongation factor DmS-II weak similarity to CYC1/CYP3 transcription activator weak similarity to human Sm protein G weak similarity to human Sm protein G weak similarity to human Sm protein G weak similarity to transcription activator Pdr4p weak similarity to transcription activator Pdr4p weak similarity to transcription factor Put3p weak similarity to transcription factors	YLR185W YPR043W YJL189W YDR012W YPL131W YNL002c YGL076c YHL045c YIL018W YFR031c-a YGL147c YNL067W YGR076c YJR094W-a YOR293W YDR025W YBR048W YPR166c YJL191W	RPL35A  RPL46 RPL2B RPL11 RLP7 RPL6A RPL4B RPL5A RPL5A RPL9B MRPL25  RPS18A RPS18B MRPL25  RPS18B MRPC CRY2	ribosomal riboso	protein protei	L37e L37a.e L39.e L4.e.B L5.e L7e L7eAA L7a.e.A L7a.e.A L8.e L8.e L9.e L9.e.c.14 m (YML25), of the large subunit S10.e S11.e S11.e S14.e S14.e S14.e S14.e S154.e
YLR067c  YAL016w  YOL042w  YER146w  YER029c  YER028c  YDR429c  YJR127c  YDL031w  YNL147w  YNL021w  YPR068c  YPL213w	AEP1 HRP1 PET309 TPD3  ZMS1	nuclear control of ATPase messenger RNA expression protein polyadenylated RNA-binding protein required for stability and translation of COX1 mRNA ser/thr phosphatase 2A, regulatory subunit A similarity to CCR4 protein similarity to human snRNP e similarity to human snRNP-associated protein B similarity to hug1p similarity to nuclear RNA binding proteins similarity to regulatory protein ADR1 similarity to snRNP proteins similarity to snRNP proteins similarity to transcription factor Rpd3p similarity to transcription factor Rpd3p similarity to U2 snRNP protein A' snRNP-related protein strong similarity to RNA helicases of the	YML017w YKR092c YKL005c YNR063w YJL124c YDR043c YIR018w YPR199c YBR239c YBR150c YGR067c	PSP2	strong similarity to Yox1p suppressor of DNA polymerase α mutation suppressor of mutant AC40 of RNA polymerase 1 and III weak similarity to <i>D. melanogaster</i> transcription elongation factor DmS-II weak similarity to CYC1/CYP3 transcription activator weak similarity to thuman Sm protein G weak similarity to thuman Sm protein G weak similarity to transcription activator Pdr4p weak similarity to transcription activator Yap1p weak similarity to transcription activator Yap1p weak similarity to transcription factor Put3p weak similarity to transcription factor Put3p weak similarity to transcription factors	YLR185W YPR043W YJL189W YDR012W YPL131W YNL002c YGL076c YHL033c YLL045c YIL045c YIL018W YFR031c-a YGL147c YNL067W YGR076c YJR094W-a YOR025W YDR025W YBR048W YPR166c YJL191W YJL190c	RPL35A  RPL46 RPL2B RPL1 RLP7 RPL6A RPL4B RPL4B RPL5B RPL5A RPL5B RPL5A RPL5B RPL5A RPL5B RPL5A RPL5B RPS24A	ribosomal riboso	protein protei	L37e L37a.e L39.e L4e.B L5e L7e.A L7a.e.A L7a.e.B L8e L9e L9e L9e.C14 m (YML25), of the large subunit S10.e S11.e S14 S14 S14 S14 S15a.e.c10
YLR067c  YAL016w  YOL042w YER146w YER029c  YER028c YDR429c YJR127c YDL031w YNL147w YNL021w YPR068c YPL213w YBL026w	AEP1 HRP1 PET309 TPD3  ZMS1	nuclear control of ATPase messenger RNA expression protein polyadenylated RNA-binding protein required for stability and translation of COX1 mRNA ser/thr phosphatase 2A, regulatory subunit A similarity to CCR4 protein similarity to human snRNP E similarity to human snRNP-associated protein B similarity to hugan snRNP-associated protein B similarity to nuclear RNA binding proteins similarity to regulatory protein ADR1 similarity to snRNP proteins similarity to transcription factor Rpd3p similarity to U2 snRNP protein A'snRNP-related protein strong similarity to RNA helicases of the DEAD box family strong similarity to RNA helicases of the DEAD box family	YML017w YKR092c YKL005c YNR063w YJL124c YDR043c YIR018w YPR199c YBR239c YBR150c YGR067c YPL133c YER116c	PSP2 SRP40	strong similarity to Yox1p suppressor of DNA polymerase α mutation suppressor of mutant AC40 of RNA polymerase 1 and III weak similarity to <i>D. melanogaster</i> transcription elongation factor DmS-II weak similarity to CYC1/CYP3 transcription activator weak similarity to thuman Sm protein G weak similarity to thuman Sm protein G weak similarity to transcription activator Pdr4p weak similarity to transcription activator Yap1p weak similarity to transcription factor Yap1p weak similarity to transcription factor Put3p weak similarity to transcription factors	YLR185W YPR043W YJR189W YJL189W YDR012W YPL131W YNL002c YGL076c YHL033c YLL045c YIL045c YIL045c YIR0167W YFR031c-a YGL147c YNL067W YGR076c  YJR094W-a YOR293W YDR025W YBR048W YPR166c YJL191W YJL191W YJL190c YLR367W YPL013c	RPL35A  RPL46 RPL28 RPL1 RLP7 RPL64 RPL48 RPL48 RPL58 RPL93 RPL93 MRPL25  RPS18A RPS18B MRP2 CRY2 RPS24A RPS24B	ribosomal ribosomal	protein protein	L37e L37ae L39ae L4e.B L5e L7e L7e.A L7ae.A L7ae.B L8e L9e L9e L9e S11e S11e.B S14 S14 S15a.e.c.10 S15a.e.c.12 S16, mitochondrial
YLR067c  YAL016w  YOL042w YER146w YER029c  YER028c YDR429c YJR127c YDL031w YNL147w YNL021w YPR068c YPL213w YBL026w YDL160c	AEP1 HRP1 PET309 TPD3  ZMS1  SNP3 DHH1	nuclear control of ATPase messenger RNA expression protein polyadenylated RNA-binding protein required for stability and translation of COX1 mRNA ser/thr phosphatase 2A, regulatory subunit A similarity to CCR4 protein similarity to human snRNP E similarity to human snRNP-associated protein B similarity to hugan snRNP-associated protein B similarity to nuclear RNA binding proteins similarity to regulatory protein ADR1 similarity to RNA helicases similarity to transcription factor Rpd3p similarity to transcription factor Rpd3p similarity to U2 snRNP protein A'snRNP-related protein strong similarity to RNA helicases of the DEAD box family	YML017w YKR092c YKL005c YNR063w YJL124c YDR043c YIR018w YPR199c YBR239c YBR150c YGR067c YPL133c YER116c	PSP2 SRP40	strong similarity to Yox1p suppressor of DNA polymerase α mutation suppressor of mutant AC40 of RNA polymerase I and III weak similarity to <i>D. melanogaster</i> transcription elongation factor DmS-II weak similarity to CYC1/CYP3 transcription activator weak similarity to human Sm protein G weak similarity to human Sm protein G weak similarity to human Sm protein G weak similarity to transcription activator Pdr4p weak similarity to transcription activator Pdr4p weak similarity to transcription factor Put3p weak similarity to transcription factors	YLR185W YPR043W YJL189W YDR012W YPL131W YNL002c YGL076c YHL033c YLL045c YIL018W YFR031c-a YGL147c YNL067W YGR076c YJR094W-a YOR293W YDR025W YBR048W YDR025W YJL191W YJL190c YLR367W YPL013c YMR143W YDL083c	RPL35A  RPL46 RPL2B RPL11 RLP7 RPL6A RPL4B RPL5A RPL9B MRPL25  RPS18A RPS18A RPS18B RPS18A RPS18B RPS24A RPS16B	ribosomal riboso	protein protei	L37e L37a.e L39.e L4.e.B L5.e L7e L7e.A L7a.e.A L7a.e.B L8.e L9.e.c14 m (YML25), of the large subunit S11.e.B S11.e.B S14.e.B S14.e.B S15a.e.c.10 S15a.e.c.12 S16, mitochondrial S16.e S16.e
YLR067c  YAL016w  YOL042w  YER146w  YER029c  YER028c  YDR429c  YJR127c  YDL031w  YNL021w  YNL021w  YNL021w  YBL026w  YDL160c  YLR147c  YLR139c	AEP1 HRP1 PET309 TPD3  ZMS1  SNP3 DHH1 SMD3 SLS1	nuclear control of ATPase messenger RNA expression protein polyadenylated RNA-binding protein required for stability and translation of COX1 mRNA ser/thr phosphatase 2A, regulatory subunit A similarity to CCR4 protein similarity to human snRNP E similarity to human snRNP-associated protein B similarity to muclear RNA binding proteins similarity to nuclear RNA binding proteins similarity to regulatory protein ADR1 similarity to snRNP proteins similarity to transcription factor Rpd3p similarity to transcription factor Rpd3p similarity to U2 snRNP protein A'snRNP-related protein strong similarity to RNA helicases of the DEAD box family strong similarity to RNA helicases of the DEAD strong similarity to RNA helicases of the DEAD box family strong similarity to small nuclear ribonucleoprotein D3 suppresses lethality of SSM4 deletion	YML017w YKR092c YKL005c YNR063w YJL124c YDR043c YIR018w YPR199c YBR239c YBR150c YGR067c YPL133c YER116c	PSP2 SRP40	strong similarity to Yox1p suppressor of DNA polymerase α mutation suppressor of mutant AC40 of RNA polymerase I and III weak similarity to D. melanogaster transcription elongation factor DmS-II weak similarity to CYC1/CYP3 transcription activator weak similarity to thuman Sm protein G weak similarity to thuman Sm protein G weak similarity to transcription activator Pdr4p weak similarity to transcription activator Pdr4p weak similarity to transcription factor Put3p weak similarity to transcription factor Put3p weak similarity to transcription factors	YLR185w YPR043w YJL189w YDR012w YPL131w YNL002c YGL076c YHL033c YLL045c YIL018w YFR031c-a YGL147c YNL067w YGR076c YJR094w-a YOR293w YDR025w YDR025w YDR025w YJR166c YJL191w YJL191w YJL190c YLR367w YPL103c YMR143w YDL083c YML083c YML024w	RPL35A  RPL46 RPL2B RPL1 RLP7 RPL6A RPL4B RPL5A RPL5A RPL5A RPL5B RPL9A RPL9B MRPL25  RPS18A RPS18B MRP2 CRY2 RPS24A RPS24B RPS16A RPS16B RPS16A RPS16B RPS16A	ribosomal riboso	protein protei	L37e L37a.e L39.e L4e.B L5e L7e L7e.A L7a.e.A L7a.e.B L8e L9e L9e L9e.co14 m (YML25), of the large subunit S10.e S11.e S11.e.B S14 S14 S15a.e.c.12 S16.e S16.e S17e.A
YLR067c  YAL016w  YOL042w  YER146w  YER029c  YER028c  YDR429c  YJR127c  YDL031w  YNL021w  YPR088c  YPL213w  YBL026w  YDL160c  YLR147c  YLR139c  RNA tra	AEP1 HRP1 PET309 TPD3  ZMS1  SNP3 DHH1 SMD3 SLS1 ensport	nuclear control of ATPase messenger RNA expression protein polyadenylated RNA-binding protein required for stability and translation of COX1 mRNA ser/thr phosphatase 2A, regulatory subunit A similarity to CCR4 protein similarity to human snRNP E similarity to human snRNP-associated protein B similarity to human snRNP-associated protein B similarity to muclear RNA binding proteins similarity to regulatory protein ADR1 similarity to RNA helicases similarity to transcription factor Rpd3p similarity to U2 snRNP protein A' snRNP-related protein strong similarity to RNA helicases of the DEAD box family strong similarity to small nuclear ribonucleoprotein D3 suppresses lethality of SSM4 deletion	YML017w YKR092c YKL005c YNR063w YJL124c YDR043c YIR018w YPR199c YBR239c YBR150c YGR067c YPL133c YER116c  Prote	PSP2 SRP40	strong similarity to Yox1p suppressor of DNA polymerase α mutation suppressor of mutant AC40 of RNA polymerase 1 and III weak similarity to <i>D. melanogaster</i> transcription elongation factor DmS-II weak similarity to CYC1/CYP3 transcription activator weak similarity to thuman Sm protein G weak similarity to <i>K. marxianus</i> Mig1 and other regulatory proteins weak similarity to transcription activator Pdr4p weak similarity to transcription activator Yap1p weak similarity to transcription factor Put3p weak similarity to transcription factors zinc-finger protein	YLR185W YPR043W YJL189W YDL131W YNL002c YGL076c YHL033c YLL045c YIL018W YFR031c-a YGL147c YNL067W YGR076c YJR094W-a YOR293W YDR025W YBR048W YDR025W YBR048W YJL191W YJL190c YLR367W YPL013c YMR143W YDL0383c YML024W YDL0383c YML024W YDR447c YDR447c YDR447c	RPL35A  RPL46 RPL2B RPL11 RLP7 RPL6A RPL4B RPL5A RPL9B MRPL26  RPS18A RPS18A RPS18B RPS18A RPS18B RPS16A RPS16B RPS16A RPS16B RPS16A RPS16B RP516A RP516B RP516A RP516B RP518A RP518B RP518A RPS28A	ribosomal riboso	protein protei	L37e L37ae L39ae L4e.B L5e L7e L7e.A L7ae.A L7ae.B L8e L9.e.C14 m (YML25), of the large subunit S11ae.B S14.B S14.B S15ae.c10 S15ae.c12 S16, mitochondrial S16ae S16e S17e.A S17e.A S17e.B S17e.B S17e.A S17e.B S18e
YLR067c  YAL016w  YOL042w  YER146w  YER029c  YER028c  YDR429c  YJR127c  YDL031w  YNL021w  YNL021w  YNL021w  YBL026w  YDL160c  YLR147c  YLR139c	AEP1 HRP1 PET309 TPD3  ZMS1  SNP3 DHH1 SMD3 SLS1 ensport	nuclear control of ATPase messenger RNA expression protein polyadenylated RNA-binding protein required for stability and translation of COX1 mRNA ser/thr phosphatase 2A, regulatory subunit A similarity to CCR4 protein similarity to human snRNP E similarity to human snRNP-associated protein B similarity to hug1p similarity to machine the similarity to RNA helicases similarity to snRNP proteins similarity to transcription factor Rpd3p similarity to RNA helicases of the DEAD box family strong similarity to small nuclear ribonucleoprotein D3 suppresses lethality of SSM4 deletion	YML017w YKR092c YKL005c YNR063w YJL124c YDR043c YIR018w YPR199c YBR239c YBR150c YGR067c YPL133c YER116c  Prote riboson YGR214w	PSP2 SRP40  SIN SYINAL PROTECTION OF THE PROTECT	strong similarity to Yox1p suppressor of DNA polymerase α mutation suppressor of mutant AC40 of RNA polymerase l and III weak similarity to <i>D. melanogaster</i> transcription elongation factor DmS-II weak similarity to CYC1/CYP3 transcription activator weak similarity to thurnan Sm protein G weak similarity to thurnan Sm protein G weak similarity to transcription activator Pdr4p weak similarity to transcription activator Pdr4p weak similarity to transcription activator Pdr4p weak similarity to transcription factor Put3p weak similarity to transcription factors zinc-finger protein	YLR185w YPR043w YJR189w YDR012w YPL131w YPL131w YPL31sw YH1032c YLL045c YIL045c YIL045c YIL067w YFR031c-a YGL147c YNL067w YGR076c YJR094w-a YOR293w YDR025w YDR025w YDR025w YJR196c YJL191w YJL1990c YLR367w YPL013c YMR143w YDL083c YMR143w YDL083c YMR143w YDL084w YDR447c YOL120c YML120c YML120c YML120c YML120c YML120c YML120c YML120c YML120c YML120c YML120c YML120c	RPL35A  RPL46 RPL2B RPL1 RLP7 RPL6A RPL4B RPL4B RPL5B RPL5A RPL5B RPL5A RPL5B RPL5A RPL5B RPL5A RPL5B RPL5A RPS18A RPS18B MRP2 CRY2 RPS24A RPS16B RPS24B RPS16A RPS16B RPS16A RPS16B RPS16B RPS16B RPS16B RPS16B RPS18B RPS18B	ribosomal riboso	protein protei	L37e L37ae L39ae L4e.B L5e L7e L7e.A L7ae.A L7ae.B L8e L9e L9e.c14 m (YML25), of the large subunit S10.e S11.e S14 S14 S15a.e.c12 S16, mitochondrial S16.e S17e.B S17e.B S17e.B S17e.B S17e.B S17e.B S18e.S18
YLR067c  YAL016w  YOL042w  YER146w  YER029c  YER028c  YDR429c  YJR127c  YDL031w  YNL021w  YPR068c  YPL213w  YBL026w  YDL160c  YLR147c  YLR139c  RNA tra  YGL097w  YMR235c	AEP1 HRP1 PET309 TPD3  ZMS1  SNP3 DHH1 SMD3 SLS1 EINSPORT SRM1 RNA1	nuclear control of ATPase messenger RNA expression protein polyadenylated RNA-binding protein required for stability and translation of COX1 mRNA ser/thr phosphatase 2A, regulatory subunit A similarity to CCR4 protein similarity to human snRNP E similarity to human snRNP-associated protein B similarity to human snRNP-associated protein B similarity to muclear RNA binding proteins similarity to regulatory protein ADR1 similarity to RNA helicases similarity to transcription factor Rpd3p similarity to RNA helicases of the DEAD box family strong similarity to small nuclear ribonucleoprotein D3 suppresses lethality of SSM4 deletion	YML017w YKR092c YKL005c YKL005c YNR063w YJL124c YDR043c YIR018w YPR199c YBR239c YBR150c YGR067c YPL133c YER116c  Prote riboson YGR214w YLR048w YCR031c	PSP2 SRP40 SRP40 NABIA NABIA NABIA CRY1	strong similarity to Yox1p suppressor of DNA polymerase α mutation suppressor of mutant AC40 of RNA polymerase land III weak similarity to D. melanogaster transcription elongation factor DmS-II weak similarity to CYC1/CYP3 transcription activator weak similarity to thuman Sm protein G weak similarity to thuman Sm protein G weak similarity to transcription activator Yap1p weak similarity to transcription activator Pdr4p weak similarity to transcription activator Yap1p weak similarity to transcription factor Put3p weak similarity to transcription factors zinc-finger protein	YLR185w YPR043w YJL189w YDR012w YPL131w YPL131w YNL002c YGL076c YHL033c YLL045c YIL018w YFR031c-a YGL147c YNL067w YGR076c YJR094w-a YOR293w YDR025w YBR048w YPR166c YJL191w YJL190c YLR367w YPL013c YMR1435w YDL033c YMR1435w YDL033c YML024w YDL024w YDR0447c YDL120c YML026c YDL121c	RPL35A  RPL46 RPL2B RPL1 RLP7 RPL6A RPL4A RPL4B RPL5B RPL9A RPL5B MRPL25  RPS18A RPS18B MRPL25  RPS16B RPS24A RPS24B RPS16B RPS16B RPS16B RPS16B RPS16B RPS16B RPS16B RPS18B	ribosomal riboso	protein protei	L37e L37ae L39ae L4e.B L5e L7e L7e.A L7ae.A L7ae.B L8e L9e L9e L9e S11e S11e S11e S11e S11e S15ae.c10 S16ae S16ae S17e S17e S18ae
YLR067c  YAL016w  YOL042w YER146w YER029c  YER028c YDR429c YJR127c YDL031w YNL147w YNL021w YPR068c YPL213w YBL026w YDL160c  YLR147c YLR139c  RNA tra YGL097w	AEP1 HRP1 PET309 TPD3  ZMS1  SNP3 DHH1 SMD3 SLS1 INSPORT	nuclear control of ATPase messenger RNA expression protein polyadenylated RNA-binding protein required for stability and translation of COX1 mRNA ser/thr phosphatase 2A, regulatory subunit A similarity to CCR4 protein similarity to human snRNP E similarity to human snRNP-associated protein B similarity to hugan snRNP-associated protein B similarity to nuclear RNA binding proteins similarity to regulatory protein ADR1 similarity to RNA helicases similarity to snRNP proteins similarity to snRNP proteins similarity to transcription factor Rpd3p similarity to U2 snRNP protein A'snRNP-related protein strong similarity to SNAP protein A'snRNP-related protein strong similarity to small nuclear ribonucleoprotein D3 suppresses lethality of SSM4 deletion	YML017w YKR092c YKL005c YNR063w YJL124c YDR043c YIR018w YPR199c YBR239c YBR150c YGR067c YPL133c YER116c  Prote riboson YGR214w YLR048w	PSP2 SRP40  SRP40  NAB1A NAB1B CRY1 RPS26 RPS26 RPS26 MRPL394	strong similarity to Yox1p suppressor of DNA polymerase α mutation suppressor of mutant AC40 of RNA polymerase 1 and III weak similarity to D. melanogaster transcription elongation factor DmS-II weak similarity to CYC1/CYP3 transcription activator weak similarity to thuman Sm protein G weak similarity to thuman Sm protein G weak similarity to transcription activator Pdr4p weak similarity to transcription activator Pdr4p weak similarity to transcription activator Yap1p weak similarity to transcription factor Put3p weak similarity to transcription factors zinc-finger protein	YLR185w YPR043w YJR189w YJL189w YDR012w YPL131w YNL002c YGL076c YHL033c YLL045c YIL045c YIL018w YFR031c-a YGL147c YNL067w YGR076c YJR094w-a YOR25w YDR025w YDR025w YDR025w YBR048w YPR166c YJL191w YJL191w YJL191w YJL190c YJL191w YDL03ac YMR143w YDL083c YMR145w YDL0847c YOL120c YMR1450w	RPL35A  RPL46 RPL2B RPL1 RPL7 RPL6A RPL4B RPL5B RPL5B RPL5A RPL5B RPL5B RPL5B RPL5B RPL5B RPL5B RPS24B RPS24B RPS24B RPS16B RPS24B RPS16B RPS1	ribosomal riboso	protein protei	L37e L37ae L37ae L39ae L4e.B L5e L7e L7e.A L7ae.A L7ae.B L8e L9e L9e L9e S11.e S11.e S114.e S15a.e.c10 S15a.e.c12 S16, mitochondrial S16.e S17e.B S18e S17e.B S18e S18e S18e S18e S18e S18e S18e S18e
YLR067c  YAL016w  YOL042w  YER146w  YER029c  YER028c  YDR429c  YJR127c  YDL031w  YNL021w  YNL021w  YPR068c  YPL213w  YBL026w  YDL160c  YLR147c  YLR139c  RNA tra  YGL097w  YMR235c  YOR1856  YLR293c	AEP1 HRP1 PET309 TPD3  ZMS1  SNP3 DHH1 SMD3 SLS1 ansport SRM1 RNA1 GSP2 GSP1	nuclear control of ATPase messenger RNA expression protein polyadenylated RNA-binding protein required for stability and translation of COX1 mRNA ser/thr phosphatase 2A, regulatory subunit A similarity to CCR4 protein similarity to human snRNP E similarity to human snRNP-associated protein B similarity to human snRNP-associated protein B similarity to muclear RNA binding proteins similarity to regulatory protein ADR1 similarity to RNA helicases similarity to RNA helicases similarity to transcription factor Rpd3p similarity to SRNA helicases of the DEAD box family strong similarity to small nuclear ribonucleoprotein D3 suppresses lethality of SSM4 deletion  GDP/GTP exchange factor for Gsp1p/Gsp2p GTPase activating protein GTP-binding protein of the ras superfamily	YML017w YKR092c YKL005c YKL005c YNR063w YJL124c YDR043c YIR018w YPR199c YBR239c YBR150c YGR067c YPL133c YER116c  Prote riboson YGR214w YLR048w YCR031c YGL189c YML009c YDL081c	PSP2 SRP40 SIN SYINAL PROTECTION SYINAL PROTECTION SYINAL PROTECTION SYINAL PROTECTION SYNAL PROTECTION SYNA	strong similarity to Yox1p suppressor of DNA polymerase α mutation suppressor of mutant AC40 of RNA polymerase l and III weak similarity to <i>D. melanogaster</i> transcription elongation factor DmS-II weak similarity to CYC1/CYP3 transcription activator weak similarity to thuman Sm protein G weak similarity to thuman Sm protein G weak similarity to transcription activator Yap1p weak similarity to transcription activator Pdr4p weak similarity to transcription activator Yap1p weak similarity to transcription factor Put3p weak similarity to transcription factors zinc-finger protein  **The State Stat	YLR185w YPR043w YPR043w YJL189w YDR012w YPL131w YNL002c YGL076c YHL033c YLL045c YIL018w YFR031c-a YGR147c YNL067w YGR076c YJR094w-a YOR293w YDR025w YDR025w YDR025w YDR025w YJR166c YJL191w YJL191w YJL190c YLR367w YPL013c YMR143w YDL03ac YML024w YDR0447c YOL120c YML026c YDL121c YNL030c YML026c YDL121c YNL030c YKR057w YJL136c	RPL35A  RPL46 RPL2B RPL1 RLP7 RPL6A RPL4B RPL5A RPL5A RPL5B MRPL25  RPS18A RPS18B MRPL25  RPS18B MRP2 RPS24A RPS18B RPS16A RPS16B RPS16B RPS16B RPS16B RPS16B RPS18EB	ribosomal riboso	protein protei	L37e L37ae L37ae L39.e L4e.B L5e L7e L7e.A L7ae.A L7ae.B L8e L9e L9e L9e L9e S11e S11e S11e S11e S15ae.c10 S15ae.c12 S16, mitochondrial S16e S17e.B S18e S18e S18e.C13 S18e.C13 S18e.C4 S19e.S S18e S18e.C13 S18e.C4 S19e.S
YLR067c  YAL016w  YOL042w YER146w YER029c  YER028c YDR429c YJR127c YDL031w YNL021w YNL021w YPR068e YPL213w YBL026w YDL160c  YLR147c  YLR139c  RNA tra YGL097w  YMR235c YOR185c YOR185c YUR293c YOR160w YGR158c	AEP1 HRP1 PET309 TPD3  ZMS1  SNP3 DHH1 SMD3 SLS1 ENSPORT SRM1 RNA1 GSP2 GSP1 MTR10 MTR3	nuclear control of ATPase messenger RNA expression protein polyadenylated RNA-binding protein required for stability and translation of COX1 mRNA ser/thr phosphatase 2A, regulatory subunit A similarity to CCR4 protein similarity to human snRNP E similarity to human snRNP-associated protein B similarity to human snRNP-associated protein B similarity to nuclear RNA binding proteins similarity to regulatory protein ADR1 similarity to RNA helicases similarity to snRNP proteins similarity to transcription factor Rpd3p similarity to U2 snRNP protein A' snRNP-related protein strong similarity to RNA helicases of the DEAD box family strong similarity to small nuclear ribonucleoprotein D3 suppresses lethality of SSM4 deletion  GDP/GTP exchange factor for Gsp1p/Gsp2p GTPase activating protein GTP-binding protein of the ras superfamily involved in mRNA transport involved in mRNA transport involved in mRNA transport	YML017w YKR092c YKL005c YNR063w YJL124c YDR043c YIR018w YPR199c YBR239c YBR150c YGR067c YPL133c YER116c  Prote riboson YGR214w YLR048w YCR031c YGL189c YML009c YDL081c YLR340w YDL130w	PSP2 SRP40  SRP40  SRP40  NABIA CRY1 RP526A  MRPL39 RPLA1 RPLA0 RPLA0 RPLA0 RPLA0	strong similarity to Yox1p suppressor of DNA polymerase α mutation suppressor of mutant AC40 of RNA polymerase l and III weak similarity to <i>D. melanogaster</i> transcription elongation factor DmS-II weak similarity to CYC1/CYP3 transcription activator weak similarity to thuman Sm protein G weak similarity to thuman Sm protein G weak similarity to thuman Sm protein G weak similarity to transcription activator Pdr4p weak similarity to transcription activator Yap1p weak similarity to transcription factor Put3p weak similarity to transcription factors zinc-finger protein  **The State of the S	YLR185W YPR043W YPR043W YDL131W YNL002c YGL076c YHL033c YLL045c YIL045c YIL018W YFR031c-a YGL147c YNL067W YFR031c-a YGL147c YNL067W YR025W YDR025W YDR025W YDR025W YDR025W YDR025W YDR025W YDR025W YDR025W YDR025W YDR025W YDR025W YDR025W YDR025W YDR025W YDR025W YDR025W YDR025W YDR030W YDL013c YMR143W YDL083c YML024W YDL120c YML026C YML036C YML	RPL35A  RPL46 RPL28 RPL17 RPL6A RPL4B RPL4B RPL5A RPL5A RPL9B MRPL25  RPS18A RPS18B MRP2C RY2 RPS16B RPS18B RPS28B RPS28B RPS28B	ribosomal riboso	protein protei	L37e L37ae L37ae L39ae L4e.B L5e L7e L7e.A L7ae.A L7ae.B L8e L8e L9e L9e L9e.C14 m (YML25), of the large subunit S10.e S11a.B S14 S15a.e.c10 S15a.e.c12 S16, mitochondrial S16e S17e.A S17e.B S18e.C3 S18e.C3 S18e.C3 S18e.C3 S18e.C3 S19.e S21e S21e S21e S21e S21e S22.e S23.e S23.e
YLR067c  YAL016w  YOL042w YER146w YER029c  YER028c YDR429c YER028c YDR429c YJR127c YDL031w YNL147w YNL021w YPR068c YL213w YBL026w YDL160c  YLR147c YLR139c  RNA tra YGL097w  YMR235c YOR186c YLR293c YOR160w	AEP1 HRP1 PET309 TPD3  ZMS1  SNP3 DHH1 SMD3 SLS1 EIRSPORT SRM1 GSP2 GSP1 MTR10	nuclear control of ATPase messenger RNA expression protein polyadenylated RNA-binding protein required for stability and translation of COX1 mRNA ser/thr phosphatase 2A, regulatory subunit A similarity to CCR4 protein similarity to CCR4 protein similarity to human snRNP E similarity to human snRNP-associated protein B similarity to hug1p similarity to muclear RNA binding proteins similarity to regulatory protein ADR1 similarity to RNA helicases similarity to transcription factor Rpd3p similarity to RNA helicases of the DEAD box family strong similarity to SRN4 deletion	YML017w YKR092c YKR092c YKL005c YNR063w YJL124c YDR043c YIR018w YPR199c YBR239c YBR150c YGR067c YPL133c YER116c  Prote riboson YGR214w YLR048w YCR031c YGR189c YML009c YDL081c YLR340w YDL130w YDL130w YDL130w YDL130w YDL130w YDL382w	PSP2 SRP40 SRP40 SRP40 NAB1A NAB1A NAB1A CRY1 RPS26A MRPL39 RPLA1 RPLA0 RPLA3 RPLA3 RPLA3 RPLA3 RPLA3	strong similarity to Yox1p suppressor of DNA polymerase α mutation suppressor of mutant AC40 of RNA polymerase I and III weak similarity to D. melanogaster transcription elongation factor DmS-II weak similarity to CYC1/CYP3 transcription activator weak similarity to thuran Sm protein G weak similarity to thuran Sm protein G weak similarity to transcription activator Pdr4p weak similarity to transcription activator Pdr4p weak similarity to transcription activator Pdr4p weak similarity to transcription factor Pur3p weak similarity to transcription factor Pur3p weak similarity to transcription factors incomplete in Since in Sinc	YLR185W YPR043W YPR043W YPR012W YPL131W YNL002c YGL076c YHL033c YLL045c YIL045c YIL045c YIL045c YIL045c YIL067W YFR031c-a YGL147c YNL067W YGR076c  YJR094W-a YOR293W YDR025W YBR048W YPR166c YJL191W YPL013c YMR143W YPL013c YMR143W YPL013c YMR143W YDL120c YMR057W YOL121c YKR057W YJL136c YGR118W YPR132W YFR132W YFR074W	RPL35A  RPL46 RPL2B RPL1 RLP7 RPL6A RPL4B RPL5A RPL5B RPL9A RPL9A RPL9B MRPL25  RPS18A RPS18B MRP2 CRY2 RPS24A RPS16B RPS24B RPS16A RPS16B RPS16B RPS18EB RPS18EB RPS18EB RPS18EB RPS18EB RPS18EB RPS18EB RPS28B RPS28B RPS28B	ribosomal riboso	protein protei	L37e L37ae L37ae L39ae L4e.B L5e L7e L7e.A L7ae.A L7ae.B L8e L9e L9e.c14 m (YML25), of the large subunit S10e S11a.B S14 S14as.c.12 S15ae.c.12 S16, mitochondrial S16ae S17a.B S18e S18e S18e S18e S18e S18e S18e S18e
YLR067c  YAL016w  YOL042w YER146w YER029c  YER028c YDR429c YJR127c YDL031w YNL021w YNL021w YPR088c YPL213w YBL026w YDL160c  YLR147c  YLR139c  RNA tra  YGL097w  YMR235c YOR188c YLR293c  YOR160w YGR168w YJL050w  YKL186c	AEP1 HRP1 PET309 TPD3  ZMS1  SNP3 DHH1 SMD3 SLS1 ENSPORT SRM1 RNA1 GSP2 GSP1 MTR10 MTR3 MTR4 MTR2	nuclear control of ATPase messenger RNA expression protein polyadenylated RNA-binding protein required for stability and translation of COX1 mRNA ser/thr phosphatase 2A, regulatory subunit A similarity to CCR4 protein similarity to human snRNP E similarity to human snRNP-associated protein B similarity to human snRNP-associated protein B similarity to muclear RNA binding proteins similarity to regulatory protein ADR1 similarity to RNA helicases similarity to transcription factor Rpd3p similarity to U2 snRNP protein A' snRNP-related protein strong similarity to RNA helicases of the DEAD box family strong similarity to small nuclear ribonucleoprotein D3 suppresses lethality of SSM4 deletion  GDP/GTP exchange factor for Gsp1p/Gsp2p GTPase activating protein GTP-binding protein of the ras superfamily involved in mRNA transport involved in nucleocytoplasmic transport of mRNA mRNA transport protein	YML017w YKR092c YKL005c YNR063w YJL124c YDR043c YIR018w YPR199c YBR139c YBR130c YGR067c YPL133c YER116c  Prote riboson YGR214w YLR048w YCR031c YGL189c YML009c YDL081c YLR340w YDL330w YDR382w YOL039w YOR369c	PSP2 SRP40 SRP40 SRP40 NAB1A NAB1A NAB1A CRY1 RPS26A MRPL39 RPLA1 RPLA0 RPLA3 RPLA3 RPLA3 RPLA3 RPLA3	strong similarity to Yox1p suppressor of DNA polymerase α mutation suppressor of mutant AC40 of RNA polymerase land III weak similarity to D. melanogaster transcription elongation factor DmS-II weak similarity to CYC1/CYP3 transcription activator weak similarity to thuman Sm protein G weak similarity to thuman Sm protein G weak similarity to transcription activator Yap1p weak similarity to transcription activator Pdr4p weak similarity to transcription activator Yap1p weak similarity to transcription factor Put3p weak similarity to transcription factors zinc-finger protein  **The State S	YLR185W YPR043W YPR043W YPR012W YPL131W YPL131W YPL131W YPL131W YPL131W YFR031c-a YGL147c YGL147c YGL076c  YJR094W-a YOR293W YDR025W YDR025W YDR025W YDR025W YDR025W YBR048W YPR166c YJL191W YJL190c YLR367W YPL013c YMR143W YDL033c YMR143W YDL033c YMR145W YDL033c YML024W YDL025C YML026C YML026C YML026C YML026C YML030c YML030c YML030c YML030c YML030c YML030c YML030c YML030c YML030c YML136C YGR118W YER074W YJL136C YGR118W YER074W YJL136C YGR118W YER074W YJL069c YLR3333c	RPL35A  RPL46 RPL2B RPL17 RPL61 RPL17 RPL64 RPL4B RPL4B RPL5B RPL93A RPL5B MRPL25  RPS18A RPS18B MRPL25  RPS16B RPS18B RPS16B RPS18B RPS1B R	ribosomal riboso	protein protei	L37e L37ae L37ae L39ae L4e.B L5e L7e L7e.A L7ae.A L7ae.B L8e L9e L9e L9e L9e S11e S11e S11e S11e S11e S11e S11e S1
YLR067c  YAL016w  YOL042w  YER146w  YER029c  YER028c  YDR429c  YJR127c  YDL031w  YNL021w  YNL021w  YNL021w  YNL021w  YR160c  YLR147c  YLR139c  RNA tra  YGL097w  YMR235c  YOR185c  YLR293c  YOR160w  YGR158c  YJL050w  YKL186c  YKL086w	AEP1 HRP1 PET309 TPD3  ZMS1  ZMS1  SNP3 DHH1 SMD3 SLS1 INSPORT SRM1 RNA1 GSP2 GSP1 MTR10 MTR3 MTR4 NUP100	nuclear control of ATPase messenger RNA expression protein polyadenylated RNA-binding protein required for stability and translation of COX1 mRNA ser/thr phosphatase 2A, regulatory subunit A similarity to CCR4 protein similarity to human snRNP E similarity to human snRNP E similarity to human snRNP-associated protein B similarity to nuclear RNA binding proteins similarity to nuclear RNA binding proteins similarity to nuclear RNA binding proteins similarity to snRNP proteins similarity to snRNP proteins similarity to transcription factor Rpd3p similarity to transcription factor Rpd3p similarity to U2 snRNP protein A' snRNP-related protein strong similarity to SnNA belicases of the DEAD box family strong similarity to small nuclear ribonucleoprotein D3 suppresses lethality of SSM4 deletion  GDP/GTP exchange factor for Gsp1p/Gsp2p GTPase activating protein GTP-binding protein GTP-binding protein GTP-binding protein GTP-binding protein of the ras superfamily involved in mRNA transport involved in mRNA transport involved in mRNA transport of mRNA mRNA transport protein	YML017w YKR092c YKL005c YNR063w YJL124c YDR043c YIR018w YPR199c YBR239c YBR150c YGR067c YPL133c YER116c Prote riboson YGR214w YLR048w YCR031c YGL189c YML009c YDL081c YLR340w YDL130w YDL130w YDR382w YOL039w YOR369c YGL0686w	PSP2 SRP40  NAB1A NAB1B CRY1 RPS26A MRPL39A RPLA1 RPLA3 RPLA3 RPLA4 RPLA2	strong similarity to Yox1p suppressor of DNA polymerase α mutation suppressor of mutant AC40 of RNA polymerase l and III weak similarity to <i>D. melanogaster</i> transcription elongation factor DmS-II weak similarity to thorus many stranscription activator weak similarity to thorus Mig1 and other regulatory proteins weak similarity to transcription activator Pdr4p weak similarity to transcription factor Put3p weak similarity to transcription factors along the similarity to transcription factors weak simi	YLR185w YPR043w YPR043w YDR012w YPL131w YPL131w YPL311w YPL311w YPL032c YLL045c YIL045c YIL045c YIL045c YIL067w YGR076c YJR094w-a YOR293w YDR025w YDR025w YDR025w YDR025w YDR025w YDR025w YDR025w YDR025w YDR025w YDR025w YDR025w YDR025w YDR025w YDR025w YDR025w YDR025w YDR025w YDR025w YDR025w YDR166c YJL191w YDL131c YDL120c YMR143w YDL120c YML024w YDL121c YML026c YDR450w YOL121c YKR057w YJL136c YJL136c YGR118w YPR132w YER074w YIL069c YLR333c YGR027c	RPL35A  RPL46 RPL2B RPL17 RPL6A RPL4B RPL4B RPL5B RPL5B RPL5B RPL5A RPL5B RPL5B RPL5B RPL5B RPL5B RPS2B RPS2B RPS2B RPS1BA RPS1BB RPS2B RPS1BB RPS1BB RPS2B RPS1BB	ribosomal riboso	protein protei	L37e L37ae L37ae L39ae L4e.B L5e L7e L7e.A L7ae.A L7ae.B L8e L9e L9e L9e S11.e S11.e S114.e S15a.e.c10 S15a.e.c12 S16, mitochondrial S16.e S17e.B S18.e S18.e S18.e S18.e S18.e S19.e S19.e S21.e S22.e S22.e S24.e S24.e S24.e S24.e
YLR067c  YAL016w  YOL042w  YER146w  YER029c  YER028c  YDR429c  YJR127c  YDL031w  YNL021w  YPR088c  YPL213w  YBL026w  YDL160c  YLR147c  YLR139c  RNA tra  YGL097w  YMR235c  YOR186c  YLR293c  YOR160w  YGR188c  YJL050w  YKL186c  YKL166c  YKL166c  YKL068w  YKL1667c  YKR082vw	AEP1 HRP1 PET309 TPD3  ZMS1  SNP3 DHH1 SMD3 SLS1 INSPORT SRM1 RNA1 GSP2 GSP1 MTR10 MTR3 MTR4  MTR2 NUP100 NUP130 NUP133	nuclear control of ATPase messenger RNA expression protein polyadenylated RNA-binding protein required for stability and translation of COX1 mRNA ser/thr phosphatase 2A, regulatory subunit A similarity to CCR4 protein similarity to human snRNP E similarity to human snRNP-associated protein B similarity to human snRNP-associated protein B similarity to nuclear RNA binding proteins similarity to regulatory protein ADR1 similarity to RNA helicases similarity to transcription factor Rpd3p similarity to U2 snRNP protein A' snRNP-related protein strong similarity to RNA helicases of the DEAD box family strong similarity to small nuclear ribonucleoprotein D3 suppresses lethality of SSM4 deletion  GDP/GTP exchange factor for Gsp1p/Gsp2p GTPase activating protein GTP-binding protein of the ras superfamily involved in mRNA transport involved in mRNA transport involved in nuclear pore protein nuclear pore protein nuclear pore protein	YML017w YKR092c YKL005c YNR063w YJL124c YDR043c YIR018w YPR199c YBR239c YBR150c YGR067c YGR067c YGR016s Prote riboson YGR214w YLR048w YCR031c YGL189c YML009c YDL081c YLR340w YDL330w YDR382w YOL039w YOR369c YGL068w YLR325c YFL0344c-a	PSP2 SRP40  NAB1A NAB1B CRY1 RPS26A MRPL39A RPLA1 RPLA3 RPLA3 RPLA4 RPLA2	strong similarity to Yox1p suppressor of DNA polymerase α mutation suppressor of mutant AC40 of RNA polymerase l and III weak similarity to <i>D. melanogaster</i> transcription elongation factor DmS-II weak similarity to CYC1/CYP3 transcription activator weak similarity to thuran Sm protein G weak similarity to thuran Sm protein G weak similarity to transcription activator weak similarity to transcription activator Pdr4p weak similarity to transcription activator Pdr4p weak similarity to transcription activator Pdr4p weak similarity to transcription factor Put3p weak similarity to transcription factors aveak similarity to transcription factors weak	YLR185W YPR043W YPR043W YPR012W YPL131W YNL002c YGL076c YHL033c YLL045c YIL045c YIL045c YIL045c YIL045c YIL067W YFR031c-a YGR147c YNL067W YDR025W YDR026C YIL191W YDL036c YMR143W YDL024W YDR447C YOL120c YML026c YDR450W YDL121c YNL0302c YKR057W YUL136c YGR118W YPR132W YPR132W YR074W YIL069sc YLR3333c YGR027C YER131W YKL1566W	RPL35A  RPL46 RPL2B RPL1 RLP7 RPL6A RPL4B RPL5A RPL5B RPL9A RPL5B MRPL25  RPS18A RPS18B MRPL25  RPS18A RPS18B MRP2 RPS24A RPS18B RPS16A RPS16B RPS16B RPS16B RPS16B RPS18EB RP	ribosomal riboso	protein protei	L37e L37ae L37ae L39ae L4e.B L5e L7e L7e.A L7ae.A L7ae.B L8e L9e L9e L9e L9e S11e S11e S11e S11e S11e S15ae.c10 S15ae.c12 S16ae S17e.A S17e.B S18e S18e S18e S18e S18e S18e S18e S18e
YLR067c  YAL016w  YOL042w YER146w YER029c  YER028c YDR429c YJR127c YDL031w YNL147w YNL021w YPR068c YLR147c  YLR139c  RNA tra YGL097w  YMR236c YOR185c YOR186c YCR185c YOR185c YJL050w YKL186c YKL186c YKL186c YKL186c YKL1866 YKL1866 YKL1866 YKL1866 YKL1866 YKL1866	AEP1 HRP1 PET309 TPD3  ZMS1  SNP3 DHH1 SMD3 SLS1 ENSPORT SRM1 RNA1 GSP1 MTR10 MTR3 MTR4 MTR2 NUP145 NUP145 NUP145 NUP145 NUP145	nuclear control of ATPase messenger RNA expression protein polyadenylated RNA-binding protein required for stability and translation of COX1 mRNA ser/thr phosphatase 2A, regulatory subunit A similarity to CCR4 protein similarity to human snRNP E similarity to human snRNP E similarity to human snRNP-associated protein B similarity to nuclear RNA binding proteins similarity to regulatory protein ADR1 similarity to regulatory protein ADR1 similarity to RNA helicases similarity to snRNP proteins similarity to snRNP proteins similarity to transcription factor Rpd3p similarity to transcription factor Rpd3p similarity to transcription factor Rpd3p similarity to U2 snRNP protein A'snRNP-related protein strong similarity to SnRNP protein at strong similarity to small nuclear ribonucleoprotein D3 suppresses lethality of SSM4 deletion  GDP/GTP exchange factor for Gsp1p/Gsp2p GTPase activating protein GTP-binding protein GTP-binding protein GTP-binding protein GTP-binding protein in TP-binding protein in TP-binding protein in TRNA transport involved in mRNA transport involved in mRNA transport involved in mRNA transport protein nuclear pore protein	YML017w YKR092c YKL005c YNR063w YJL124c YDR043c YIR018w YPR199c YBR239c YBR150c YGR067c YPL133c YER116c  Prote riboson YGR214w YCR031c YGL189c YML009c YDL081c YGL189c YML009c YDL031c YGR326w YDR382cw YDR382cw YDR382cw YOR369c YGL068w YOR369c YGL068w YUR325c	PSP2 SRP40  NAB1A NAB1B CRY1 RPS26A MRPL39A RPLA1 RPLA3 RPLA3 RPLA4 RPLA2	strong similarity to Yox1p suppressor of DNA polymerase α mutation suppressor of mutant AC40 of RNA polymerase 1 and III weak similarity to <i>D. melanogaster</i> transcription elongation factor DmS-II weak similarity to thuman Sm protein G weak similarity to thuman Sm protein G weak similarity to thuman Sm grotein G weak similarity to transcription activator Pdr4p weak similarity to transcription activator Pdr4p weak similarity to transcription activator Pdr4p weak similarity to transcription activator Pap1p weak similarity to transcription factor Put3p weak similarity to transcription factors weak similari	YLR.185W YPR043W YPR043W YPR012W YPL131W YNL002c YGL076c YHL033c YLL045c YIL045c YIL045c YIL045c YIL045c YIR094W-a YGR076c  YJR094W-a YOR293W YDR025W YR166c YJL191W YJL190c YLR367W YPL013c YMR143W YPL013c YMR143W YDR120c YMR165C YDR450W YOL121c YML026c YDR450W YOL121c YML026c YDR450W YOL121c YKR057W YJL136C YJR132W YR132W YR1069c YLR333C YGR027C YER131W YKL156W YHR021c	RPL35A  RPL46 RPL2B RPL18 RPL1 RLP7 RPL6A RPL4B RPL4B RPL5B RPL9B MRPL25  RPS18A RPS18B MRPL25  RPS18B MRP2 RPS24A RPS18B RP516A RPS16B RP516A RP516B RP516A RP516B RP516A RP516B RP516A RP518EB RP516A RP516B RP518EB	ribosomal riboso	protein protei	L37e L37ae L37ae L39ae L4e.B L5e L7e.A L7ae.A L7ae.B L8e L9e L9e L9e.C14 m (YML25), of the large subunit S10.e S11a.B S14 S15a.e.c10 S15a.e.c12 S16, mitochondrial S16e S17e.A S17e.B S18.e.C3 S18.e.C4 S18.e.C3 S18.e.C4 S18.e.C3 S18.e.C4 S19.e S21e S21e S21e S21e S21e S22e S25e.C7 S26e-C5 S27e S27e
YLR067c  YAL016w  YOL042w  YER146w  YER029c  YER028c  YDR429c  YJR127c  YDL031w  YNL021w  YPR068c  YPL13w  YBL026w  YDL160c  YLR147c  YLR139c  RNA tra  YGL097w  YMR235c  YOR185c  YUR293c  YOR160w  YKL186c  YKL067c  YKL068w  YKL067c  YKR082w  YGL092w  YGL092w  YGL192w  YGL192w  YGL192w  YGL192w  YGL192w  YGL192w  YGL172w	AEP1 HRP1 PET309 TPD3  ZMS1  ZMS1  SNP3 DHH1  SMD3 SLS1 INSPORT  SRM1 RNA1 GSP2 GSP1 MTR10 MTR3 MTR4 MTR2 NUP100 NUP120 N	nuclear control of ATPase messenger RNA expression protein polyadenylated RNA-binding protein required for stability and translation of COX1 mRNA ser/thr phosphatase 2A, regulatory subunit A similarity to CCR4 protein similarity to human snRNP E similarity to human snRNP E similarity to human snRNP-associated protein B similarity to nuclear RNA binding proteins similarity to regulatory protein ADR1 similarity to regulatory protein ADR1 similarity to regulatory protein ADR1 similarity to transcription factor Rpd3p similarity to transcription factor Rpd3p similarity to transcription factor Rpd3p similarity to U2 snRNP protein A snRNP-related protein strong similarity to SNA helicases of the DEAD box family strong similarity to small nuclear ribonucleoprotein D3 suppresses lethality of SSM4 deletion  GDP/GTP exchange factor for Gsp1p/Gsp2p GTPase activating protein GTP-binding protein GTP-binding protein GTP-binding protein of the ras superfamily involved in mRNA transport involved in mRNA transport involved in nuclear pore protein	YML017w YKR092c YKR092c YKL005c YNR063w YJL124c YDR043c YIR018w YPR199c YBR239c YBR150c YGR067c YPL133c YER116c  Prote riboson YGR214w YLR048w YCR031c YGL189c YML009c YDL031c YLR340w YDL130w YDL130w YDR382w YOL039kw YOR369c YGL068w YLR325c YFL034c-a YFR032c-a YFR032c-a YLR061w YMR142c	PSP2 SRP40 SRP40  NAB1A NAB1A NAB1A CRY1 RPS26A MRPL39/ RPLA0 RPLA1 RPLA0 RPLA2 RPLA2 RS12	strong similarity to Yox1p suppressor of DNA polymerase α mutation suppressor of mutant AC40 of RNA polymerase l and III weak similarity to <i>D. melanogaster</i> transcription elongation factor DmS-II weak similarity to CYC1/CYP3 transcription activator weak similarity to thuman Sm protein G weak similarity to thuman Sm protein G weak similarity to transcription activator weak similarity to transcription activator Pdr4p weak similarity to transcription activator Pdr4p weak similarity to transcription activator Pdr4p weak similarity to transcription factor Put3p weak similarity to transcription factors weak s	YLR185W YPR043W YPR043W YPR012W YPL131W YNL002c YGL076c YHL033c YLL045c YIL045c YIL045c YIL045c YIL045c YIL045c YIL067W YFR031c-a YGL147c YGR076c  YJR094W-a YOR293W YDR025W YBR048W YPR166c YJL191W YJL191W YJL191W YJL191W YPL013c YMR143W YPL013c YMR143W YPL013c YMR143W YPL013c YMR057W YOL121c YNL302c YKR057W YJL136c YGR118W YPR132W YFR074W YJL136c YGR118W YPR021c YCR064W YHR021c YDR064W YHR021c YDR064W YHR021c YDR064W YHR021c	RPL35A  RPL46 RPL2B RPL1 RLP7 RPL6A RPL4B RPL4B RPL5B RPL9A RPL5B RPL9A RPL9B MRPL25  RPS18A RPS18B MRP2 CRY2 RPS24A RPS16B RPS16B RPS16B RPS16B RPS18EA RP516B RPS18EA RP51B RPS18EA RP55B RPS28B RPS28B RPS28B RPS28B RPS28A RP55B RPS28A RP55B RPS28A RP55B RPS28A RP55B RPS28A RP55B RPS27B RPS28A RP55B RPS27B RPS27B RPS31B RPS31A RPS27B RPS31B RPS31A RPS27B RPS31B RPS31A RPS27B RPS31B	ribosomal riboso	protein protei	L37e L37ae L37ae L39ae L4e.B L5e L7e L7e.A L7ae.A L7ae.B L8e L9e L9e L9e L9e.c14 m (YML25), of the large subunit S10e S11ae S11ae S14 S15ae.c12 S16ae.c12 S16ae.c13 S16ae.c13 S16ae.c13 S16ae.c13 S17e.B S18ae.c13 S18ae.c4 S19ae S18ae.c4 S19ae S18ae.c4 S19ae S21e S21e S21e S21e S23ae S24e S24e S24e S24e S25e.c7 S26e-c5 S27e S27e S27e S27e S27e S27e S27e S27e
YLR067c  YAL016w  YOL042w YER146w YER029c  YER028c YDR429c YJR127c YDL031w YNL021w YNL021w YPR088c YPL213w YBL026w YDL160c  YLR147c  YLR139c  RNA tra  YGL097w  YMR235c YOR185c YOR185c YUR293c YOR160w YKL160c YKL186c YKL068w YKL0657c YKR082w YGL092w YJL061w YDR192c YGL172w YJD161w YDR4322w YDR4322w	AEP1 HRP1 PET309 TPD3  ZMS1  SNP3 DHH1 SMD3 SLS1 ENSPORT SRM1 RNA1 GSP2 GSP1 MTR10 MTR3 MTR4  MTR2 NUP133 NUP142 NUP133 NUP142 NUP29 NUP49 NUP82 NUP49 NUP82 NPL3	nuclear control of ATPase messenger RNA expression protein polyadenylated RNA-binding protein required for stability and translation of COX1 mRNA ser/thr phosphatase 2A, regulatory subunit A similarity to CCR4 protein similarity to human snRNP E similarity to human snRNP-associated protein B similarity to human snRNP-associated protein B similarity to regulatory protein ADR1 similarity to regulatory protein ADR1 similarity to RNA helicases similarity to snRNP proteins similarity to snRNP proteins similarity to transcription factor Rpd3p similarity to U2 snRNP protein A' snRNP-related protein strong similarity to RNA helicases of the DEAD box family strong similarity to small nuclear ribonucleoprotein D3 suppresses lethality of SSM4 deletion  GDP/GTP exchange factor for Gsp1p/Gsp2p GTPase activating protein GTP-binding protein of the ras superfamily involved in mRNA transport involved in mRNA transport involved in mRNA transport involved in nucleacytoplasmic transport of mRNA mRNA transport protein nuclear pore protein	YML017w YKR092c YKL005c YKL005c YNR063w YJL124c YDR043c YIR018w YPR199c YBR150c YGR07c YPL133c YER116c  Prote riboson YGR214w YLR048w YCR031c YGL189c YML009c YDL081c YLR340w YDL330w YDL330w YDL330w YDR382w YOL039w YOL039w YOL039w YOL039w YOL039w YOL039w YOL039w YOR036c YFL034c-a YFR032c-a YFR032c-a YFR032c-a YFR032c-a YLR061w YMR142c YPL183w-c YPL183w-c YPL183w-c YR183w-c YR183w-c YR187bw	PSP2 SRP40  SRP40  SRP40  SRP40  NAB1A NAB1A CRY1 RP526 AMRPL39 RPLA1 RPLA0 RPLA3 RPLA4 RPLA2 RS12  GRC5	strong similarity to Yox1p suppressor of DNA polymerase α mutation suppressor of mutant AC40 of RNA polymerase land III weak similarity to D. melanogaster transcription elongation factor DmS-II weak similarity to CYC1/CYP3 transcription activator weak similarity to thuman Sm protein G weak similarity to thuman Sm protein G weak similarity to transcription activator Pdr4p weak similarity to transcription activator Pdr4p weak similarity to transcription activator Pdr4p weak similarity to transcription factor Put3p weak similarity to transcription factor Put3p weak similarity to transcription factors weak s	YLR185W YPR043W YPR043W YPR012W YPL131W YPL131W YPL131W YPL131W YPL131W YFR031c-a YGL147c YGL147c YGL076c  YJR094W-a YOR293W YDR025W YBR048W YPR166c YJL191W YJL190c YLR367W YPL013c YMR145W YPL013c YML024W YDR047C YOL120c YML026c YDR050W YDR132W YDR057W YLS057W YLS057W YLS057W YLS05W YR132W YER074W YLS06W YHR021c YLR3333C YGR027C YER131W YKL156W YHR021c YDR064W YLR264W YOR167c YLR388W	RPL35A  RPL46 RPL2B RPL17 RPL61 RPL17 RPL64 RPL4B RPL4B RPL5B RPL5B RPL93A RPL5B MRPL25  RPS18A RPS18B MRPL25  RPS166A RPS16B RPS18BB RPS16B RPS18BB RPS16B RPS18BB RPS1BBB RPS1BBBB RPS1BBB RPS1BBBB RPS1BBB RPS1BBB RPS1BBB RPS1BBB RPS1BBB RPS1BBB RPS1BBBB RPS1BB	ribosomal riboso	protein protei	L37e L37ae L37ae L37ae L37ae L39e L4e.B L5e L7e L7e.A L7ae.A L7ae.B L8e L9e L9e L9e L9e S11e S11e S11e S11e S11e S11e S11e S1
YLR067c  YAL016w  YOL042w YER146w YER029c  YER028c YJR127c YJL031w YNL147w YNL021w YPR068c YPL213w YBL026w YLR147c YLR139c  RNA tra YGL097w  YMR235c YOR160w YGR158c YJL050w YKL186c YKL066w YKL186c YKL066w YKL057c YKR082w YGL092w YDR192c YGR192c YGR192c YGR192c YGR192c YGR192c YGR192c	AEP1 HRP1 PET309 TPD3  ZMS1  ZMS1  SNP3 DHH1  SMD3 SLS1  INSPORT  SRM1  RNA1 GSP2 GSP1  MTR10 MTR3 MTR4 NUP100 NUP120 NUP120 NUP120 NUP120 NUP145 NUP42 NUP43 NUP82 NPL3 NAB2	nuclear control of ATPase messenger RNA expression protein polyadenylated RNA-binding protein required for stability and translation of COX1 mRNA ser/thr phosphatase 2A, regulatory subunit A similarity to CR4 protein similarity to human snRNP E similarity to human snRNP E similarity to human snRNP-associated protein B similarity to nuclear RNA binding proteins similarity to regulatory protein ADR1 similarity to regulatory protein ADR1 similarity to regulatory protein ADR1 similarity to RNA helicases similarity to snRNP proteins similarity to transcription factor Rpd3p similarity to transcription factor Rpd3p similarity to U2 snRNP protein A'snRNP-related protein strong similarity to SnANP protein A'snRNP-related protein strong similarity to small nuclear ribonucleoprotein D3 suppresses lethality of SSM4 deletion  GDP/GTP exchange factor for Gsp1p/Gsp2p GTPase activating protein GTP-binding protein GTP-binding protein GTP-binding protein of the ras superfamily involved in mRNA transport involved in mRNA transport involved in mRNA transport involved in mRNA transport involved in nuclear pore protein	YML017w YKR092c YKL005c YNR063w YJL124c YDR043c YIR018w YPR199c YBR239c YBR150c YGR067c YPL133c YER116c  Prote riboson YGR214w YLR048w YCR031c YGL189c YML009c YDL30w YDL30w YDL30w YDL30w YDR382w YOL039w YOL039w YOL039w YOL039w YOL039w YOL039w YOL039w YLR041w YMR142c YFL183w=2 YLR061w YMR142c YPL183w=2	PSP2 SRP40 SRP40 NAB1A NAB1B CRY1 RP526A MRPL39A RPLA1 RPLA3 RPLA4 RPLA2 RS12	strong similarity to Yox1p suppressor of DNA polymerase α mutation suppressor of mutant AC40 of RNA polymerase land III weak similarity to <i>D. melanogaster</i> transcription elongation factor DmS-II weak similarity to CYC1/CYP3 transcription activator weak similarity to CYC1/CYP3 transcription activator weak similarity to thuman Sm protein G weak similarity to transcription activator Pdr4p weak similarity to transcription activator Pdr4p weak similarity to transcription activator Pdr4p weak similarity to transcription factor Pur3p weak similarity to transcription factor Pur3p weak similarity to transcription factors weak similarity to transcripti	YLR.185W YPR043W YPR043W YPR012W YPL131W YNL002C YGL076C YHL033C YLL045C YIL045C YIL045C YIL045C YIL045C YIR094W-a YGR076C  YJR094W-a YOR293W YDR025W YR166C YJL191W YJL190C YLR367W YJL190C YMR057W YJL136C YDR045W YR132W YR1333C YGR113W YR1333C YGR113W YKL156W YR1333C YGR027C YGR113W YKL156W YHR021C YDR064W YLR264W YCR167C	RPL35A  RPL46 RPL2B RPL17 RPL6A RPL18 RPL18 RPL4B RPL4B RPL5B RPL9A RPL9A RPL9A RPL9B RPL9A RPS18A RPS18B RPS18A RPS18B RPS16B RPS24A RPS16B RPS16B RPS18EB RP	ribosomal riboso	protein protei	L37e L37e L37ae L39e L4e.B L5e L7e L7e.A L7ae.A L7ae.B L8e L9e L9e.c14 m (YML25), of the large subunit S10.e S11.e S14.e S16ae.c12 S16.mitochondrial S16e S17e.B S18e.c13 S18e.c4 S17e.B S18e.C13 S17e.B S18e.C13 S17e.B S18e.C13 S17e.B S18e.C13 S18e.C3 S18e.C3 S18e.C3 S18e.C3 S18e.C3 S18e.C3 S18e.C3 S2e.C3 S2

	RP10A RP10B	ribosomal protein S3a.e ribosomal protein S3a.e	YLR289w	GUF1	strong similarity to E. coli elongation factor-type GTP-binding protein lepa	tRNA sy	ntheta	ses
YJR145c	RPS7B	ribosomal protein S4.e.c10	YDL084w		strong similarity to nuclear RNA helicase		ALA1	alanyl-tRNA synthetase, cytosolic
YHR203c YBR251w	RPS7A MRPS5	ribosomal protein S4.e.c8 ribosomal protein S5, mitochondrial	YDR021w		(DEAD family) strong similarity to translation initiation	YHR091c YCR024c	MSR1	arginyl-tRNA synthetase, mitochondrial asn-tRNA synthetase, mitochondrial
YJR123w	RPS5	ribosomal protein S5.e		0004	factor eIF4A	YHR019c	DED81	asparaginyl-tRNA-synthetase
YBR181c YPL090c	RPS101 RPS10B	ribosomal protein S6.e ribosomal protein S6.e	YKL010c YLR005w	SOS1 SSL1	suppressor of sis1 TFIIH subunit (transcription initiation	YPL104w YLL018c	MSD1 DPS1	aspartate-tRNA ligase, mitochondrial aspartyl-tRNA synthetase, cytosolic
YBL072c	RPS8A	ribosomal protein S8.e			factor), factor B	YOR168w	GLN4	glutaminyl-tRNA synthetase
YER102w YBR146w	RPS8B MRPS9	ribosomal protein S8.e ribosomal protein S9, mitochondrial	YKR084c	HBS1	translation elongation factor eEF1 α subunit homologue	YOL033w YBR121c	MSE1 GRS1	glutamyl-tRNA synthetase, mitochondrial glycine-tRNA ligase
YPL081w	RPS13B	ribosomal protein S9.e.A	YPR080w	TEF1	translation elongation factor eEF1	YPR033c	HTS1	histidine-tRNA ligase, mitochondrial
YBR189w YGR085c	SUP46 RPL16B	ribosomal protein S9.e.B ribosomal protein YL16.B	YBR118w	TEF2	α-A subunit, cytosolic translation elongation factor eEF1	YPL040c YBL076c	ISM1 ILS1	isoleucine-tRNA ligase, mitochondrial isoleucyl-tRNA synthetase
YKR006c	MRPL13	ribosomal protein YmL13, mitochondrial			α-A subunit, cytosolic	YPL160w	CDC60	leucine-tRNA ligase, cytosolic
	MRPL2 MRPL20	ribosomal protein YmL2, mitochondrial ribosomal protein YmL20, mitochondrial	YPL048w	CAM1	translation elongation factor eEF1, α subunit	YLR382c YDR037w	NAM2 KRS1	leucine-tRNA ligase, mitochondrial lysyl-tRNA synthetase, cytosolic
YBR282w		ribosomal protein YmL27, mitochondrial	YKL081w	TEF4	translation elongation factor eEF1,		MSK1	lysyl-tRNA synthetase, mitochondrial
YDR462w YNL252c		ribosomal protein YmL28, mitochondrial ribosomal protein YmL30, mitochondrial	VALOODA	EFB1	γ subunit	YGR264c YGR171c	MES1 MSM1	methionyl-tRNA synthetase methionyl-tRNA synthetase
	MRPL31	ribosomal protein YmL30, mitochondrial	YAL003w YOR133w	EFT1	translation elongation factor eEF1β translation elongation factor eEF2	YPR047w	MSF1	phenylalanine-tRNA ligase α subunit,
YCR003w		ribosomal protein YmL32, mitochondrial	YDR385w		translation elongation factor eEF2	VEL 000+	FRS2	mitochondrial
	MRPL36 MRPL37	ribosomal protein YmL36, mitochondrial ribosomal protein YmL37, mitochondrial	YLR249w YNL014w	YEF3	translation elongation factor eEF3 translation elongation factor eEF3	YFL022c	FR52	phenylalanine-tRNA ligase β subunit, cytosolic
/PL173w	1400/44	ribosomal protein YmL40, mitochondrial	VAII 400 -		homologue	YLR060w	FRS1	phenylalanyl-tRNA synthetase, α subunit,
YMR225c YPL249c-a		ribosomal protein YmR44, mitochondrial ribosomal protein, cytoplasmic	YNL163c YLR069c	MEF1	translation elongation factor eEF4 translation elongation factor G,	YHR011w		cytosolic seryl-tRNA synthetase
YML025c		ribosomal protein, mitochondrial			mitochondrial	YDR023w	SES1	seryl-tRNA synthetase, cytosolic
YDR347w YGR084c		ribosomal protein, mitochondrial ribosomal protein, mitochondrial	YOR187w	TUF1	translation elongation factor TU, mitochondrial	YNL247w YER087w		similarity to cysteinyl-tRNA synthetases similarity to E. coli prolyl-tRNA synthetase
YKL003c	MRP17	ribosomal protein, mitochondrial	YJL102w	MEF2	translation elongation factor,	YDR341c		strong similarity to arginine-tRNA ligase
YDR405w YHL004w		ribosomal protein, mitochondrial ribosomal protein, mitochondrial	YOL023w	IFM1	mitochondrial translation initiation factor 2, mitochondrial			and mitochondrial arginyl-tRNA synthetase
YKL167c	MRP49	ribosomal protein, mitochondrial	YNL244c	SUI1	translation initiation factor 3 (eIF3)	YGL245w		strong similarity to glutamine-tRNA ligase
YKL142w YLR312w-a		ribosomal protein, mitochondrial ribosomal protein, mitochondrial	YKR059w YMR260c	TIF1 TIF11	translation initiation factor 4A translation initiation factor eIF1A	YPR081c		strong similarity to glycyl-tRNA synthetases
YBL038w	MRPL16	ribosomal protein, mitochondrial	YPL237w	SUI3	translation initiation factor eIF2 β subunit	YHR020w		strong similarity to human glutamyl-prolyl
YMR193w YMR024w	MRPL24	ribosomal protein, mitochondrial	YJR007w	SUI2 GCD11	translation initiation factor eIF2, α subunit		MOT⁴	tRNA synthetase
YMR286w	MRPL33	ribosomal protein, mitochondrial ribosomal protein, mitochondrial	YER025w YKR026c	GCD11 GCN3	translation initiation factor eIF2, γ subunit translation initiation factor eIF2B, 34K,	YKL194c YIL078w	MST1 THS1	threonine-tRNA ligase, mitochondrial threonyl tRNA synthetase, cytosolic
YLR439w	MRPL4	ribosomal protein, mitochondrial			α subunit	YOL097c	WRS1	tryptophan-tRNA ligase
YHR147c YGR220c	MRPL9	ribosomal protein, mitochondrial ribosomal protein, mitochondrial	YLR291c	GCD7	translation initiation factor eIF2B, 43K subunit	YDR268w	MSW1	tryptophanyl-tRNA synthetase, mitochondrial
YDR337w	MRPS28	ribosomal protein, mitochondrial	YGR083c	GCD2	translation initiation factor eIF2B, 71K (δ)	YPL097w	MSY1	tyrosyl-tRNA synthetase
YNL137c YOR158w		ribosomal protein, mitochondrial ribosomal protein, mitochondrial	YDR211w	GCD6	subunit translation initiation factor eIF2B, ε 81K	YGR185c YGR094w	TYS1 VAS1	tyrosyl-tRNA synthetase valyl-tRNA synthetase
/CR046c	PETCR46	ribosomal protein, mitochondrial			subunit			
YFR049w YJR113c	YMR31	ribosomal protein, mitochondrial similarity to mitochondrial ribosomal	YOR260w YOR361c	GCD1 PRT1	translation initiation factor eIF2B, γ subunit translation initiation factor eIF3 subunit	otner pi	otein-s	synthesis activities
		protein S7	YMR146c	TIF34	translation initiation factor eIF3, P39		SSB1	heat-shock protein of HSP70 family
YHR148w YDR116c		similarity to ribosomal protein similarity to ribosomal protein L1	YNL062c	GCD10	subunit translation initiation factor eIF3, RNA-	YNL209w	SSB2	heat-shock protein of HSP70 family, cytosolic
YOR150w		similarity to ribosomal protein L13			binding subunit	YGR147c	NAT2	N-acetyltransferase for N-terminal
YNL284c YEL050c		similarity to ribosomal protein L15 similarity to ribosomal protein L2	YJL138c YPR163c	TIF2 TIF3	translation initiation factor eIF4A translation initiation factor eIF4B	YJR066w	TOR1	methionine
YELU5UC YLR009w		similarity to ribosomal protein L2 similarity to ribosomal protein L24.e.B	YPK163C YOL139C	CDC33	translation initiation factor eIF4B translation initiation factor eIF4E	YDL044c	MTF2	phosphatidylinositol 3-kinase protein involved in mRNA splicing and
YDR115w		similarity to ribosomal protein L34	YPR041w	TIF5	translation initiation factor eIF5			protein synthesis, mitochondrial
VDD007						VDI 040	NIAT-	protoin NI cook its and see a fine it
		similarity to ribosomal protein L5 similarity to ribosomal protein S13	YEL034w YJR047c	HYP2 ANB1	translation initiation factor eIF5A.1 translation initiation factor eIF5A.2	YDL040c YJL023c	NAT1 PET130	protein N-acetyltransferase subunit protein synthesis protein, mitochondrial
YNL081c YDR041w		similarity to ribosomal protein L5 similarity to ribosomal protein S13 similarity to ribosomal proteins	YEL034w YJR047c YGL169w	HYP2 ANB1 SUA5	translation initiation factor eIF5A.1 translation initiation factor eIF5A.2 translation initiation protein	YJL023c YMR005w	PET130 MPT1	protein synthesis protein, mitochondrial required for protein synthesis
YNL081c YDR041w		similarity to ribosomal protein L5 similarity to ribosomal protein S13 similarity to ribosomal proteins similarity to Rpl10p and S.solfataricus	YEL034w YJR047c	HYP2 ANB1	translation initiation factor eIF5A.1 translation initiation factor eIF5A.2	YJL023c	PET130	protein synthesis protein, mitochondrial required for protein synthesis required to maintain RHO <sup>+</sup> mitochondrial
YNL081c YDR041w YKL009w	NHP2	similarity to ribosomal protein L5 similarity to ribosomal protein S13 similarity to ribosomal proteins similarity to Rpl10p and S.solfataricus ribosomal protein L10 strong similarity to high-mobility group	YEL034w YJR047c YGL169w	HYP2 ANB1 SUA5 SUP45	translation initiation factor eIF5A.1 translation initiation factor eIF5A.2 translation initiation protein translational release factor	YJL023c YMR005w YBL080c YHR189w	PET130 MPT1 PET112	protein synthesis protein, mitochondrial required for protein synthesis required to maintain RHO <sup>+</sup> mitochondrial DNA similarity to peptidyl-tRNA hydrolases
YNL081c YDR041w YKL009w YDL208w	NHP2	similarity to ribosomal protein L5 similarity to ribosomal protein S13 similarity to ribosomal proteins similarity to Rpl10p and S.solfataricus ribosomal protein L10 strong similarity to high-mobility group (HMG) family	YEL034w YJR047c YGL169w YBR143c <b>transla</b> t	HYP2 ANB1 SUA5 SUP45 <b>tional c</b>	translation initiation factor eIF5A.1 translation initiation factor eIF5A.2 translation initiation protein translational release factor	YJL023c YMR005w YBL080c	PET130 MPT1	protein synthesis protein, mitochondrial required for protein synthesis required to maintain RHO+ mitochondrial DNA
YNL081c YDR041w YKL009w YDL208w YEL026w		similarity to ribosomal protein L5 similarity to ribosomal protein S13 similarity to ribosomal proteins similarity to Rpl10p and S.solfataricus ribosomal protein L10 strong similarity to high-mobility group (HMG) family strong similarity to high-mobility group-like protein Nhp2p	YEL034w YJR047c YGL169w YBR143c	HYP2 ANB1 SUA5 SUP45 <b>tional co</b>	translation initiation factor eIF5A.1 translation initiation factor eIF5A.2 translation initiation protein translational release factor	YJL023c YMR005w YBL080c YHR189w	PET130 MPT1 PET112	protein synthesis protein, mitochondrial required for protein synthesis required to maintain RHO <sup>+</sup> mitochondrial DNA similarity to peptidyl-tRNA hydrolases
YNL081c YDR041w YKL009w YDL208w YEL026w	NHP2 RPS30B	similarity to ribosomal protein L5 similarity to ribosomal protein S13 similarity to ribosomal proteins similarity to Rpl10p and S.solfataricus ribosomal protein L10 strong similarity to high-mobility group (HMG) family strong similarity to high-mobility group-like protein Nhp2p strong similarity to human ubiquitin-like	YEL034w YJR047c YGL169w YBR143c <i>transla</i> i YMR282c YBR120c	HYP2 ANB1 SUA5 SUP45 <b>tional co</b> AEP2 CBP6	translation initiation factor eIF5A.1 translation initiation factor eIF5A.2 translation initiation protein translational release factor  pontrol  2'-O-ribosyl phosphate transferase apo-cytochrome b pre-mRNA processing protein	YJL023c YMR005w YBL080c YHR189w YLL039c	PET130 MPT1 PET112 UBI4	protein synthesis protein, mitochondrial required for protein synthesis required to maintain RHO* mitochondrial DNA similarity to peptidyl-tRNA hydrolases ubiquitin
YNL081c YDR041w YKL009w YDL208w YEL026w YOR182c		similarity to ribosomal protein L5 similarity to ribosomal protein S13 similarity to ribosomal proteins S13 similarity to Rpl10p and S.solfataricus ribosomal protein L10 strong similarity to high-mobility group (HMG) family strong similarity to high-mobility group-like protein Nhp2p strong similarity to human ubiquitin-like protein/ribosomal protein S30 strong similarity to Mycoplasma	YEL034W YJR047c YGL169W YBR143c <i>translat</i> YMR282c YBR120c YPL029W	HYP2 ANB1 SUA5 SUP45 <b>tional co</b> AEP2 CBP6 SUV3	translation initiation factor eIF5A.1 translation initiation factor eIF5A.2 translation initiation protein translational release factor  pontrol  2'-O-ribosyl phosphate transferase apo-cytochrome b pre-mRNA processing protein ATP-dependent RNA helicase, mitochondrial	YJL023c YMR005w YBL080c YHR189w YLL039c	PET130 MPT1 PET112 UBI4	protein synthesis protein, mitochondrial required for protein synthesis required to maintain RHO' mitochondrial DNA similarity to peptidyl-tRNA hydrolases ubiquitin
YNL081c YDR041w YKL009w YDL208w YEL026w YOR182c YNR037c		similarity to ribosomal protein L5 similarity to ribosomal protein S13 similarity to ribosomal protein S13 similarity to Rpl10p and S.solfataricus ribosomal protein L10 strong similarity to high-mobility group (HMG) family strong similarity to high-mobility group-like protein Nhp2p strong similarity to human ubiquitin-like protein/ribosomal protein S30 strong similarity to Mycoplasma ribosomal protein S19	YEL034w YJR047c YGL169w YBR143c <i>transla</i> i YMR282c YBR120c	HYP2 ANB1 SUA5 SUP45 <b>tional co</b> AEP2 CBP6 SUV3	translation initiation factor eIF5A.1 translation initiation factor eIF5A.2 translation initiation protein translational release factor  portrol  2'-O-ribosyl phosphate transferase apo-cytochrome b pre-mRNA processing protein ATP-dependent RNA helicase, mitochondrial component of mitochondrial translation	YJL023c YMR005w YBL080c YHR189w YLL039c	PET130 MPT1 PET112 UBI4	protein synthesis protein, mitochondrial required for protein synthesis required to maintain RHO* mitochondrial DNA similarity to peptidyl-tRNA hydrolases ubiquitin
YNL081c YDR041w YKL009w YDL208w YEL026w YOR182c YNR037c YNL185c	RPS30B	similarity to ribosomal protein L5 similarity to ribosomal protein S13 similarity to ribosomal proteins S13 similarity to Rpl10p and S.solfataricus ribosomal protein L10 strong similarity to high-mobility group (HMG) family strong similarity to high-mobility group-like protein Nhp2p strong similarity to human ubiquitin-like protein/ribosomal protein S30 strong similarity to Mycoplasma	YEL034W YJR047c YGL169W YBR143c <i>translat</i> YMR282c YBR120c YPL029W	HYP2 ANB1 SUA5 SUP45 <b>tional co</b> AEP2 CBP6 SUV3 PET127	translation initiation factor eIF5A.1 translation initiation factor eIF5A.2 translation initiation protein translational release factor  pontrol  2'-O-ribosyl phosphate transferase apo-cytochrome b pre-mRNA processing protein ATP-dependent RNA helicase, mitochondrial	YJL023c YMR005w YBL080c YHR189w YLL039c	PET130 MPT1 PET112 UBI4	protein synthesis protein, mitochondrial required for protein synthesis required to maintain RHO' mitochondrial DNA similarity to peptidyl-tRNA hydrolases ubiquitin
YNL081c YDR041w YKL009w YDL208w YEL026w YOR182c YNR037c YNL185c YER056c-a	RPS30B	similarity to ribosomal protein L5 similarity to ribosomal protein S13 similarity to ribosomal proteins S13 similarity to Rpl10p and S.solfataricus ribosomal protein L10 strong similarity to high-mobility group (HMG) family strong similarity to high-mobility group-like protein Nhp2p strong similarity to human ubiquitin-like protein ribosomal protein S30 strong similarity to human ubiquitin-like protein/ribosomal protein S30 strong similarity to Mycoplasma ribosomal protein S19 strong similarity to ribosomal protein L11 strong similarity to ribosomal protein L11 strong similarity to ribosomal protein L134.e	YEL034W YJR047c YGL169W YBR143c <i>transla</i> t YMR282c YBR120c YPL029W YOR017W	HYP2 ANB1 SUA5 SUP45 <b>tional co</b> AEP2 CBP6 SUV3 PET127	translation initiation factor eIF5A.1 translation initiation factor eIF5A.2 translation initiation protein translational release factor  pontrol  2'-O-ribosyl phosphate transferase apo-cytochrome b pre-mRNA processing protein ATP-dependent RNA helicase, mitochondrial component of mitochondrial translation system component of the Tor signalling pathway cytochrome b translational activator	YJL023c YMR005w YBL080c YHR189w YLL039c Protein YEL030w YKL073w	PET130 MPT1 PET112 UBI4 ein de folding	protein synthesis protein, mitochondrial required for protein synthesis required to maintain RHO' mitochondrial DNA similarity to peptidyl-tRNA hydrolases ubiquitin  stination  and stabilization  heat-shock protein of HSP70 family chaperone of the ER lumen
YNL081c YDR041w YKL009w YDL208w YEL026w YOR182c YNR037c YNL185c YER056c-a YMR230w	RPS30B	similarity to ribosomal protein L5 similarity to ribosomal protein S13 similarity to ribosomal protein S13 similarity to Rpl10p and S.solfataricus ribosomal protein L10 strong similarity to high-mobility group (HMG) family strong similarity to high-mobility group-like protein Nhp2p strong similarity to human ubiquitin-like protein K10somal protein S30 strong similarity to human ubiquitin-like protein/ribosomal protein S30 strong similarity to Mycoplasma ribosomal protein S19 strong similarity to ribosomal protein L11 strong similarity to ribosomal protein L34.e	YEL034W YJR047c YGL169W YBR143c translat YMR282c YBR120c YPL029W YOR017W YMR028W YDR197W	HYP2 ANB1 SUA5 SUP45 <b>tional co</b> AEP2 CBP6 SUV3 PET127 TAP42	translation initiation factor eIFSA.1 translation initiation factor eIFSA.2 translation initiation protein translational release factor  pontrol  2'-O-ribosyl phosphate transferase apo-cytochrome b pre-mRNA processing protein ATP-dependent RNA helicase, mitochondrial component of mitochondrial translation system component of the Tor signalling pathway	YJL023c YMR005w YBL080c YHR189w YLL039c Protein YEL030w	PET130 MPT1 PET112 UBI4 Pin de	protein synthesis protein, mitochondrial required for protein synthesis required to maintain RHO' mitochondrial DNA similarity to peptidyl-tRNA hydrolases ubiquitin  Stination  and stabilization  heat-shock protein of HSP70 family chaperone of the ER lumen chaperonin of the TCP1 ring complex,
YNL081c YDR041w YRL009w YPL208w YPL026w YOR182c YNR037c YNL185c YER056c-a YMR230w YNR036c YNR036c YNL096c YNL096c	RPS30B	similarity to ribosomal protein L5 similarity to ribosomal protein S13 similarity to ribosomal proteins S13 similarity to Rpl10p and S.solfataricus ribosomal protein L10 strong similarity to high-mobility group (HMG) family strong similarity to high-mobility group-like protein Nhp2p strong similarity to human ubiquitin-like protein Nhp2p strong similarity to human ubiquitin-like protein Nribosomal protein S30 strong similarity to Mycoplasma ribosomal protein S19 strong similarity to ribosomal protein L11 strong similarity to ribosomal protein S10 strong similarity to ribosomal protein S10 strong similarity to ribosomal protein S12 strong similarity to ribosomal protein S12 strong similarity to ribosomal protein S12 strong similarity to ribosomal protein S7	YEL034W YJR047c YGL169W YBR143c <i>translat</i> YMR282c YBR120c YPL029W YOR017W YMR028W YDR197W YNL216W	HYP2 ANB1 SUA5 SUP45 tional co AEP2 CBP6 SUV3 PET127 TAP42 CBS2 RAP1	translation initiation factor eIFSA1 translation initiation factor eIFSA2 translation initiation protein translational release factor  portrol  2'-O-ribosyl phosphate transferase apo-cytochrome b pre-mRNA processing protein ATP-dependent RNA helicase, mitochondrial component of mitochondrial translation system component of the Tor signalling pathway cytochrome b translational activator protein DNA-binding protein with repressor and activator activity	YJL023c YMR005w YBL080c YHR189w YLL039c Protein YEL030w YKL073w	PET130 MPT1 PET112 UBI4 ein de folding	protein synthesis protein, mitochondrial required for protein synthesis required to maintain RHO' mitochondrial DNA similarity to peptidyl-tRNA hydrolases ubiquitin  Stination  and stabilization  heat-shock protein of HSP70 family chaperone of the ER lumen chaperonin of the TCP1 ring complex, cytosolic chaperonin of the TCP1 ring complex,
YNLL081c YDR041w YKL009w YDL208w YDL208w YOR182c YNR037c YNL185c YER056c-a YMR230w YNR036c YNL096c YLR167w	RPS30B	similarity to ribosomal protein L5 similarity to ribosomal protein S13 similarity to ribosomal protein S13 similarity to Rpl10p and S.solfataricus ribosomal protein L10 strong similarity to high-mobility group (HMG) family strong similarity to high-mobility group-like protein Nhp2p strong similarity to human ubiquitin-like protein Nibosomal protein S30 strong similarity to human ubiquitin-like protein/ribosomal protein S30 strong similarity to Mycoplasma ribosomal protein S19 strong similarity to ribosomal protein L11 strong similarity to ribosomal protein S10 strong similarity to ribosomal protein S10 strong similarity to ribosomal protein S12 strong similarity to ribosomal protein S12 strong similarity to ribosomal protein S12 strong similarity to ribosomal protein S77 ubiquitin/ribosomal protein S273	YEL034w YJR047c YGL169w YBR143c <b>transla</b> i YMR282c YBR120c YPL029w YOR017w YMR028w YDR197w YNL216w YER054c	HYP2 ANB1 SUA5 SUP45 SUP45 AEP2 CBP6 SUV3 PET127 TAP42 CBS2 RAP1 GIP2	translation initiation factor eIFSA1 translation initiation factor eIFSA2 translation initiation protein translational release factor control  2'-O-ribosyl phosphate transferase apo-cytochrome b pre-mRNA processing protein ATP-dependent RNA helicase, mitochondrial component of mitochondrial translation system component of the Tor signalling pathway cytochrome b translational activator protein DNA-binding protein with repressor and activator activity Glo7p-interacting protein	YJL023c YMR005w YBL080c YHR189w YLL039c  Prote protein YEL030w YKL073w YIL142w YJL014w	PET130 MPT1 PET112  UBI4  LHS1 CCT2  CCT3	protein synthesis protein, mitochondrial required for protein synthesis required to maintain RHO' mitochondrial DNA similarity to peptidyl-tRNA hydrolases ubiquitin  Stination  and stabilization  heat-shock protein of HSP70 family chaperone of the ER lumen chaperonin of the TCP1 ring complex, cytosolic haperonin of the TCP1 ring complex, cytosolic chaperonin of the TCP1 ring complex, cytosolic
YNL081c YDR041W YKL009W YKL009W YDL208W YEL026W YOR182c YNR037c YNL185c YER056c-a YMR230W YMR036c YMR036c YMR188c	RPS30B	similarity to ribosomal protein L5 similarity to ribosomal protein S13 similarity to ribosomal protein S13 similarity to ribosomal proteins similarity to Rpl10p and S.solfataricus ribosomal protein L10 strong similarity to high-mobility group (HMG) family strong similarity to high-mobility group-like protein Nhp2p strong similarity to human ubiquitin-like protein Nhp2p strong similarity to human ubiquitin-like protein Npsosmal protein S30 strong similarity to Mycoplasma ribosomal protein S19 strong similarity to ribosomal protein L11 strong similarity to ribosomal protein L14 strong similarity to ribosomal protein S10 strong similarity to ribosomal protein S10 strong similarity to ribosomal protein S17 ubiquitin/ribosomal protein S27 uveak similarity to 30S ribosomal protein S17	YEL034W YJR047c YGL169W YBR143c <b>translai</b> YMR282c YBR120c YPL029W YOR017W YMR028W YDR197W YNL216W YER054c YMR080c YGR072cW	HYP2 ANB1 SUA5 SUP45 tional co AEP2 CBP6 SUV3 PET127 TAP42 CBS2 RAP1 GIP2 NAM7 UPF3	translation initiation factor eIFSA1 translation initiation factor eIFSA2 translation initiation protein translational release factor  portrol  2'-O-ribosyl phosphate transferase apo-cytochrome b pre-mRNA processing protein ATP-dependent RNA helicase, mitochondrial component of mitochondrial translation system component of the Tor signalling pathway cytochrome b translational activator protein DNA-binding protein with repressor and activator activity Glc7p-interacting protein nonsense-mediated mRNA decay protein nonsense-mediated mRNA decay protein	YJL023c YMR005w YBL080c YHR189w YLL039c  Protein YEL030w YKL073w YIL142w YJL014w YDR212w	PET130 MPT1 PET112  UBI4  LHS1 CCT2  CCT3  CCT1	protein synthesis protein, mitochondrial required for protein synthesis required to maintain RHO' mitochondrial DNA similarity to peptidyl-tRNA hydrolases ubiquitin  stination  and stabilization  heat-shock protein of HSP70 family chaperone of the ER lumen chaperonin of the TCP1 ring complex, cytosolic chaperonin of the TCP1 ring complex, cytosolic component of chaperonin-containing T-complex
YNLL081c YDR041W YKL009W YYL009W YDL208W YPL026W YOR182c YNR037c YNL185c YFR056c-a YMR230W YMR036c YNL036c YNL036c YNL036c YNL036c	RPS30B	similarity to ribosomal protein L5 similarity to ribosomal protein S13 similarity to ribosomal protein S13 similarity to Rph10p and S.solfataricus ribosomal protein L10 strong similarity to high-mobility group (HMG) family strong similarity to high-mobility group-like protein Nhp2p strong similarity to human ubiquitin-like protein/ribosomal protein S30 strong similarity to human ubiquitin-like protein/ribosomal protein S19 strong similarity to ribosomal protein L11 strong similarity to ribosomal protein L34.e strong similarity to ribosomal protein S10 strong similarity to ribosomal protein S12 strong similarity to ribosomal protein S12 strong similarity to ribosomal protein S12 strong similarity to ribosomal protein S7 ubiquitin/ribosomal protein S27 weak similarity to 305 ribosomal protein	YEL034W YJR047c YGL169W YBR143c  translat YMR282c YBR120c YPL029W YOR017W YMR028W YDR197W YNL216W YER054c YMR080c	HYP2 ANB1 SUA5 SUP45 tional co AEP2 CBP6 SUV3 PET127 TAP42 CBS2 RAP1 GIP2 NAM7	translation initiation factor eIFSA1 translation initiation factor eIFSA2 translation initiation protein translational release factor control  2'-O-ribosyl phosphate transferase apo-cytochrome b pre-mRNA processing protein ATP-dependent RNA helicase, mitochondrial component of mitochondrial translation system component of the Tor signalling pathway cytochrome b translational activator protein DNA-binding protein with repressor and activator activity (3Ic7p-interacting protein nonsense-mediated mRNA decay protein	YJL023c YMR005w YBL080c YHR189w YLL039c  Prote protein YEL030w YKL073w YIL142w YJL014w	PET130 MPT1 PET112  UBI4  LHS1 CCT2  CCT3	protein synthesis protein, mitochondrial required for protein synthesis required to maintain RHO' mitochondrial DNA similarity to peptidyl-tRNA hydrolases ubiquitin  Stination  and stabilization  heat-shock protein of HSP70 family chaperone of the ER lumen chaperonin of the TCP1 ring complex, cytosolic chaperonin of the TCP1 ring complex, cytosolic component of chaperonin-containing T-complex component of chaperonin-containing
YNL081c YDR041W YKL009W YDL208W YDL208W YOR182c YNR037c YNL185c YER056c-a YMR230W YNR036c YNR036c YNR096c YLR167W YMR188c YDL202W	RPS30B UBI3	similarity to ribosomal protein L5 similarity to ribosomal protein S13 similarity to ribosomal protein S13 similarity to ribosomal proteins similarity to Rpl10p and S.solfataricus ribosomal protein L10 strong similarity to high-mobility group (HMG) family strong similarity to high-mobility group-like protein Nhp2p strong similarity to human ubiquitin-like protein Nhp2p strong similarity to human ubiquitin-like protein Npsosmal protein S30 strong similarity to Mycoplasma ribosomal protein S19 strong similarity to ribosomal protein L11 strong similarity to ribosomal protein L14 strong similarity to ribosomal protein S10 strong similarity to ribosomal protein S10 strong similarity to ribosomal protein S17 ubiquitin/ribosomal protein S27 uveak similarity to 30S ribosomal protein S17	YEL034W YJR047c YGL169W YBR143c <b>translai</b> YMR282c YBR120c YPL029W YOR017W YMR028W YDR197W YNL216W YER054c YMR080c YGR072cW	HYP2 ANB1 SUA5 SUP45 tional co AEP2 CBP6 SUV3 PET127 TAP42 CBS2 RAP1 GIP2 NAM7 UPF3 NMD2	translation initiation factor eIFSA1 translation initiation factor eIFSA2 translation initiation protein translational release factor  portrol  2'-O-ribosyl phosphate transferase apo-cytochrome b pre-mRNA processing protein ATP-dependent RNA helicase, mitochondrial component of mitochondrial translation system component of the Tor signalling pathway cytochrome b translational activator protein DNA-binding protein with repressor and activator activity Glc7p-interacting protein nonsense-mediated mRNA decay protein	YJL023c YMR005w YBL080c YHR189w YLL039c  Protein YEL030w YKL073w YIL142w YJL014w YDR212w	PET130 MPT1 PET112  UBI4  LHS1 CCT2  CCT3  CCT1	protein synthesis protein, mitochondrial required for protein synthesis required to maintain RHO' mitochondrial DNA similarity to peptidyl-tRNA hydrolases ubiquitin  Stination  and stabilization  heat-shock protein of HSP70 family chaperone of the ER lumen chaperonin of the TCP1 ring complex, cytosolic chaperonin of the TCP1 ring complex, cytosolic component of chaperonin-containing T-complex component of chaperonin-containing T-complex component of chaperonin-containing T-complex component of chaperonin-containing T-complex component of chaperonin-containing
YNL081c YDR041w YKL009w YDL208w YPL026w YOR182c YNR037c YNL185c YER056c-a YMR230w YNR036c YNL096c YLR167w YMR188c YDL202w **Tanslat**	RPS30B UBI3	similarity to ribosomal protein L5 similarity to ribosomal protein S13 similarity to ribosomal protein S13 similarity to Rpl10p and S.solfataricus ribosomal protein L10 strong similarity to high-mobility group (HMG) family strong similarity to high-mobility group-like protein Nhp2p strong similarity to human ubiquitin-like protein Nhp2p strong similarity to Mycoplasma ribosomal protein S30 strong similarity to ribosomal protein L11 strong similarity to ribosomal protein S10 strong similarity to ribosomal protein S10 strong similarity to ribosomal protein S12 strong similarity to ribosomal protein S7 ubiquitin/ribosomal protein S27a weak similarity to 30S ribosomal protein S17 weak similarity to ribosomal protein	YEL034W YJR047c YGL169W YBR143c <b>transla</b> i YMR282c YBR120c YPL029W YOR017W YMR028W YDR197W YNL216W YER054c YMR080c YGR072W YHR077c YMR064W	HYP2 ANB1 SUA5 SUP45 tional co CBP6 SUV3 PET127 TAP42 CBS2 RAP1 GIP2 NAM7 UPF3 NMD2 AEP1	translation initiation factor eIFSA1 translation initiation factor eIFSA2 translation initiation protein translational release factor control  2'-O-ribosyl phosphate transferase apo-cytochrome b pre-mRNA processing protein ATP-dependent RNA helicase, mitochondrial component of mitochondrial translation system component of the Tor signalling pathway cytochrome b translational activator protein DNA-binding protein with repressor and activator activity Glo7p-interacting protein nonsense-mediated mRNA decay protein RNA expression protein	YJL023c YMR005w YHR189w YLL039c  Protein YEL030w YKL073w YIL142w YJL014w YDR212w YDL143w YJL111w	PET130 MPT1 PET112  UBI4  in de folding  LHS1 CCT2 CCT3 CCT1 CCT4 CCT7	protein synthesis protein, mitochondrial required for protein synthesis required to maintain RHO' mitochondrial DNA similarity to peptidyl-tRNA hydrolases ubiquitin  Stination  and stabilization  heat-shock protein of HSP70 family chaperone of the ER lumen chaperonin of the TCP1 ring complex, cytosolic chaperonin of the TCP1 ring complex, cytosolic component of chaperonin-containing T-complex
YNLL081c YDR041W YYDR041W YYDL208W YPL026W YYDR182c YNR037c YNL185c YER056c-a YMR230W YNR036c YNL096c	RPS30B  UBI3  tion (initition)  RPLA1	similarity to ribosomal protein L5 similarity to ribosomal protein S13 similarity to ribosomal protein S13 similarity to Rpl10p and S.solfataricus ribosomal protein L10 strong similarity to high-mobility group (HMG) family strong similarity to high-mobility group-like protein Nhp2p strong similarity to human ubiquitin-like protein Nhp2p strong similarity to Mycoplasma ribosomal protein S30 strong similarity to ribosomal protein L11 strong similarity to ribosomal protein S10 strong similarity to ribosomal protein S10 strong similarity to ribosomal protein S12 strong similarity to ribosomal protein S7 ubiquitin/ribosomal protein S27a weak similarity to 30S ribosomal protein S17 weak similarity to ribosomal protein	YEL034W YJR047c YGL169W YBR143c <i>translat</i> YMR282c YBR120c YPL029W YOR017W YMR028W YDR197W YNL216W YER054c YMR080c YGR072W YHR077c	HYP2 ANB1 SUA5 SUP45 tional co AEP2 CBP6 SUV3 PET127 TAP42 CBS2 RAP1 GIP2 NAM7 UPF3 NMD2	translation initiation factor eIFSA1 translation initiation factor eIFSA2 translation initiation protein translational release factor  portrol  2'-O-ribosyl phosphate transferase apo-cytochrome b pre-mRNA processing protein ATP-dependent RNA helicase, mitochondrial component of mitochondrial translation system component of the Tor signalling pathway cytochrome b translational activator protein DNA-binding protein with repressor and activator activity Glc7p-interacting protein nonsense-mediated mRNA decay protein	YJL023c YMR005w YHR189w YLL039c  Protein YEL030w YKL073w YIL142w YJL014w YDR212w YDL143w	PET130 MPT1 PET112  UBI4  LHS1 CCT2  CCT3  CCT1  CCT4	protein synthesis protein, mitochondrial required for protein synthesis required to maintain RHO' mitochondrial DNA similarity to peptidyl-tRNA hydrolases ubiquitin  Stination  and stabilization  heat-shock protein of HSP70 family chaperone of the ER lumen chaperonin of the TCP1 ring complex, cytosolic chaperonin of the TCP1 ring complex, cytosolic component of chaperonin-containing T-complex component of chaperonin-containing T-complex component of chaperonin-containing T-complex component of chaperonin-containing T-complex component of chaperonin-containing
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YNLL081c YDR041W YYKL009W YDL208W YYL026W YYNR037c YNL185c YER056c-a YMR230W YMR038C YNL096c	RPS30B  UBI3  tion (initition)  RPLA1	similarity to ribosomal protein L5 similarity to ribosomal protein S13 similarity to ribosomal protein S13 similarity to Rpl10p and S.solfataricus ribosomal protein L10 strong similarity to high-mobility group (HMG) family strong similarity to high-mobility group-like protein Nhp2p strong similarity to human ubiquitin-like protein Nhp2p strong similarity to human ubiquitin-like protein/Inbosomal protein S30 strong similarity to Mycoplasma ribosomal protein S19 strong similarity to ribosomal protein L11 strong similarity to ribosomal protein L14 strong similarity to ribosomal protein S12 ubiquitin/ribosomal protein S27 weak similarity to 30S ribosomal protein S17 weak similarity to ribosomal protein sittinon, elongation and	YEL034W YJR047c YGL169W YBR143c  translat YMR282c YBR120c YPL029W YOR017W YMR028W YDR197W YNL216W YER054c YMR080c YGR072c YMR064W YPL179W YFR009W YLR203c	HYP2 ANB1 SUA5 SUP45 tional ca AEP2 CBP6 SUV3 PET127 TAP42 CBS2 RAP1 GIP2 NAM7 VIPF3 NMD2 AEP1 GCN20	translation initiation factor eIFSA1 translation initiation factor eIFSA2 translation initiation protein translational release factor  portrol  2'-O-ribosyl phosphate transferase apo-cytochrome b pre-mRNA processing protein ATP-dependent RNA helicase, mitochondrial component of mitochondrial translation system component of the Tor signalling pathway cytochrome b translational activator protein DNA-binding protein with repressor and activator activity Glc7p-interacting protein nonsense-mediated mRNA decay protein nonsense-mediated mRNA decay protein nonsense-mediated mRNA decay protein posphoprotein phosphoprotein protein phosphoprotein protein phosphoprotein phosphatase positive effector of Gcn2p possibly involved in translational activation of COX1 and COB mRNA	YJL023c YMR005w YHR189w YLL039c  Protein YEL030w YKL073w YIL142w YJL014w YDR212w YJL111w YJL111w YJL008c YDR188w	PET130 MPT1 PET112  UBI4  Sin de folding  LHS1 CCT2 CCT3 CCT1 CCT4 CCT7 CCT8	protein synthesis protein, mitochondrial required for protein synthesis required to maintain RHO' mitochondrial DNA similarity to peptidyl-tRNA hydrolases ubiquitin  Stination  and stabilization  heat-shock protein of HSP70 family chaperone of the ER lumen chaperonin of the TCP1 ring complex, cytosolic chaperonin of the TCP1 ring complex, cytosolic component of chaperonin-containing T-complex (§ subunit)
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YNL081c YDR041W YYDR041W YYDR041W YYDR041W YYDL208W YYEL026W YYDR182c YNR037c YNL185c YER056c-a YMR230W YNL086c YLR167W YNL096c YLR167W YNL096c YLR167W YMR188c YDL202W ***Tanslat*** ***Tanslat*** ***Tanslat** **Tanslat** ***Tanslat** **Tanslat** **Tanslat	RPS30B  UBI3  tion (initition)  RPLA1 NIP1 PAN2 SUP35 SUP35 MAP2 MSS1 MRF1	similarity to ribosomal protein L5 similarity to ribosomal protein S13 similarity to ribosomal protein S13 similarity to ribosomal proteins similarity to Rpl10p and S.solfataricus ribosomal protein L10 strong similarity to high-mobility group (HMG) family strong similarity to high-mobility group-like protein Nhp2p strong similarity to human ubiquitin-like protein Nhp2p strong similarity to ribosomal protein S10 strong similarity to ribosomal protein L11 strong similarity to ribosomal protein S10 strong similarity to ribosomal protein S10 strong similarity to ribosomal protein S12 strong similarity to ribosomal protein S12 strong similarity to ribosomal protein S12 strong similarity to 30S ribosomal protein S17 weak similarity to ribosomal protein S18 strong similarity to ribosomal	YEL034W YJR047c YGL169W YBR143c  translat YMR282c YBR120c YPL029W YOR017W YMR028W YDR197W YNL216W YER054c YMR080c YGR072W YHR077c YMR064W YPL179W YFR009W YFR009W YLR203c YBL058W YNL139C YLR067c YMR257c	HYP2 ANB1 SUA5 SUP45  tional ca  AEP2 CBP6 SUV3  PET127  TAP42 CBS2  RAP1 GIP2 NAM7 UPF3 NIMD2  AEP1 PPO1 GCN20 MSS51  SHP1 FLR1 PET309  PET1111	translation initiation factor eIFSA1 translation initiation factor eIFSA2 translation initiation protein translational release factor  portrol  2'-O-ribosyl phosphate transferase apo-cytochrome b pre-mRNA processing protein ATP-dependent RNA helicase, mitochondrial component of mitochondrial translation system component of mitochondrial translation system component of the Tor signalling pathway cytochrome b translational activator protein DNA-binding protein with repressor and activator activity Glc7p-interacting protein nonsense-mediated mRNA decay protein nonsense-mediated mRNA decay protein nonsense-mediated mRNA decay protein phosphoprotein phosphatase positive effector of Gcn2p possibly involved in translational activation of COX1 and COB mRNA potential regulatory subunit for Glc7p regulatory protein required for translation of COX2 mRNA ser/thr phosphoprotein phosphatase 1, catalytic subunit ser/thr phosphoprotein phosphatase 1,	YJL023c YMR005w YHR189w YLL039c  Protein YEL030w YKL073w YIL142w YJL014w YDR212w YJL111w YJL018e YDR188w YDR155c YML078w YOR288c YML078w YFR048c YDR619w YFL016c	PET130 MPT1 PET112  UBI4  LHS1 CCT2  CCT3  CCT1  CCT4  CCT7  CCT8  CCT6  CPH1 CPR3  MPD1 CA11 FKB2  MDJ1	protein synthesis protein, mitochondrial required for protein synthesis required to maintain RHO' mitochondrial DNA similarity to peptidyl-tRNA hydrolases ubiquitin <b>stination and stabilization</b> heat-shock protein of HSP70 family chaperone of the ER lumen chaperonin of the TCP1 ring complex, cytosolic chaperonin of the TCP1 ring complex, cytosolic chaperonin-containing T-complex component of chaperonin-containing T-complex component of chaperonin-containing T-complex component of chaperonin-containing T-complex component of chaperonin-containing T-complex (ζ subunit) cyclophilin (peptidylprolyl isomerase) cyclophilin (peptidylprolyl isomerase), mitochondrial disulphide isomerase related protein dnal homologue FK506/rapamycin-binding protein of the ER heat-shock protein - chaperone
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YNL081c YDL081c YDR041W YKL009W YDL208W YFEL026W YOR182c YNR037c YNL185c YER056c-a YMR230W YNR038c	RPS30B  UBI3  tion (initition)  RPLA1 NIP1 PAN2 SUP35 SUP35 MAP2 MSS1 MRF1	similarity to ribosomal protein L5 similarity to ribosomal protein S13 similarity to ribosomal protein S13 similarity to ribosomal proteins similarity to Rpl10p and S.solfataricus ribosomal protein L10 strong similarity to high-mobility group (HMG) family strong similarity to high-mobility group-like protein Nhp2p strong similarity to human ubiquitin-like protein Nhp2p strong similarity to ribosomal protein S10 strong similarity to ribosomal protein L11 strong similarity to ribosomal protein S10 strong similarity to ribosomal protein S10 strong similarity to ribosomal protein S12 strong similarity to ribosomal protein S12 strong similarity to ribosomal protein S12 strong similarity to 30S ribosomal protein S17 weak similarity to ribosomal protein S18 strong similarity to ribosomal	YEL034W YJR047c YGL169W YBR143c  translat YMR282c YBR120c  YPL029W YOR017W YMR028W YDR197W YNL216W YER054c YMR080c YGR072W YHR077c YMR064W YPL179W YPL179W YPL199W YL79W YR054C YGR072W YHR0677c YMR064W YPL139C YL79W YMR067c YMR257c YER133W	HYP2 ANB1 SUA5 SUP45 tional cd AEP2 CBP6 SUV3 PET127 TAP42 CBS2 RAP1 GIP2 NAM7 UPF3 NMD2 AEP1 PPQ1 GCN20 MSS51 SHP1 RLR1 PET309 PET111 GLC7	translation initiation factor eIFSA1 translation initiation factor eIFSA2 translation initiation protein translational release factor  portrol  2'-O-ribosyl phosphate transferase apo-cytochrome b pre-mRNA processing protein ATP-dependent RNA helicase, mitochondrial component of mitochondrial translation system component of mitochondrial translation system component of the Tor signalling pathway cytochrome b translational activator protein DNA-binding protein with repressor and activator activity Glc7p-interacting protein nonsense-mediated mRNA decay protein nonsense-mediated mRNA decay protein nonsense-mediated mRNA decay protein phosphoprotein phosphatase positive effector of Gcn2p possibly involved in translational activation of COX1 and COB mRNA potential regulatory subunit for Glc7p regulatory protein required for translation of COX2 mRNA ser/thr phosphoprotein phosphatase 1, catalytic subunit ser/thr phosphoprotein phosphatase 1,	YJL023c YMR005w YHR189w YLL039c  Protein YEL030w YKL073w YIL142w YJL014w YDR212w YJL111w YJL018e YDR188w YDR155c YML078w YOR288c YML078w YFR048c YDR619w YFL016c	PET130 MPT1 PET112  UBI4  LHS1 CCT2  CCT3  CCT1  CCT4  CCT7  CCT8  CCT6  CPH1 CPR3  MPD1 CA11 FKB2  MDJ1	protein synthesis protein, mitochondrial required for protein synthesis required to maintain RHO' mitochondrial DNA similarity to peptidyl-tRNA hydrolases ubiquitin <b>stination and stabilization</b> heat-shock protein of HSP70 family chaperone of the ER lumen chaperonin of the TCP1 ring complex, cytosolic chaperonin of the TCP1 ring complex, cytosolic chaperonin of the TCP1 ring complex, cytosolic component of chaperonin-containing T-complex component of chaperonin-containing T-complex component of chaperonin-containing T-complex component of chaperonin-containing T-complex (ζ subunit) cyclophilin (peptidylprolyl isomerase) cyclophilin (peptidylprolyl isomerase), mitochondrial disulphide isomerase related protein dnal homologue FK508/rapamycin-binding protein of the ER heat-shock protein - chaperone
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YNL081c YDR041w YYKL009w YPL026w YPL026w YYOR182c YNR037c YNL185c YER056c-a YMR230w YNR036c YNL096c	RPS30B  UBI3  tion (initition)  RPLA1 NIP1 PAN2 SUP35 SIS1 MAP2 MSS1  MRF1 TIF4632 TIF4631	similarity to ribosomal protein L5 similarity to ribosomal protein S13 similarity to ribosomal protein S13 similarity to Rpl10p and S.solfataricus ribosomal protein L10 strong similarity to high-mobility group (HMG) family strong similarity to high-mobility group-like protein Nhp2p strong similarity to high-mobility group-like protein Nhp2p strong similarity to human ubiquitin-like protein Nhp2p strong similarity to human ubiquitin-like protein Nhp2p strong similarity to ribosomal protein S10 strong similarity to ribosomal protein L11 strong similarity to ribosomal protein L11 strong similarity to ribosomal protein S10 strong similarity to ribosomal protein S10 strong similarity to ribosomal protein S12 strong similarity to ribosomal protein S12 strong similarity to ribosomal protein S17 ubiquitin/ribosomal protein S27a weak similarity to ribosomal protein S17 ubiquitin/ribosomal protein s18 acidic ribosomal protein al associated with 40s ribosomal subunit component of Pab1p-stimulated poly(A) ribonuclease eukaryotic peptide chain release factor GTP-binding subunit nethionine aminopeptidase, isoform 2 mitochondrial GTPase involved in expression of COX1 mitochondrial peptide chain release factor mRNA cap-binding protein (elF4F), 150K subunit mRNA CAP-binding protein (elF4F), 20K	YEL034W YJR047c YGL169W YJR047c YGL169W YBR143c  translait  YMR282c YBR120c  YPL029W YOR017W YMR028W YDR197W YNL216W YER054c YMR080c YGR072W YHR077c YMR064W YPL179W YFR009W YFR009W YFR009W YRL036c YBL058W YNL139c YLR067c YMR257c YER133W YOR178c YDR283c YGR222W YBR024W	HYP2 ANB1 SUD45 SUD45 SUP45 tional ca  AEP2 CBP6 SUV3 PET127 TAP42 CBS2 RAP1 GIP2 NAM7 UPF3 NIMD2 AEP1 PPO1 GCN20 MSS51 SHP1 RLR1 PET309 PET111 GLC7 GAC1 GCN2 PET64 SCO2	translation initiation factor eIFSA.1 translation initiation factor eIFSA.2 translation initiation protein translational release factor  pontrol  2'-O-ribosyl phosphate transferase apo-cytochrome b pre-mRNA processing protein ATP-dependent RNA helicase, mitochondrial component of mitochondrial translation system component of fitochondrial translation system component of the Tor signalling pathway cytochrome b translational activator protein DNA-binding protein with repressor and activator activity Glc7p-interacting protein nonsense-mediated mRNA decay protein nonsense-mediated mRNA decay protein nonsense-mediated mRNA decay protein possense-mediated mRNA decay protein possense-mediated mRNA decay protein activation of ATPase messenger RNA expression protein phosphoprotein phosphatase positive effector of Gcn2p possibly involved in translational activation of COX1 and COB mRNA potential regulatory subunit for Glc7p regulatory protein required for stability and translation of COX1 mRNA ser/thr phosphoprotein phosphatase 1, catalytic subunit ser/thr protein kinase splicing protein and translational activator, mitochondrial strong similarity to Sco1p	YJL023c YMR005w YRB080c  Protein YEL030w YKL073w YJL142w YJL0144w YDR212w YDL143w YJL111w YJL008c YDR188w YDR155c YML078w YOR288c YER048c YDR59w YFL016c YOR232w YJR045c	PET130 MPT1 PET112  UBI4  PET112  UBI4  PET112  UBI4  PET112  UBI4  PET112  CCT2  CCT3  CCT1  CCT4  CCT7  CCT8  CCT6  CPH1  CPR3  MPD1  CAJ1  FKB2  MDJ1  MGE1  HSP60  SSC1	protein synthesis protein, mitochondrial required for protein synthesis required to maintain RHO' mitochondrial DNA similarity to peptidyl-tRNA hydrolases ubiquitin  Stination  and stabilization  heat-shock protein of HSP70 family chaperone of the ER lumen chaperonin of the TCP1 ring complex, cytosolic chaperonin of the TCP1 ring complex, cytosolic chaperonin of the TCP1 ring complex, cytosolic component of chaperonin-containing T-complex component of chaperonin-containing T-complex component of chaperonin-containing T-complex (S subunit) cyclophilin (peptidylprolyl isomerase) cyclophilin (peptidylprolyl isomerase) cyclophilin (peptidylprolyl isomerase) mitochondrial disulphide isomerase related protein dnaJ homologue FK506/rapamycin-binding protein of the ER heat-shock protein - chaperone heat-shock protein - chaperone, mitochondrial heat-shock protein 70-related protein, mitochondrial heat-shock protein 70-related protein, mitochondrial heat-shock protein 70-related protein, mitochondrial
YNL081c YDL081c YDR041W YKL009W YEL026W YDL208W YFL026W YOR182c YNR037c YNL185c YFR056c-a YMR230W YNR036c YNL096c YNL096c YNL096c YNL096c YNL096c YNL096c YNL091c YMR309c YGL094c YDR172W YNL007c YBL091c YMR023c YGL143c YGL049c YGR162W YOR276W YFR165W	RPS30B  UBI3  tion (initition)  RPLA1 NIP1 PAN2 SUP35 SIS1 MAP2 MSS1 MRF1 TIF4632 TIF4631 CAF20 PAB1	similarity to ribosomal protein L5 similarity to ribosomal protein S13 similarity to ribosomal protein S13 similarity to ribosomal proteins similarity to Rpl10p and S.solfataricus ribosomal protein L10 strong similarity to high-mobility group (I+MG) family strong similarity to high-mobility group-like protein Nhp2p strong similarity to high-mobility group-like protein Nhp2p strong similarity to human ubiquitin-like protein Nhp2p strong similarity to human ubiquitin-like protein Nhp2p strong similarity to ribosomal protein L11 strong similarity to ribosomal protein L11 strong similarity to ribosomal protein L13 strong similarity to ribosomal protein S10 strong similarity to ribosomal protein S10 strong similarity to ribosomal protein S12 strong similarity to ribosomal protein S17 weak similarity to ribosomal protein S27a weak similarity to ribosomal protein S17 weak similarity to ribosomal protein S18 weak similarity to ribosomal protein S17 weak similarity to ribosomal protein S18 weak similarity to riboso	YEL034W YJR047c YGL169W YJR047c YGL169W YBR143c  translat YMR282c YBR120c YPL029W YOR017W YMR028W YDR197W YNL216W YER054c YMR080c YGR072W YHR077c YMR064W YPL179W YFR009W YLR203c YBL058W YNL139c YLR067c YMR257c YER133W YOR178c YDR283c YGR222W YBR024W YGL195W YDL069c	HYP2 ANB1 SUA5 SUP45  tional co  AEP2 CBP6 SUV3  PET127  TAP42 CBS2  RAP1 GIP2 NAM7 UP3 NMD2  AEP1 PPQ1 GCN20 MSS61 SHP1 RLR1 PET309  PET111 GLC7 GAC1 GCN2 PET64 SCO2 GCN1 CBS1	translation initiation factor eIFSA.1 translation initiation factor eIFSA.2 translation initiation protein translational release factor  pontrol  2'-O-ribosyl phosphate transferase apo-cytochrome b pre-mRNA processing protein ATP-dependent RNA helicase, mitochondrial component of mitochondrial translation system component of mitochondrial translation system component of the Tor signalling pathway cytochrome b translational activator protein DNA-binding protein with repressor and activator activity Glo7p-interacting protein nonsense-mediated mRNA decay protein nonsense-mediated mRNA decay protein nonsense-mediated mRNA decay protein posense-mediated mRNA decay protein posense-mediated mRNA decay protein posense-mediated mRNA decay protein consense-mediated mRNA decay protein phosphoprotein phosphatase positive effector of Gcn2p possibly involved in translational activation of COX1 and COB mRNA potential regulatory subunit for Glc7p regulatory protein required for stability and translation of COX1 mRNA required for translation of COX2 mRNA ser/thr phosphoprotein phosphatase 1, catalytic subunit ser/thr protein kinase splicing protein and translational activator, mitochondrial strong similarity to Sco1p translational activator of cob mRNA	YIL023c YMR005w YMR189w YLL039c  Protein YEL030w YKL073w YIL142w YDL143w YJL014w YJL008c YDR188w YDR155c YML078w YOR288c YCR648e	PET130 MPT1 PET112  UBI4  Sin de folding  LHS1 CCT2  CCT3  CCT1  CCT4  CCT7  CCT8  CCT6  CPH1 CPH2  MPD1 FKB2  MDJ1 MGE1 HSP60	protein synthesis protein, mitochondrial required for protein synthesis required to maintain RHO' mitochondrial DNA similarity to peptidyl-tRNA hydrolases ubiquitin  Stination  and stabilization  heat-shock protein of HSP70 family chaperone of the ER lumen chaperonin of the TCP1 ring complex, cytosolic chaperonin of the TCP1 ring complex, cytosolic component of chaperonin-containing T-complex (\$\xi\$ subunity cyclophilin (peptidylprolyl isomerase) cyclophilin (peptidylprolyl isomerase) cyclophilin (peptidylprolyl isomerase), mitochondrial disulphide isomerase related protein dnal homologue FK506/rapamycin-binding protein of the ER heat-shock protein - chaperone heat-shock protein - chaperone heat-shock protein - chaperone, mitochondrial heat-shock protein of HSP70 family heat-shock protein of HSP70 family, leat-shock protein of HSP70 family, heat-shock protein of HSP70 family,
YNL081c YDR041w YYL009w YDL208w YPL026w YOR182c YNR037c YNL185c YER056c-a YMR230w YNL096c YLR167w YNL096c YLR167w YNL096c YLR167w YNL091c YMR309c YGL094c YDL01c YMR023c YDL01c YNL096c YDR172w YNL097c YGL094c YNL096c YDR172w YNL097c YGL094c YRL096c YRL094c YRL096c YRL094c YRL096c YRL094c YRL096c YRL094c YRL096c YRR096c YRR09c YRR096c YRR096c YRR096c YRR09c YRR09c YRR09c YRR09c YRR09c YRR0	UBI3  tion (initition)  RPLA1 NIP1 PAN2 SUP35 SIS1 MAP2 MSS1 MRF1 TIF4632 TIF4631 CAF20	similarity to ribosomal protein L5 similarity to ribosomal protein S13 similarity to ribosomal protein S13 similarity to ribosomal proteins similarity to Rpl10p and S.solfataricus ribosomal protein L10 strong similarity to high-mobility group (I-IMG) family strong similarity to high-mobility group-like protein Nhp2p strong similarity to human ubiquitin-like protein Nhp2p strong similarity to ribosomal protein S10 strong similarity to ribosomal protein L11 strong similarity to ribosomal protein S10 strong similarity to ribosomal protein S10 strong similarity to ribosomal protein S10 strong similarity to ribosomal protein S12 strong similarity to ribosomal protein S12 strong similarity to ribosomal protein S12 strong similarity to 30S ribosomal protein S17 weak similarity to ribosomal protein S17 weak similarity to ribosomal protein s11 associated with 40s ribosomal protein s14 associated with 40s ribosomal protein s14 associated with 40s ribosomal subunit component of Pab1p-stimulated poly(A) ribonuclease eukaryotic peptide chain release factor GTP-binding subunit heat-shock protein methionine aminopeptidase, isoform 2 mitochondrial GTPase involved in expression of COX1 mitochondrial geptide chain release factor mRNA cap-binding protein (elF4F), 130K subunit mRNA cap-binding protein (elF4F), 20K subunit mRNA polyadenylate-binding protein similarity to elongation factor 2 eFT1	YEL034W YJR047c YGL169W YJR047c YGL169W YBR143c  translait YMR282c YBR120c YPL029W YOR017W YMR028W YDR197W YNL216W YER054c YMR080c YGR072cW YHR077c YMR064W YPL179W YFR009W YL79W YFR009W YL79W YR067c YMR257c YMR257c YMR257c YMR257c YMR257c YMR257c YMR257c YMR257c YR133W YOR178c	HYP2 ANB1 SUA5 SUP45  tional ca  AEP2 CBP6 SUV3 PET127 TAP42 CBS2 RAP1 GIP2 NAMD2 AEP1 PP01 GCN20 MSS51 SHP1 RLR1 PET309 PET111 GCC7 GAC1 GCN2 PET54 SCO2 GCN1	translation initiation factor eIFSA.1 translation initiation factor eIFSA.2 translation initiation protein translational release factor  pontrol  2'-O-ribosyl phosphate transferase apo-cytochrome b pre-mRNA processing protein ATP-dependent RNA helicase, mitochondrial component of mitochondrial translation system component of the Tor signalling pathway cytochrome b translational activator protein DNA-binding protein with repressor and activator activity Glc7p-interacting protein nonsense-mediated mRNA decay protein nonsense-mediated mRNA decay protein nonsense-mediated mRNA decay protein nonsense-mediated mRNA decay protein posphoprotein phosphatase positive effector of Gcn2p possibly involved in translational activation of COX1 and COB mRNA potential regulatory subunit for Glc7p regulatory protein required for translation of COX2 mRNA ser/thr phosphoprotein phosphatase 1, catalytic subunit ser/thr phosphoprotein phosphatase 1, regulatory subunit ser/thr phosphoprotein phosphatase 1, regulatory subunit ser/thr phosphoprotein phosphatase 1, regulatory subunit ser/thr protein kinase splicing protein and translational activator, mitochondrial strong similarity to Sco1p translational activator of coto mRNA translational activator of cytochrome c	YJL023c YMR005w YMR189w YLL039c  Protein YEL030w YKL073w YJL104W YDR212w YDL143w YJL111w YJL008c YDR188w YDR165c YML078w YOR288c YCR048c YDR519w YFL016c YOR232w YJR045c YAL005c YLL024c	PET130 MPT1 PET112  UBI4  Sin de folding  LHS1 CCT2  CCT3  CCT1  CCT4  CCT7  CCT8  CCT6  CPH1 CPR3  MPD1 CAl1 FKB2  MDJ1 MGE1 HSP60  SSC1  SSA1 SSA2	protein synthesis protein, mitochondrial required for protein synthesis required to maintain RHO' mitochondrial DNA similarity to peptidyl-tRNA hydrolases ubiquitin  Stination  and stabilization  heat-shock protein of HSP70 family chaperone of the ER lumen chaperonin of the TCP1 ring complex, cytosolic chaperonin of the TCP1 ring complex, cytosolic component of chaperonin-containing T-complex component of chaperonin-containing T-complex component of chaperonin-containing T-complex (5 subunit) component of chaperonin-containing T-complex (5 subunit) cyclophilin (peptidylprolyl isomerase) cyclophilin (peptidylprolyl isomerase), mitochondrial disulphide isomerase related protein dnal homologue FK506/rapamycin-binding protein of the ER heat-shock protein - chaperone heat-shock protein - chaperone, mitochondrial heat-shock protein fHSP70 family, cytosolic
YMR188c YDL202w translat termina YDL081c YMR309c YGL094c YDR172w YNL007c YBL091c YMR023c YGL143c YGL049c YGR162w YOR276w YER165w YKL173w YKL173w YKL173w YGR201c	RPS30B  UBI3  tion (initition)  RPLA1 NIP1 PAN2 SUP35 SIS1 MAP2 MSS1 MRF1 TIF4632 TIF4631 CAF20 PAB1	similarity to ribosomal protein L5 similarity to ribosomal protein S13 similarity to ribosomal protein S13 similarity to ribosomal proteins similarity to Rpl10p and S.solfataricus ribosomal protein L10 strong similarity to high-mobility group (I-IMG) family strong similarity to high-mobility group-like protein Nhp2p strong similarity to human ubiquitin-like protein Nhp2p strong similarity to human ubiquitin-like protein Nhp2p strong similarity to human ubiquitin-like protein Nhp2p strong similarity to ribosomal protein S10 strong similarity to ribosomal protein L11 strong similarity to ribosomal protein L13 strong similarity to ribosomal protein S10 strong similarity to ribosomal protein S12 strong similarity to ribosomal protein S17 weak similarity to ribosomal protein S17 weak similarity to ribosomal protein s17 weak similarity to ribosomal protein s18 acidic ribosomal protein and acidic ribosomal protein al associated with 40s ribosomal protein s18 acidic ribosomal protein s18 acidic ribosomal protein s19 acidic ribosomal protein s10 acidic ribosomal protein s10 acidic ribosomal protein s11 associated with 40s ribosomal protein s11 as	YEL034W YJR047c YGL169W YJR047c YGL169W YBR143c  translat  YMR282c YBR120c  YPL029W YOR017W YMR028W YDR197W YNL216W YER054c YMR080c YGR072W YHR077c YMR064W YPL179W YFR009W YLR203c YBL058W YNL139c YLR067c YMR257c YER133W YOR178c YDR283c YGR222W YBR024W YGL195W YDL069c YER153c YNR045W	HYP2 ANB1 SUA5 SUP45 tional co  AEP2 CBP6 SUV3 PET127 TAP42 CBS2 RAP1 GIP2 NAM7 UPF3 NMD2 AEP1 PPQ1 GCN20 MSS51 PET309 PET111 GLC7 GAC1 GCN2 PET64 SCO2 GCN1 CBS1 PET122 PET494	translation initiation factor eIFSA.1 translation initiation factor eIFSA.2 translation initiation protein translational release factor  pontrol  2'-O-ribosyl phosphate transferase apo-cytochrome b pre-mRNA processing protein ATP-dependent RNA helicase, mitochondrial component of mitochondrial translation system component of mitochondrial translation system component of the Tor signalling pathway cytochrome b translational activator protein DNA-binding protein with repressor and activator activity Glo7p-interacting protein nonsense-mediated mRNA decay protein nonsense-mediated mRNA decay protein nonsense-mediated mRNA decay protein phosphoprotein phosphatase positive effector of Gcn2p possibly involved in translational activation of COX1 and COB mRNA potential regulatory subunit for Glc7p regulatory protein required for stability and translation of COX1 mRNA required for translation of COX2 mRNA ser/thr phosphoprotein phosphatase 1, regulatory subunit ser/thr protein kinase spilcing protein and translational activator, mitochondrial strong similarity to Sco1p translational activator of cob mRNA translational activator of cytochrome c oxidase subunit III translational activator, mitochondrial	YIL023c YMR005w YHR189w YLL039c  Protein YEL030w YKL073w YIL142w YDL142w YDL143w YDL143w YJL111w YDR155c YML078w YOR288c YER048c YDR165e YDR165e YDR165e YDR165e YDR25e YJR045c YJR045c YAL005c YLL024c YDR171w	PET130 MPT1 PET112  UBI4  LHS1 CCT2 CCT3 CCT1 CCT4 CCT7 CCT8 CCT6 CPH1 CPR3  MPD1 CAl1 FKB2 MD1 MGE1 HSP60 SSC1 SSA1 SSA2 HSP42	protein synthesis protein, mitochondrial required for protein synthesis required to maintain RHO' mitochondrial DNA similarity to peptidyl-tRNA hydrolases ubiquitin  Stination  and stabilization  heat-shock protein of HSP70 family chaperone of the ER lumen chaperonin of the TCP1 ring complex, cytosolic chaperonin of the TCP1 ring complex, cytosolic component of chaperonin-containing T-complex (5 subunit) cyclophilin (peptidylprolyl isomerase) cyclophil
YNLL081c YDR041w YYDL208w YPL208w YPL208w YYDL208w YYDL208w YYDR182c YNR037c YNL185c YER056c-a YMR230w YNR036c YNL186c YNR036c YNR036c YNR036c YNR188c YDL202w  ***translat** **termina** YDL081c YMR309c YGL094c YDR172w YNL007c Y8L091c YYMR023c YGL049c YGL049c YGR162w YOR276w YER165w YCR165w YCR165w YCH173w YHR015w YHR015w YHR1615w YHR1615w YHR1615w	RPS30B  UBI3  tion (initition)  RPLA1 NIP1 PAN2 SUP35 SIS1 MAP2 MSS1 MRF1 TIF4632 TIF4631 CAF20 PAB1	similarity to ribosomal protein L5 similarity to ribosomal protein S13 similarity to ribosomal protein S13 similarity to ribosomal proteins similarity to Rpl10p and S.solfataricus ribosomal protein L10 strong similarity to high-mobility group (HMG) family strong similarity to high-mobility group-like protein Nhp2p strong similarity to high-mobility group-like protein Nhp2p strong similarity to human ubiquitin-like protein Nhp2p strong similarity to human ubiquitin-like protein S10 somal protein S19 strong similarity to ribosomal protein L11 strong similarity to ribosomal protein L14 strong similarity to ribosomal protein S10 strong similarity to ribosomal protein S11 weak similarity to ribosomal protein S11 associated with 40s ribosomal subunit component of Pab1p-stimulated poly(A) ribonuclease eukaryotic peptide chain release factor GTP-binding subunit heat-shock protein methionine aminopeptidase, isoform 2 mitochondrial GTPase involved in expression of COX1 mitochondrial peptide chain release factor mRNA cap-binding protein (elF4F), 130K subunit mRNA cAP-binding protein (elF4F), 150K subunit mRNA polyadenylate-binding protein imilarity to elongation factor 2 eFT1 similarity to PES4 PAB-like protein	YEL034W YJR047c YGL169W YJR047c YGL169W YBR143c  translat YMR282c YBR120c  YPL029W YOR017W YMR028W YDR197W YNL216W YER054c YMR080c YGR072W YHR077c YMR064W YPL179W YFR099W YLR203c YBL058W YNL139c YLR067c YMR257c YMR257c YMR257c YMR257c YMR257c YMR257c YMR257c YDR283c YDR283c YDR283c YDR283c YDR283c YDR283c YBR024W YGL195W YDL069c YER153c	HYP2 ANB1 SUA5 SUP45  tional ca  AEP2 CBP6 SUV3 PET127 TAP42 CBS2 RAP1 GIP2 NAM7 UPF3 NMD2 AEP1 PP01 GCN20 MSS51 SHP1 RLR1 RLR1 CGCC GAC1 GCN2 PET64 CGS1 PET122	translation initiation factor eIFSA.1 translation initiation factor eIFSA.2 translation initiation protein translational release factor  pontrol  2'-O-ribosyl phosphate transferase apo-cytochrome b pre-mRNA processing protein ATP-dependent RNA helicase, mitochondrial component of mitochondrial translation system component of the Tor signalling pathway cytochrome b translational activator protein DNA-binding protein with repressor and activator activity Glc7p-interacting protein nonsense-mediated mRNA decay protein nonsense-mediated mRNA decay protein nonsense-mediated mRNA decay protein posense-mediated mRNA decay protein nonsense-mediated mRNA decay protein nonsense-mediated mRNA decay protein phosphoprotein phosphatase positive effector of Gn2p possibly involved in translational activation of COX1 and COB mRNA potential regulatory subunit for Glc7p regulatory protein required for translation of COX2 mRNA prequired for translation of COX2 mRNA ser/thr phosphoprotein phosphatase 1, regulatory subunit ser/thr phosphoprotein phosphatase 1, regulatory subunit ser/thr phosphoprotein phosphatase 1, regulatory subunit ser/thr protein kinase splicing protein and translational activator ranslational activator translational activator translational activator translational activator of cob mRNA translational activator of cytochrome c	YJL023c YMR005w YMR189w YLL039c  Protein YEL030w YKL073w YJL104W YDR212w YDL143w YJL111w YJL008c YDR188w YDR165c YML078w YOR288c YCR048c YDR519w YFL016c YOR232w YJR045c YAL005c YLL024c	PET130 MPT1 PET112  UBI4  Sin de folding  LHS1 CCT2  CCT3  CCT1  CCT4  CCT7  CCT8  CCT6  CPH1 CPR3  MPD1 CAl1 FKB2  MDJ1 MGE1 HSP60  SSC1  SSA1 SSA2	protein synthesis protein, mitochondrial required for protein synthesis required to maintain RHO' mitochondrial DNA similarity to peptidyl-tRNA hydrolases ubiquitin  Stination  and stabilization  heat-shock protein of HSP70 family chaperone of the ER lumen chaperonin of the TCP1 ring complex, cytosolic chaperonin of the TCP1 ring complex, cytosolic component of chaperonin-containing T-complex (5 subunit) cyclophilin (peptidylprolyl isomerase) cyclophilin (peptidylprolyl isomerase) cyclophilin (peptidylprolyl isomerase) cyclophilin (peptidylprolyl isomerase) mitochondrial disulphide isomerase related protein dnal homologue FK506/rapamycin-binding protein of the ER heat-shock protein - chaperone heat-shock protein - chaperone heat-shock protein f HSP70 family heat-shock protein of HSP70 family, cytosolic heat-shock protein with similarity to

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YHR057c	CYP2	peptidyl-prolyl cis-trans isomerase	YBR162w-a		secretory pathway protein	YKL134c	(MIP1)	mitochondrial intermediate peptidase
YCR069w YDR304c	SCC3 CYP5	peptidyl-prolyl <i>cis-trans</i> isomerase peptidyl-prolyl <i>cis-trans</i> isomerase D	YBR097w YPL243w		ser/thr protein kinase signal recognition particle protein	YLR163c YHR024c	MAS1 MAS2	mitochondrial processing peptidase mitochondrial processing peptidase,
10113040	CIFS	(cyclophilin D) of the ER	YPL210c	SRP72	signal recognition particle protein	111110240	IVIAOZ	catalytic 53K (α) subunit
YNL135c	FPR1	peptidyl-prolyl cis-trans isomerase, FK506-	YDR292c	SRP101	signal recognition particle receptor, α	YMR150c	IMP1	mitochondrial protease
YML074c	NPI46	binding protein proline <i>cis-trans</i> isomerase	YML105c	SEC65	subunit signal recognition particle subunit	YPR051w YGR147c	MAK3 NAT2	N-acetyltransferase N-acetyltransferase for N-terminal
YDR518w	EUG1	protein disulphide isomerase	YDL092w	SRP14	signal recognition particle subunit			methionine
YCL043c YJR097w	PDI1	protein disulphide-isomerase similarity to Caj1p	YKL122c YPR088c	SRP21 SRP54	signal recognition particle subunit signal recognition particle subunit	YBR247c YLR195c	ENP1 NMT1	N-glycosylation protein N-myristoyltransferase
YBR044c		similarity to carry similarity to chaperonin HSP60 proteins	YOR285w	JHF 54	similarity to <i>D. melanogaster</i> heat-shock	YJL002c	OST1	oligosaccharyltransferase α subunit
YOL088c		similarity to disulphide isomerases and ER60 proteases	VODOOO		protein 67B2	YEL002c	WBP1 SWP1	oligosaccharyltransferase β subunit
YNL077w		similarity to dnaJ protein homologue YDJ1	YOR286w		similarity to <i>D. melanogaster</i> heat-shock protein 67B2	YMR149w YOR103c	OST2	oligosaccharyltransferase δ subunit oligosaccharyltransferase ε subunit
YMR161w	HLJ1	similarity to dnaJ proteins	YHR110w		similarity to human gp25L2 protein	YOR085w	OST3	oligosaccharyltransferase γ subunit
YIR004w YLR090w	XDI1	similarity to DNAJ-like proteins similarity to <i>E. coli</i> dnaJ	YAR002c-a YKL154w		similarity to mammalian gp25L protein similarity to mouse signal recognition	YDL232w YGL022w	OST4 STT3	oligosaccharyltransferase subunit oligosaccharyltransferase subunit
YJL073w		similarity to heat-shock proteins			particle receptor β subunit	YFL045c	SEC53	phosphomannomutase
YNR028w		similarity to peptidylprolyl isomerase Scc3p	YKL196c YMR018w		similarity to Sec22p similarity to tetratricopeptide-repeat	YPR122w YEL060c	AXL1 PRB1	protease protease B, vacuolar
YIL005w		similarity to protein disulphide isomerases			protein PAS10	YLR389c	STE23	protease involved in a-factor processing
YLR369w		strong similarity to heat-shock protein 70- related proteins	YMR214w YNL304w	SCJ1	similarity to to <i>E. coli</i> dnaJ similarity to Ypt1p and other GTP-binding	YCL043c YKL019w	PDI1 RAM2	protein disulphide-isomerase protein farnesyltransferase, α subunit
YLR449w		strong similarity to peptidylprolyl	TIVESOTIV		proteins	YDL090c	RAM1	protein farnesyltransferase, β subunit
YJR064w	CCT5	isomerase FRP3	YER101c	AST2	strong similarity to Ast1p	YHR013c YDL040c	ARD1 NAT1	protein N-acetyltransferase subunit protein N-acetyltransferase subunit
YFR041c	0015	T-complex protein 1, $\epsilon$ subunit weak similarity to dnaJ-like heat-shock	YOR016c		strong similarity to FUN54 protein, similarity to hamster COP-coated vesicle	YIL085c	KTR7	putative α-1,2-mannosyltransferase
VAII 007=		proteins	VCI 000		membrane protein	YGL194c	RTL1	putative deacetylase
YNL227c		weak similarity to dnaJ-like proteins	YGL002w YER087c-a	SEB1	strong similarity to human gp25L2 protein strong similarity to mammalian Sec61β	YNL029c YGR199w	KTR5 PMT6	putative mannosyltransferase putative mannosyltransferase
protein	targetii	ng, sorting and translocation	.,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,		subunit	YKL193c	SDS22	regulatory subunit for the mitotic function
YKL073w	LHS1	chaperone of the ER lumen	YCR099c YCR100c		strong similarity to Pep1p strong similarity to Pep1p	YNL048w	ALG11	of type I protein phosphatase required for asparagine-linked
YGL206c	CHC1	clathrin heavy chain	YCR101c		strong similarity to Pep1p			glycosylation
YOL062c YPL259c	APM4 APM1	clathrin-associate protein YAP54 clathrin-associated protein	YIL173w YJL222w		strong similarity to Pep1p strong similarity to Pep1p	YLR088w	GAA1	required for attachment of GPI anchor onto proteins
YBR288c	APM3	clathrin-associated protein complex,	YBR283c		strong similarity to Sec61p	YPL050c	MNN9	required for complex N-glycosylation
YDL212w	SHR3	medium subunit endoplasmic reticulum membrane protein	YOR327c YOR329c	SNC2 SCD5	strong similarity to synaptobrevin suppressor of clathrin deficiency	YJR010c-a YML055w	SPC1 SPC2	signal peptidase 10.8K subunit signal peptidase 18K subunit
YBL040c	ERD2	ER lumen protein-retaining receptor	YHR050w	SMF2	suppressor of clatifit deliciency suppressor of mitochondrial matrix	YIR022w	SEC11	signal sequence processing protein
YER019c-a YLR378c	SEB2 SEC61	ER protein-translocation complex subunit ER protein-translocation complex subunit	YOR036w	DED10	mutant	YDL042c YER005w	SIR2	silencing regulatory protein similarity to Gda1p
YPL094c	SEC62	ER protein-translocation complex subunit	YLR148w	PEP3	syntaxin (T-SNARE) vacuolar membrane protein	YMR223w		similarity to duarp similarity to human putative ubiquitin
YOR254c	SEC63	ER protein-translocation complex subunit	YBL017c	PEP1	vacuolar protein sorting/targeting protein	VDD000		carboxyl-terminal hydrolase
YBR171w YLR292c	SEC66 SEC72	ER protein-translocation complex subunit ER protein-translocation complex subunit	YJL053w YOR132w	PEP8 VPS17	vacuolar protein sorting/targeting protein vacuolar protein sorting-associated	YDR098c		similarity to <i>Legionella</i> glutaredoxin-like protein
YDR086c	SSS1	ER protein-translocation complex subunit		1/000=	protein	YER174c		similarity to Legionella glutaredoxin-like
YOR089c YKR014c	VPS21 YPT52	GTP-binding protein GTP-binding protein of the RAB family	YNR006w	VPS27	vacuolar protein sorting-associated protein	YGL257c		protein similarity to Mnn1p
YNL093w	YPT53	GTP-binding protein of the RAB family	YGL095c	VPS45	vacuolar protein sorting-associated	YIL014w		similarity to Mnn1p
YOR270c	VPH1	(RAS superfamily) H*-ATPase V0 domain 95K subunit,	YJL154c	VPS35	protein vacuolar protein-sorting protein	YPR131c YDL093w	PMT5	similarity to N-acetyltransferases similarity to O-mannosyltransferases
		vacuolar	YDR323c	PEP7	vacuolar segregation protein		7 77770	Pmt1p-Pmt4p
		heat-shock protein of HSP70 family						
YAL005c	SSA1 FRS1		YPL045w	VPS16	vacuolar sorting protein	YDR307w YDR245w	MANNIO	similarity to Pmt1p
YCR075c YGR028w	ERS1 MSP1	intracellular protein transport protein intra-mitochondrial sorting protein	YDR495c YLR396c	VPS3 VPS33	vacuolar sorting protein vacuolar sorting protein vacuolar sorting protein	YDR245w	MNN10	similarity to <i>S. pombe</i> galactosyltransferase
YCR075c	ERS1 MSP1	intracellular protein transport protein intra-mitochondrial sorting protein involved in Golgi retention and vacuolar	YDR495c YLR396c YAL002w	VPS3 VPS33 VPS8	vacuolar sorting protein vacuolar sorting protein vacuolar sorting protein	YDR245w YLR066w	MNN10	similarity to <i>S. pombe</i> galactosyltransferase similarity to signal peptidase
YCR075c YGR028w	ERS1 MSP1	intracellular protein transport protein intra-mitochondrial sorting protein	YDR495c YLR396c YAL002w YML097c	VPS3 VPS33 VPS8 VPS9	vacuolar sorting protein vacuolar sorting protein vacuolar sorting protein vacuolar sorting protein	YDR245w	MNN10	similarity to <i>S. pombe</i> galactosyltransferase similarity to signal peptidase similarity to to α-1,3-mannosyltransferase similarity to ubiquitin-activating enzymes
YCR075c YGR028w YOR069w YLR347c YOL122c	ERS1 MSP1 VPS5 KAP95 SMF1	intracellular protein transport protein intra-mitochondrial sorting protein involved in Golgi retention and vacuolar sorting karyopherin-β manganese transporter	YDR495c YLR396c YAL002w YML097c	VPS3 VPS33 VPS8 VPS9	vacuolar sorting protein vation (glycosylation, acylation,	YDR245w YLR066w YNR059w YPL003w YPR180w	MNN10	similarity to <i>S. pombe</i> galactosyltransferase similarity to signal peptidase similarity to to $\alpha$ -13-mannosyltransferase similarity to ubiquitin-activating enzymes similarity to ubiquitin-activating enzymes
YCR075c YGR028w YOR069w YLR347c	ERS1 MSP1 VPS5 KAP95	intracellular protein transport protein intra-mitochondrial sorting protein involved in Golgi retention and vacuolar sorting karyopherin-β	YDR495c YLR396c YAL002w YML097c	VPS3 VPS33 VPS8 VPS9 modification, p	vacuolar sorting protein vacuolar sorting protein vacuolar sorting protein vacuolar sorting protein	YDR245w YLR066w YNR059w YPL003w	MNN10	similarity to <i>S. pombe</i> galactosyltransferase similarity to signal peptidase similarity to to α-1,3-mannosyltransferase similarity to ubiquitin-activating enzymes
YCR075c YGR028w YOR069w YLR347c YOL122c YKR001c	ERS1 MSP1 VPS5 KAP95 SMF1 VPS1	intracellular protein transport protein intra-mitochondrial sorting protein involved in Golgi retention and vacuolar sorting karyopherin-β manganese transporter member of the dynamin family of GTPases mitochondrial chaperonin	YDR495c YLR396c YAL002w YML097c <b>protein</b> <b>myristy</b> <b>process</b>	VPS3 VPS33 VPS8 VPS9 modific vlation, p	vacuolar sorting protein vation (glycosylation, acylation, palmitylation, farnesylation and	YDR245w YLR066w YNR059w YPL003w YPR180w YGL087c	MNN10  KTR3	similarity to <i>S. pombe</i> galactosyltransferase similarity to signal peptidase similarity to to $\alpha$ -13-mannosyltransferase similarity to ubiquitin-activating enzymes similarity to ubiquitin-activating enzymes similarity to ubiquitin-protein ligase similarity to $\alpha$ -1,2-
YCR075c YGR028w YOR069w YLR347c YOL122c YKR001c	ERS1 MSP1 VPS5 KAP95 SMF1 VPS1	intracellular protein transport protein intra-mitochondrial sorting protein involved in Golgi retention and vacuolar sorting karyopherin-β manganese transporter member of the dynamin family of GTPases	YDR495c YLR396c YAL002w YML097c <b>protein</b> <b>myristy</b>	VPS3 VPS33 VPS8 VPS9 modificulation, psing)	vacuolar sorting protein vation (glycosylation, acylation,	YDR245w YLR066w YNR059w YPL003w YPR180w YGL087c YIR039c		similarity to <i>S. pombe</i> galactosyltransferase galactosyltransferase similarity to signal peptidase similarity to to α-1,3-mannosyltransferase similarity to ubiquitin-activating enzymes similarity to ubiquitin-protein ligase similarity to vapap strong similarity to γapap strong similarity to γapap strong similarity to α-1,2-mannosyltransferase
YCR075c YGR028w YOR069w YLR347c YOL122c YKR001c	ERS1 MSP1 VPS5 KAP95 SMF1 VPS1	intracellular protein transport protein intra-mitochondrial sorting protein involved in Golgi retention and vacuolar sorting karyopherin-β manganese transporter member of the dynamin family of GTPases mitochondrial chaperonin mitochondrial inner membrane import translocase subunit mitochondrial inner membrane import	YDR495c YLR396c YAL002w YML097c <b>protein</b> <b>myristy</b> <b>process</b> YJR131w YDR483w YER001w	VPS3 VPS33 VPS8 VPS9 modificiation, psing) MNS1 KRE2 MNN1	vacuolar sorting protein vation (glycosylation, acylation, palmitylation, farnesylation and	YDR245W YLR066W YNR059W YPL003W YPR180W YGL087c YIR039c YBR205W YBR199W	KTR3 KTR4	similarity to <i>S. pombe</i> galactosyltransferase similarity to signal peptidase similarity to to α-1,3-mannosyltransferase similarity to ubiquitin-activating enzymes similarity to ubiquitin-activating enzymes similarity to ubiquitin-protein ligase similarity to τραβρ strong similarity to α-1,2-mannosyltransferase strong similarity to α-1,2-mannosyltransferase
YCR075c YGR028w YOR069w YLR347c YOL122c YKR001c YOR020c YNR017w YJL143w	ERS1 MSP1 VPS5 KAP95 SMF1 VPS1 HSP10 MAS6	intra-cellular protein transport protein intra-mitochondrial sorting protein involved in Golgi retention and vacuolar sorting karyopherin-β manganese transporter member of the dynamin family of GTPases mitochondrial chaperonin mitochondrial inner membrane import translocase subunit mitochondrial inner membrane import translocase subunit mitochondrial inner membrane import translocase subunit	YDR495c YLR396c YAL002w YML097c <b>protein</b> <b>myristy</b> <b>process</b> YJR131w YDR483w YER001w YGL038c	VPS3 VPS33 VPS8 VPS9 <b>modific</b> (lation, p sing) MNS1 KRE2 MNN1 OCH1	vacuolar sorting protein vation (glycosylation, acylation, palmitylation, farnesylation and α-1,2-mannosidase α-1,2-mannosyltransferase α-1,3-mannosyltransferase α-1,6-mannosyltransferase α-1,6-mannosyltransferase	YDR245w YLR066w YNR059w YPL003w YPR180w YGL087c YIR039c YBR205w	KTR3	similarity to <i>S. pombe</i> galactosyltransferase galactosyltransferase similarity to signal peptidase similarity to to α-1,3-mannosyltransferase similarity to ubiquitin-activating enzymes similarity to ubiquitin-protein ligase similarity to Yap3p strong similarity to α-1,2- mannosyltransferase strong similarity to α-1,2- mannosyltransferase strong similarity to α-1,2- mannosyltransferase strong similarity to α-1,2-
YCR075c YGR028w YOR069w YLR347c YOL122c YKR001c YOR020c YNR017w YJL143w YIL022w	ERS1 MSP1 VPS5 KAP95 SMF1 VPS1 HSP10 MAS6 TIM17	intracellular protein transport protein intra-mitochondrial sorting protein involved in Golgi retention and vacuolar sorting karyopherin-β manganese transporter member of the dynamin family of GTPases mitochondrial chaperonin mitochondrial inner membrane import translocase subunit	YDR495c YLR396c YAL002w YML097c <b>protein</b> <b>myristy</b> <b>process</b> YJR131w YDR483w YER001w YGL038c YBR164c YKL157w	VPS3 VPS33 VPS8 VPS9 modific (lation, psing) MNS1 KRE2 MNN1 OCH1 ARL1 APE2	vacuolar sorting protein vation (glycosylation, acylation, palmitylation, farnesylation and	YDR245W YLR066W YNR059W YPL003W YPR180W YGL087c YIR039c YBR205W YBR199W	KTR3 KTR4	similarity to <i>S. pombe</i> galactosyltransferase similarity to signal peptidase similarity to to $\alpha$ -1,3-mannosyltransferase similarity to ubiquitin-activating enzymes similarity to ubiquitin-activating enzymes similarity to ubiquitin-protein ligase similarity to $\alpha$ -1,2-mannosyltransferase strong similarity to $\alpha$ -1,2-mannosyltra
YCR075c YGR028w YOR069w YLR347c YOL122c YKR001c YOR020c YNR017w YJL143w	ERS1 MSP1 VPS5 KAP95 SMF1 VPS1 HSP10 MAS6 TIM17	intracellular protein transport protein intra-mitochondrial sorting protein involved in Golgi retention and vacuolar sorting karyopherin-β manganese transporter member of the dynamin family of GTPases mitochondrial chaperonin mitochondrial inner membrane import translocase subunit mitochondrial inner membrane protease	YDR495c YLR396c YAL002w YML097c protein myristy proces: YJR131w YDR483w YER001w YGL038c YBR164c YKL157w YJR062c	VPS3 VPS3 VPS9 VPS9 modific vlation, I sing) MNS1 KRE2 MNN1 OCH1 ARL1 APE2 NTA1	vacuolar sorting protein vation (glycosylation, acylation, palmitylation, farnesylation and α-12-mannosidase α-1,2-mannosyltransferase α-1,3-mannosyltransferase α-1,6-mannosyltransferase ADP-ribosylation factor amino-petridase yscll amino-terminal amidase	YDR245w YLR066w YNR059w YPR180w YPR180w YGL087c YIR039c YBR206w YBR199w YPL053c YPL051w	KTR3 KTR4	similarify to <i>S. pombe</i> galactosyltransferase similarity to signal peptidase similarity to signal peptidase similarity to to α-1,3-mannosyltransferase similarity to ubiquitin-activating enzymes similarity to ubiquitin-activating enzymes similarity to ubiquitin-protein ligase similarity to γ4p3p strong similarity to α-1,2-mannosyltransferase strong similarity to α-1,2-mannosyltransferase strong similarity to α-1,2-mannosyltransferase strong similarity to α-1,2-mannosyltransferase Kre2p strong similarity to α-1,2-mannosyltransferase strong similarity to α-
YCR075c YGR028w YOR069w YLR347c YOL122c YKR001c YOR020c YNR017w YJL143w YIL022w	ERS1 MSP1 VPS5 KAP95 SMF1 VPS1 HSP10 MAS6 TIM17	intracellular protein transport protein intra-mitochondrial sorting protein involved in Golgi retention and vacuolar sorting karyopherin-β manganese transporter member of the dynamin family of GTPases mitochondrial chaperonin mitochondrial inner membrane import translocase subunit mitochondrial inner membrane protease subunit mitochondrial inner membrane protease subunit mitochondrial outer membrane import	YDR495c YLR396c YAL002w YML097c <b>protein</b> <b>myristy</b> <b>proces:</b> YJR131w YDR483w YER001w YGL038c YBR164c YKL157w YJR062c YGL017w YPL154c	VPS3 VPS3 VPS9 VPS9 modific (lation, p sing) MNS1 KRE2 MNN1 OCH1 ARL1 APE2 NTA1 ATE1 PEP4	vacuolar sorting protein vacuolar sorting pro	YDR245w YLR066w YNR059w YPL003w YPR180w YGL087c YIR039c YBR205w YBR199w YPL053c YPL051w YLR121c YOR099w	KTR3 KTR4 KTR6	similarity to <i>S. pombe</i> galactosyltransferase galactosyltransferase similarity to signal peptidase similarity to to α-13-mannosyltransferase similarity to ubiquitin-activating enzymes similarity to ubiquitin-activating enzymes similarity to ubiquitin-protein ligase similarity to ubiquitin-protein ligase similarity to α-12-mannosyltransferase strong similarity to α-12-mannosyltransferase strong similarity to α-12-mannosyltransferase Kre2p strong similarity to α-12-mannosyltransferase Kre2p strong similarity to aspartylproteases strong similarity to aspartylproteases strong similarity to mannosyltransferases
YCR075c YGR028w YOR069w YLR347c YOL122c YKR001c YOR020c YNR017w YJL143w YIL022w YMR035w	ERS1 MSP1 VPS5 KAP95 SMF1 VPS1 HSP10 MAS6 TIM17 TIM44 IMP2	intracellular protein transport protein intra-mitochondrial sorting protein involved in Golgi retention and vacuolar sorting karyopherin-β manganese transporter member of the dynamin family of GTPases mitochondrial chaperonin mitochondrial inner membrane import translocase subunit mitochondrial inner membrane protease subunit mitochondrial inner membrane protease subunit mitochondrial outer membrane import receptor subunit	YDR495c YLR396c YAL002w YML097c protein myristy process: YJR131w YDR483w YER001w YGL038c YBR164c YKL157w YJR062c YGL017w YPL154c YLR120c	VPS3 VPS3 VPS8 VPS9 VPS9 modific (lation, psing) MNS1 KRE2 MNN1 OCH1 ARL1 APE2 NTA1 APE2 NTA1 APE4 YAP3	vacuolar sorting protein vacuolar sorting pro	YDR245W YLR066W YNR059W YPL003W YPR180W YGL087c YJR039c YBR206W YPL053c YPL051W YLR121c YOR099W YCR083W	KTR3 KTR4 KTR6	similarity to <i>S. pombe</i> galactosyltransferase similarity to signal peptidase similarity to to α-1,3-mannosyltransferase similarity to ubiquitin-activating enzymes similarity to ubiquitin-activating enzymes similarity to ubiquitin-protein ligase similarity to γ4p3p strong similarity to α-1,2- mannosyltransferase strong similarity to α-1,2- mannosyltransferase strong similarity to α-1,2- mannosyltransferase strong similarity to α-1,2- strong similarity to α-1,2- strong similarity to α-1,2- strong similarity to α-1,2- strong similarity to appartylproteases strong similarity to aspartylproteases strong similarity to mannosyltransferases strong similarity to mannosyltransferases strong similarity to thoredoxin
YCR075c YGR026w YOR069w YLR347c YOL122c YKR001c YOR020c YNR017w YJL143w YIL022w YMR035w YNL131w YGR082w	ERS1 MSP1 VPS5 KAP95 SMF1 VPS1 HSP10 MAS6 TIM17 TIM44 IMP2 TOM22	intracellular protein transport protein intra-mitochondrial sorting protein involved in Golgi retention and vacuolar sorting karyopherin-β manganese transporter member of the dynamin family of GTPases mitochondrial chaperonin mitochondrial inner membrane import translocase subunit mitochondrial outer membrane import receptor subunit mitochondrial outer membrane import receptor subunit, 20K	YDR495c YLR396c YAL002w YML097c protein myristy proces: YJR131w YER001w YGL038c YBR164c YKL167w YJR062c YGL017w YPL154c YLR120c YDL41w YBR110c	VPS3 VPS3 VPS9 Modific (lation, l sing) MNS1 KRE2 MNN1 OCH1 ARL1 APE2 NTA1 ATE1 YAP3 BPL1 ALG1	vacuolar sorting protein vacuolar sorting pro	YDR245w YLR066w YNR059w YPL003w YPR180w YGL087c YJR309c YBR205w YPL053c YPL051w YLR121c YOR099w YCR083w YOR339c	KTR3 KTR4 KTR6	similarity to <i>S. pombe</i> galactosyltransferase galactosyltransferase similarity to signal peptidase similarity to to α-13-mannosyltransferase similarity to ubiquitin-activating enzymes similarity to ubiquitin-activating enzymes similarity to ubiquitin-protein ligase similarity to ubiquitin-protein ligase similarity to α-12-mannosyltransferase strong similarity to α-12-mannosyltransferase strong similarity to α-12-mannosyltransferase strong similarity to α-12-mannosyltransferase Kre2p strong similarity to aspartylproteases strong similarity to aspartylproteases strong similarity to thioredoxin strong similarity to thioredoxin strong similarity to ubiquitin conjugating enzymes
YCR075c YGR028w YCR069w YLR347c YOL122c YKR001c YOR020c YNR017w YJL143w YIL022w YMR035w YNL131w	ERS1 MSP1 VPS5 KAP95 SMF1 VPS1 HSP10 MAS6 TIM17 TIM44 IMP2	intracellular protein transport protein intra-mitochondrial sorting protein involved in Golgi retention and vacuolar sorting karyopherin-β manganese transporter member of the dynamin family of GTPases mitochondrial chaperonin mitochondrial inner membrane import translocase subunit mitochondrial inner membrane import receptor subunit mitochondrial outer membrane import receptor subunit, 20K mitochondrial outer membrane import receptor subunit, 20K mitochondrial outer membrane import receptor subunit, 20K mitochondrial outer membrane import mitochondrial outer membrane import	VDR495c YLR396c YLR396c protein myristy process YJR131w YDR483w YER001w YGL038c YBR164c YKL157w YJR062c YGL017w YPL164c YLR120c YDL141v	VPS3 VPS3 VPS8 VPS9 modific (lation, ) sing) MNS1 KRE2 MNN1 OCH1 ARL1 APE2 NTA1 ATE1 PEP4 YAP3 BPL1	vacuolar sorting protein vacuolar sorting pro	YDR245W YLR066W YNR059W YPL003W YPR180W YGL087c YJR039c YBR206W YPL053c YPL051W YLR121c YOR099W YCR083W	KTR3 KTR4 KTR6	similarity to <i>S. pombe</i> galactosyltransferase galactosyltransferase similarity to signal peptidase similarity to to α-1,3-mannosyltransferase similarity to ubiquitin-activating enzymes similarity to ubiquitin-activating enzymes similarity to ubiquitin-protein ligase similarity to γ2p3p strong similarity to α-1,2- mannosyltransferase strong similarity to α-1,2- mannosyltransferase strong similarity to α-1,2- mannosyltransferase strong similarity to α-1,2- strong similarity to aspartylproteases strong similarity to to aspartylproteases strong similarity to thioredoxin strong similarity to thioredoxin strong similarity to tubiquitin conjugating
YCR075c YGR026w YOR069w YLR347c YOL122c YKR001c YOR020c YNR017w YJL143w YIL022w YMR035w YNL131w YGR082w	ERS1 MSP1 VPS5 KAP95 SMF1 VPS1 HSP10 MAS6 TIM17 TIM44 IMP2 TOM22 TOM20 TOM37	intracellular protein transport protein intra-mitochondrial sorting protein involved in Golgi retention and vacuolar sorting karyopherin-β manganese transporter member of the dynamin family of GTPases mitochondrial chaperonin mitochondrial inner membrane import translocase subunit mitochondrial inner membrane import receptor subunit duter membrane import receptor subunit, 20K mitochondrial outer membrane import receptor subunit, 37K mitochondrial outer membrane import receptor subunit, 37K mitochondrial outer membrane import receptor subunit, 37K mitochondrial outer membrane import mitochondrial outer membrane import receptor subunit, 37K mitochondrial outer membrane import	VDR495c YLR396c YAL002w YML097c <b>protein</b> <b>myristy</b> <b>proces:</b> YJR131w YER001w YGL038c YGL038c YGL031r YPL154c YL157w YPL154c YL1120c YDL141w YBR110w YBR110w YBR110w YGL038c	VPS3 VPS3 VPS8 VPS9 modific (lation, I sing) MNS1 KRE2 MNN1 OCH1 ARL1 APE2 NTA1 ATE1 PEP4 YAP3 BPL1 ALG1 ALG1 KEX1	vacuolar sorting protein vation (glycosylation, acylation, palmitylation, farnesylation and α-12-mannosidase α-1,2-mannosyltransferase α-1,3-mannosyltransferase α-1,3-mannosyltransferase α-1,6-mannosyltransferase ADP-ribosylation factor amino-peridase yscll amino-terminal amidase arginyl tRNA transferase aspartyl protease aspartyl protease aspartyl protease aspergillopepsin biotin holocarboxylase synthetase β-mannosyltransferase carboxypeptidase (YSC-α) dolichl-Pglucose synthetase	YDR245w YLR066w YNR059w YPL003w YPR180w YGL087c YJR309c YBR205w YPL053c YPL051w YLR121c YOR099w YCR083w YOR339c	KTR3 KTR4 KTR6	similarify to <i>S. pombe</i> galactosyltransferase similarity to signal peptidase similarity to to α-1,3-mannosyltransferase similarity to ubiquitin-activating enzymes similarity to ubiquitin-activating enzymes similarity to ubiquitin-protein ligase similarity to γ4p3p strong similarity to α-1,2- mannosyltransferase strong similarity to α-1,2- strong similarity to α-1,2- strong similarity to α-1,2- strong similarity to α-1,2- strong similarity to appartylproteases strong similarity to aspartylproteases strong similarity to mannosyltransferases strong similarity to thioredoxin strong similarity to ubiquitin-activating enzymes strong similarity to ubiquitin-activating enzymes
YCR075c YGR028w YOR069w YCR069w YLR347c YOL122c YKR001c YOR020c YNR017w YJL143w YIL022w YMR035w YNL131w YGR082w YMR060c YMR203w	ERS1 MSP1 VPS5 KAP95 SMF1 VPS1 HSP10 MAS6 TIM17 TIM44 IMP2 TOM22 TOM20 TOM37	intracellular protein transport protein intra-mitochondrial sorting protein involved in Golgi retention and vacuolar sorting karyopherin-β manganese transporter member of the dynamin family of GTPases mitochondrial chaperonin mitochondrial inner membrane import translocase subunit mitochondrial inner membrane import receptor subunit, 20K mitochondrial outer membrane import receptor subunit, 20K mitochondrial outer membrane import receptor subunit, 37K mitochondrial outer membrane import receptor subunit, 40K	VDR495c YLR396c YLR396c Protein myristy process YJR131w YER001w YGL038c YR16364 YKL167w YJR062c YGL017w YPL164c YL18120c YDL141w YBR1160w YGL276 YJR143c	VPS3 VPS3 VPS8 VPS9 modific (lation, I sing) MNS1 KRE2 MNN1 OCH1 APE1 APE1 APE1 PEP4 YAP3 BPL1 ALG1 KEX1 ALG6 PMT4	vacuolar sorting protein vacuolar sorting pro	YDR245w YLR066w YNR059w YPL003w YPR180w YPR180w YRR05ey YBR205w YBR205w YPL063c YPL063c YPL051w YLR121c YOR099w YCR083w YOR339c YPR066w YML111w	KTR3 KTR4 KTR6 KTR1	similarity to <i>S. pombe</i> galactosyltransferase galactosyltransferase similarity to signal peptidase similarity to to α-1,3-mannosyltransferase similarity to ubiquitin-activating enzymes similarity to ubiquitin-activating enzymes similarity to ubiquitin-protein ligase similarity to γ2p3p strong similarity to α-1,2-mannosyltransferase strong similarity to α-1,2-mannosyltransferase strong similarity to α-1,2-mannosyltransferase strong similarity to α-1,2-mannosyltransferase strong similarity to ΔDP-ribosylation factors strong similarity to aspartylproteases strong similarity to mannosyltransferases strong similarity to thioredoxin strong similarity to thioredoxin strong similarity to ubiquitin-activating enzymes strong similarity to ubiquitin-activating enzymes strong similarity to ubiquitin-activating enzymes
YCR075c YGR028w YCR069w YLR347c YOL122c YKR001c YOR020c YNR017w YJL143w YIL022w YMR035w YNL131w YGR082w YMR060c YMR203w YOR045w	ERS1 MSP1 WPS5 KAP95 SMF1 VPS1 HSP10 MAS6 TIM17 TIM44 IMP2 TOM22 TOM20 TOM37 TOM40 TOM6	intracellular protein transport protein intra-mitochondrial sorting protein involved in Golgi retention and vacuolar sorting karyopherin-β manganese transporter member of the dynamin family of GTPases mitochondrial chaperonin mitochondrial inner membrane import translocase subunit mitochondrial inner membrane protease subunit mitochondrial outer membrane import receptor subunit, 20K mitochondrial outer membrane import receptor subunit, 37K mitochondrial outer membrane import receptor subunit, 40K mitochondrial outer membrane import receptor subunit, 40K mitochondrial outer membrane import receptor subunit, 40K mitochondrial outer membrane import receptor subunit, 6K	VDR495c YLR396c YLR396c protein myristy process YJR131w YDR483w YER001w YGL038c YBR164c YKL157w YJR062c YGL017w YPL154c YLR120c VDL141u YBR110w YGL027c	VPS3 VPS3 VPS8 VPS9 modific (lation, l sing) MNS1 KRE2 MNN1 OCH1 ARL1 APE2 NTA1 PEP4 YAP3 BPL1 ALG1 KEX1 ALG1 KEX1	vacuolar sorting protein vacuolar sorting pro	YDR245w  YLR066w YNR059w YPL003w YPR180w YGL087c Y1R039c YBR205w  YPL053c  YPL051w  YLR019c YCR083w YOR339c  YPR066w  YML111w YGL226c-a	KTR3 KTR4 KTR6 KTR1	similarity to <i>S. pombe</i> galactosyltransferase galactosyltransferase similarity to signal peptidase similarity to to α-1,3-mannosyltransferase similarity to ubiquitin-activating enzymes similarity to ubiquitin-protein ligase similarity to ubiquitin-protein ligase similarity to γ4p3p strong similarity to α-1,2- mannosyltransferase strong similarity to α-1,2- mannosyltransferase strong similarity to α-1,2- mannosyltransferase strong similarity to α-1,2- strong similarity to α-1,2- strong similarity to α-1,2- strong similarity to appartylproteases strong similarity to aspartylproteases strong similarity to mannosyltransferase strong similarity to thoredoxin strong similarity to ubiquitin-activating enzymes strong similarity to ubiquitin-activating enzymes strong similarity to ubiquitination protein Bul1p subunit of N-oligosaccharyltransferase, ξ subunit
YCR075c YGR028w YOR069w YCR069w YLR347c YOL122c YKR001c YOR020c YNR017w YJL143w YIL022w YMR035w YNL131w YGR082w YMR060c YMR203w	ERS1 MSP1 VPS5 KAP95 SMF1 VPS1 HSP10 MAS6 TIM17 TIM44 IMP2 TOM22 TOM20 TOM37	intracellular protein transport protein intra-mitochondrial sorting protein involved in Golgi retention and vacuolar sorting karyopherin-β manganese transporter member of the dynamin family of GTPases mitochondrial chaperonin mitochondrial inner membrane import translocase subunit mitochondrial inner membrane import receptor subunit, 20K mitochondrial outer membrane import receptor subunit, 37K mitochondrial outer membrane import receptor subunit, 37K mitochondrial outer membrane import receptor subunit, 40K mitochondrial outer membrane import receptor subunit, 40K mitochondrial outer membrane import receptor subunit, 6K mitochondrial outer membrane import receptor subunit, 6K mitochondrial outer membrane import receptor subunit, 6K mitochondrial outer membrane import	VDR495c YLR396c YLR306c Protein myristy process YJR131w YER001w YGL038c YBR164c YKL157w YJR062c YGL017w YPL154c YLR120c YDL141w YBR110w YGL032c YPL227c YJR143c YDL212w YNL238w	VPS3 VPS3 VPS8 VPS9 modific (lation, l sing) MNS1 KRE2 MNN1 OCH1 ARL1 APE2 NTA1 APE2 NTA1 APE1 ALG1 KEX1 ALG5 PMT4 SHR3 KEX2	vacuolar sorting protein vacuolar sorting pro	YDR245w YLR066w YNR059w YPL003w YPR180w YPR180w YRR05ey YBR205w YBR205w YPL063c YPL063c YPL051w YLR121c YOR099w YCR083w YOR339c YPR066w YML111w	KTR3 KTR4 KTR6 KTR1	similarity to <i>S. pombe</i> galactosyltransferase galactosyltransferase similarity to signal peptidase similarity to to α-1,3-mannosyltransferase similarity to ubiquitin-activating enzymes similarity to ubiquitin-activating enzymes similarity to ubiquitin-activating enzymes similarity to ubiquitin-protein ligase similarity to α-1,2-mannosyltransferase strong similarity to α-1,2-mannosyltransferase strong similarity to α-1,2-mannosyltransferase strong similarity to α-1,2-mannosyltransferase Kre2p strong similarity to ΔDP-ribosylation factors strong similarity to aspartylproteases strong similarity to mannosyltransferases strong similarity to thioredoxin strong similarity to thioredoxin strong similarity to ubiquitin conjugating enzymes strong similarity to ubiquitin-activating enzymes
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YCR075c YGR028w YCR069w YLR347c YOL122c YKR001c YOR020c YNR017w YJL143w YIL022w YMR035w YNL131w YGR082w YMR060c YMR203w YOR045w YNL070w YNL121c YMR150c YJL034w YMR091c YMR091c YDR432w YLR191w YPR047w YNL106c YBL069w YLR168c YDR2244w	ERS1 MSP1 WPS5 KAP95 SMF1 VPS1 HSP10 MAS6 TIM17 TIM44 IMP2 TOM22 TOM20 TOM37 TOM40 TOM6 TOM7 TOM70 IMP1 KAR2 NPL4 NPL3 PAS20 MSF1 PIE3 AST1 (MSF1) PAS10	intracellular protein transport protein intra-mitochondrial sorting protein involved in Golgi retention and vacuolar sorting karyopherin-β manganese transporter member of the dynamin family of GTPases mitochondrial chaperonin mitochondrial inner membrane import translocase subunit mitochondrial inner membrane import receptor subunit mitochondrial outer membrane import receptor subunit, 20K mitochondrial outer membrane import receptor subunit, 37K mitochondrial outer membrane import receptor subunit, 40K mitochondrial outer membrane import receptor subunit, 40K mitochondrial outer membrane import receptor subunit, 7K mitochondrial outer membrane import receptor subunit, 7K mitochondrial outer membrane specialized import receptor mitochondrial protease nuclear fusion protein nuclear protein localization factor nuclear protein localization factor and ER translocation component nucleolar protein protein involved in protein import phenylalanine-tRNA ligase α subunit, mitochondrial protein involved in protein probably involved in intramitochondrial protein sorting putative peroxisomal targeting signal receptor required for correct localization of Sec12p required for retention of luminal ER	VDR495c YLR396c YLR396c YLR396c Protein myristy proces: YJR131w YER001w YGL038c YBR1684c YKL167w YJR062e YGL017w YPL164c YKL167w YJR143c YPL227c YDL141w YBR110w YGL203c YPL227c YJR143c YDL212w YNL238w YDR331w YDR31w YDR31w YDR310c YGL155w YPR176c YGL056c YGL056c YGL057c	VPS3 VPS3 VPS3 VPS9 VPS9 modific (lation, I sing) MNS1 KRE2 MNN1 OCH1 ARL1 APE2 NTA1 ALG1 PEP4 YAP3 BPL1 ALG5 PMT4 ALG6 FMT4 SHR3 KEX1 ALG6 ALG8 STE14 MSI4 CDC43 BET1 ALG6 ALG6 ALG8 ALG6 ALG8 ALG6 ALG6 ALG6 ALG6 ALG7 CYC2 ALG2 CYC2 ALG2 ALG7 RMT1 PMT1 PMT1 PMT1 PMT1 PMT2 PMT3 RHK1	vacuolar sorting protein valorar sorting protein valorar sorting protein valorar sorting protein valorar sorting protein	YDR245w YLR066w YNR059w YPL005w YPL003w YPR180w YPR180w YPL051w YPL051w YPL051w YLR121c YOR099w YCR083w YOR339c YPR066w YML111w YGL226c-a YEL056w YIR075w YGR026w YGR096w YJR075w YGR096w YJR075w YGR096w YJR075w YGR096w YJR075w YGR096w YJR075w YGR096w YJR075w YJR075w YJR075w YGR096w YJR075w YGR090w YJR075w YGR090w YJR075w YJR075w YJR075w YJR092w YJR092w YJR075w YJR092w YJR075w YJR092w	KTR3 KTR4 KTR6  KTR1  OST5  HAT2  HOC1 TRX1 TRX2 STE13 BUL1 CDC34 PAS2 QRIB RAD6 UBC12 UBC13 UBC13 UBC6 UBC6 UBC6 UBC8 UBC9 UBC9 UBC9 UBC11	similarity to <i>S. pombe</i> galactosyltransferase galactosyltransferase similarity to signal peptidase similarity to to α-1,3-mannosyltransferase similarity to ubiquitin-activating enzymes similarity to ubiquitin-activating enzymes similarity to ubiquitin-activating enzymes similarity to γ2p3p strong similarity to α-1,2- mannosyltransferase strong similarity to ADP-ribosylation factors strong similarity to aspartylproteases strong similarity to thoredoxin strong similarity to thioredoxin strong similarity to ubiquitin-conjugating enzymes strong similarity to ubiquitin-activating enzyme ubiquitin-conjugating enzyme
YCR075c YGR078c YGR028w YCR069w YLR347c YOL122c YKR001c YOR020c YNR017w YJL143w YIL022w YMR035w YNL131w YGR082w YMR060c YMR203w YOR045w YML070w YNL121c YMR150c YJL034w YMR091c YBR170c YDR432w YR191w YPR047w YNL106c YBL069w YLR168c YDR244w YCL001w YDR015c	ERS1 MSP1 VPS5 KAP95 SMF1 VPS1 HSP10 MAS6 TIM17 TIM44 IMP2 TOM22 TOM20 TOM37 TOM40 TOM6 TOM7 TOM6 TOM7 TOM6 TOM7 TOM6 TOM7 TOM8 NPL6 NPL6 NPL1 NPL3 PAS20 MSF1 PIE3 AST1 (MSF1) PAS10 RER1 ERD1 MAF1	intracellular protein transport protein intra-mitochondrial sorting protein involved in Golgi retention and vacuolar sorting karyopherin-β manganese transporter member of the dynamin family of GTPases mitochondrial chaperonin mitochondrial inner membrane import translocase subunit mitochondrial inner membrane import receptor subunit mitochondrial outer membrane import receptor subunit mitochondrial outer membrane import receptor subunit, 20K mitochondrial outer membrane import receptor subunit, 40K mitochondrial outer membrane import receptor subunit, 40K mitochondrial outer membrane import receptor subunit, 7K mitochondrial outer membrane import receptor subunit, 7K mitochondrial outer membrane specialized import receptor mitochondrial outer membrane specialized import receptor mitochondrial protein muclear protein localization factor and ER translocation component nuclear protein localization factor and ER translocation component phenylalanine-tRNA ligase α subunit, mitochondrial phosphated phosphatese PMA1 protein targeting protein probably involved in intramitochondrial protein sorting putative peroxisomal targeting signal receptor required for correct localization of Sec12p required for retention of Iuminal ER proteins required for sorting of Mod5p	VDR495c YLR396c YLR396c YLR306v YML097c Protein myristy proces: YJR131w YER001w YGL038c YGL038c YGL017w YPL154c YLR120c YDL141w YBR110c YDL141w YBR110c YDL141w YBR110c YDL141w YBR110c YDL141w YBR110c YDL141w YBR10c YDL141w YBR10c YDL154c YLR120c YDL154c YRL120c YDL154c YRL120c YDL154c YRL120c YDL154c YRL120c YDL154c YRL165c YDL154c YDL154c YDL154c YDL154c YDL154c YDL154c YDL154c YRL165c	VPS3 VPS3 VPS3 VPS8 VPS9 modific (lation, I sing)  MNS1 KRE2 MNN1 OCH1 ARL1 AFE1 PEP4 YAP3 BPL1 ALG1 ALG5 PMT4 SHR3 KEX1 ALG5 PMT4 SHR3 KEX2 GPI8 STE14 MSI4 CDC43 BET4 ALG6 GCN5 BET4 ALG6 GDA1 GCN5 GCN5 CYT2 PMT1 PMT1 PMT2 PMT3 RIK11 MAP1	vacuolar sorting protein vacuolar sorting	YDR245w  YLR066w YNR059w YPL005w YPL003w YPR180w YPL053c YPL051w  YPL053c  YPL051w  YLR121c YOR099w YOR083w YOR339c  YPR066w  YML111w  YGL226c-a YPR066w  YML111w  YGR025w YMR075w YLR043c YGR209c YOR219c YMR275c YOR219c YMR275c YDR054c YGR133w YMR022w YMR022w YDR056y YER1064w YDR056y YER1064w YDR056y YER1064w YDR1370w YEL012w YDR0564w YDR059c YER1050w YEL1012w YDR136c YER1105w YKL210w YJR093w	KTR3 KTR4 KTR6  KTR1  OST5  HAT2  HOC1 TRX1 TRX1 TRX2 QRIB RAD6 UBC1 UBC13 UBC5 UBC3 UBC9 RSP5 UBA1 VUH1	similarity to S. pombe galactosyltransferase similarity to signal peptidase similarity to to α-1,3-mannosyltransferase similarity to ubiquitin-activating enzymes similarity to α-1,2- mannosyltransferase strong similarity to α-1,2- mannosyltransferase strong similarity to α-1,2- mannosyltransferase strong similarity to ΔDP-ribosylation factors strong similarity to aspartylproteases strong similarity to aspartylproteases strong similarity to thoredoxin strong similarity to thoredoxin strong similarity to ubiquitin-activating enzymes strong similarity to ubiquitination protein Bul 1p subunit of N-oligosaccharyltransferase, ζ subunit subunit of the major yeast histone acetyltransferase suppressor of pkc1 thioredoxin I thioredoxin peryme ubiquitin-conjugating enzyme
YCR075c YGR028w YCR069w YLR347c YOL122c YKR001c YOR020c YNR017w YJL143w YIL022w YMR035w YNL131w YGR082w YMR060c YMR203w YOR045w YNL070w YNL121c YMR150c YJL034w YMR091c YMR091c YMR091c YBL106c YDR432w YLR191w YPR047w YNL106c YBL069w YLR168c YDR244w YCL001w YDR2414c	ERS1 MSP1 VPS5 KAP95 SMF1 VPS1 HSP10 MAS6 TIM17 TIM44 IMP2 TOM22 TOM20 TOM37 TOM40 TOM6 TOM7 TOM6 TOM7 TOM6 TOM7 TOM6 TOM7 TOM8 NPL6 NPL6 NPL1 NPL3 PAS20 MSF1 PIE3 AST1 (MSF1) PAS10 RER1 ERD1 MAF1	intracellular protein transport protein intra-mitochondrial sorting protein involved in Golgi retention and vacuolar sorting karyopherin-β manganese transporter member of the dynamin family of GTPases mitochondrial chaperonin mitochondrial inner membrane import translocase subunit mitochondrial outer membrane import receptor subunit and translocase subunit mitochondrial outer membrane import receptor subunit, 20K mitochondrial outer membrane import receptor subunit, 40K mitochondrial outer membrane import receptor subunit, 40K mitochondrial outer membrane import receptor subunit, 6K mitochondrial outer membrane import receptor subunit, 7K mitochondrial outer membrane import receptor subunit, 8K mitochondrial outer membrane import receptor subunit, 7K mitochondrial outer membrane import receptor subunit, 7K mitochondrial protein localization factor and ER translocation component nuclear protein localization fact	VDR495c YLR396c YLR396c YLR396c Protein myristy process YJR311W YER001W YGL038c YBR164c YKL167W YJR062c YGL017W YPL154c YLR120c YDL414W YBR110W YGL203c YDL414W YBR110W YGL203c YDL412W YDL212W YDL212W YDL212W YDL212W YDL213W YDR310W YDR310C YGR370c YGL155W YGR370c YGL155W YPR176c YJL031c YOR002W YGR1065c YJL031c YGR065c YDL095W YAL039c YKL087c YGL065c YDL095W YAL029c YKL087c YGR252W YBL095W YBL09	VPS3 VPS3 VPS3 VPS8 VPS9 modific (lation, I sing)  MNS1 KRE2 MNN1 OCH1 ARL1 AFE1 PEP4 YAP3 BPL1 ALG1 ALG5 PMT4 SHR3 KEX1 ALG5 PMT4 SHR3 KEX2 GPI8 STE14 MSI4 CDC43 BET4 ALG6 GCN5 BET4 ALG6 GDA1 GCN5 GCN5 CYT2 PMT1 PMT1 PMT2 PMT3 RIK11 MAP1	vacuolar sorting protein vacuolar sorting vacuolar	YDR245w YLR066w YNR059w YPL005w YPL003w YPR180w YPL053c YPL053c YPL051w YLR121c YOR090w YCR083w YOR339c YPR066w YML111w YGL226c-a YEL056w YJR075w YLR043c YGR209c YOR219c YMR275c YMR275c YDR056c YMR275c YDR056c YMR275c YDR056c YGR209c YMR275c YDR056c YGR209c YMR275c YDR056c YGR209c YMR275c YDR056c YGR209c YMR275c YDR056c YDR0	KTR3 KTR4 KTR6  KTR1  OST5  HAT2  HOC1 TRX1 TRX2 STE13 BUL1 CDC34 PAS2 QRIB RAD6 UBC12 UBC12 UBC13 UBC6 UBC8 UBC9 UBC8 UBC8 UBC9 UBC8 UBC8 UBC9 UBC4 TYUH1 ALG7	similarity to <i>S. pombe</i> galactosyltransferase similarity to signal peptidase similarity to to α-1,3-mannosyltransferase similarity to ubiquitin-activating enzymes similarity to ubiquitin-activating enzymes similarity to ubiquitin-activating enzymes similarity to ubiquitin-protein ligase similarity to yap3p strong similarity to α-1,2- mannosyltransferase Kre2p strong similarity to aspartylproteases strong similarity to aspartylproteases strong similarity to mannosyltransferases strong similarity to ubiquitin conjugating enzymes strong similarity to ubiquitin-activating enzymes strong similarity to ubiquitin-activating enzymes strong similarity to ubiquitination protein Bul 1p subunit of N-oligosaccharyltransferase, ζ subunit subunit of the major yeast histone acetyltransferase suppressor of <i>pkc1</i> thioredoxin I type IV dipeptidyl aminopeptidase ubiquitin-conjugating enzyme

וז א/וו ארו	STE24	zinc metallo-protease	YGR105w	VMA21	vacuolar ATPase assembly integral	YDR054c	CDC34	ubiquitin-conjugating enzyme
assemb	ly of pr	otein complexes	YHR060w	VMA22	membrane protein vacuolar ATPase assembly protein	YMR022w YDR177w	UBC1	ubiquitin-conjugating enzyme ubiquitin-conjugating enzyme
/GR214w	ΝΛΡ1Λ	40S ribosomal protein p40 homologue A	YDR495c	VPS3	vacuolar sorting protein	YLR306w YDR092w	UBC12	ubiquitin-conjugating enzyme ubiquitin-conjugating enzyme
LR048w	NAB1B	40S ribosomal protein p40 homologue B	proteol	ysis		YBR082c	UBC4	ubiquitin-conjugating enzyme
PL195w	YKS4	α- or γ- adaptin, large subunit of the clathrin-associated protein(AP) complex	YPL149w	APG5	involved in autophagy and nutrient	YDR059c YER100w	UBC5 UBC6	ubiquitin-conjugating enzyme ubiquitin-conjugating enzyme
BL037w	APL3	α-adaptin, large subunit of the clathrin-			starvation	YDL064w	UBC9	ubiquitin-conjugating enzyme
OR094w	ARF3	associated protein(AP) complex ADP-ribosylation factor 3	YOL013c YLR207w	HRD1 HRD3	involved in degradation of Hmg2p involved in degradation of Hmg2p	YDR139c YER125w	RSP5	ubiquitin-like protein ubiquitin-protein ligase
BL022c	PIM1	ATP-dependent protease, mitochondrial	YMR174c	PAI3	protease A (ysca) inhibitor IA3	YKL210w	UBA1	ubiquitin-protein ligase
KL135c GR261c	APL2 YKS5	β-adaptin β-adaptin, large subunit of the clathrin-	YNL015w YCL052c	PBI2 PBN1	proteinase B inhibitor 2 required for Prb1p expression	YGR184c YDR069c	UBR1 DOA4	ubiquitin-protein ligase ubiquitin-specific protease
/DD105-	MOH	associated protein(AP) complex	YHR132c		similarity to carboxypeptidase	YDL122w	UBP1	ubiquitin-specific protease
'BR195c	MSI1	chromatin assembly complex, subunit p50	YNR069c YBR227c		similarity to central part of Bul1p similarity to E. coli ATP-binding protein	YER144c YJR099w	UBP5 YUH1	ubiquitin-specific protease ubiquitin-specific protease
PR018w	RLF2	chromatin assembly complex, subunit	VNII 100 av		clpX	YOR124c YER151c	UBP2 UBP3	ubiquitin-specific proteinase ubiquitin-specific proteinase
'LR170c	APS1	p90 clathrin-associated protein (AP) complex,	YNL186w		similarity to human putative ubiquitin carboxy-terminal hydrolase			
′JR058c	APS2	small subunit AP19 clathrin-associated protein 17, small	YIL137c YKR038c		similarity to <i>M. musculus</i> aminopeptidase similarity to Qri7p	lysosoma YBR286w	I <b>l and vac</b> APE3	cuolar degradation aminopeptidase Y, vacuolar
		subunit	YER047c		similarity to regulatory subunit Yta6p of	YKL103c	LAP4	aminopeptidase yscl, vacuolar
JR005w	YAP80	clathrin-associated protein complex, β subunit	YCR045c		26S proteasome similarity to serin proteases	YPL154c YMR297w	PEP4 PBC:1	aspartyl protease carboxypeptidase y, serine-type protea
'JL024c	APS3	clathrin-associated protein(AP) complex,	YER078c		similarity to X-Pro aminopeptidase II	YHR028c	DAP2	dipeptidyl aminopeptidase B
′ER058w	PET117	small subunit cytochrome c oxidase assembly factor	YBR139w YBL067c	UBP13	strong similarity to carboxypeptidase ubiquitin carboxyl-terminal hydrolase	YJL172w YEL060c	CPS1 PRB1	Gly-X carboxypeptidase YSCS protease B, vacuolar
PL132w	COX11	cytochrome c oxidase assembly protein	YOL111c	05, 10	weak similarity to human ubiquitin-like	YOR003w	YSP3	subtilisin-like protease III
'ML129c 'DR079w		cytochrome c oxidase assembly protein cytochrome c oxidase assembly protein			protein GDX	other sub	cellular d	legradation
'LR038c	COX12	cytochrome c oxidase subunit VIB	cytoplasn			YDR144c	MKC7	aspartyl protease of the periplasmic
MR256c DL067c	COX7 COX9	cytochrome c oxidase subunit VII cytochrome c oxidase subunit VIIA	YFR052w YIL075c	NIN1 SEN3	26S proteasome regulatory subunit 26S proteasome regulatory subunit	YBL022c	PIM1	space ATP-dependent protease, mitochondria
/ER141w	COX15	cytochrome oxidase assembly factor	YOR259c	CRL13	26S proteasome subunit	YIL015w	BAR1	barrierpepsin
'ER154w 'BL007c	OXA1 SLA1	cytochrome oxidase biogenesis protein cytoskeleton assembly control protein	YPR103w YFR050c	PRE2 PRE4	26S proteasome subunit 26S proteasome subunit	YBR201w YER017c	DER1 AFG3	involved in degradation proteins in the protease of the SEC18/CDC48/PAS1
/NL243w	SLA2	cytoskeleton assembly control protein	YOR157c YGR253c	PUP1	26S proteasome subunit			family of ATPases (AAA)
/LR393w /NL315c	ATP11	F1F0 ATPase complex assembly protein F1F0-ATPase complex assembly protein	YER094c	PUP2 PUP3	26S proteasome subunit 26S proteasome subunit	YPR024w	YME1	protease of the SEC18/CDC48/PAS1 family of ATPases (AAA)
/JL180c /PL172c	ATP12	F1F0-ATPase complex assembly protein	YGL048c	SUG1	26S proteasome subunit	YMR089c	YTA12	protease of the SEC18/CDC48/PAS1
PL1720 PL231w	COX10 FAS2	farnesyl transferase fatty-acyl-CoA synthase, α subunit	YHR200w YER021w	SUN1 SUN2	26S proteasome subunit 26S proteasome subunit	YCL057w	PRD1	family of ATPases (AAA) proteinase yscD
/PR029c	APL4	γ-adaptin, large subunit of the clathrin-	YOR117w	YTA1 YTA2	26S proteasome subunit	YHR113w		similarity to vacuolar aminopeptidase
/DL192w		associated protein(AP) complex GTP-binding protein of the ARF family	YDR394w YKL145w	YTA3	26S proteasome subunit 26S proteasome subunit	YFR006w		Lap4p/Ape1p similarity to X-Pro dipeptidases
DL137w KL119c	ARF2 VPH2	GTP-binding protein of the ARF family H <sup>+</sup> -ATPase assembly protein, vacuolar	YGR270w YOR362c	YTA7 PRE10	26S proteasome subunit 26S proteasome subunit C1	othorn	rotoin d	destination activities
/PL234c	TFP3	H+ATPase V0 domain 17K subunit,	YER012w	PRE1	26S proteasome subunit C11			iestination activities
YLR447c	VMA6	vacuolar H <sup>+</sup> -ATPase V0 domain 36K subunit,	YGR135w YML092c	PRE9 PRE8	26S proteasome subunit Y13 26S proteasome subunit Y7	YDR258c	HSP78	heat-shock protein of clpb family of AT dependent proteases, mitochondrial
		vacuolar	YGL011c	SCL1	26S proteasome subunit YC7α/Y8	YDL104c	QRI7	similarity to <i>H. influenzae</i>
/OR270c	VPH1	H*-ATPase V0 domain 95K subunit, vacuolar	YMR314w YNL239w	PRE5 LAP3	26S proteasome subunit, α-type aminopeptidase of cysteine protease	YDR415c		sialoglycoprotease (gcp) strong similarity to bacterial leucyl
OR332w	VMA4	H <sup>+</sup> -ATPase V1 domain 27K subunit,			family	TDIATOC		aminopeptidase
/KL080w	VMA5	vacuolar H <sup>+</sup> -ATPase V1 domain 42K subunit,	YJR062c YGL017w	NTA1 ATE1	amino-terminal amidase arginyl tRNA transferase		_	
		vacuolar	YDL132w	CDC53	controls G1/S transition	Trans	nort	facilitation
YLL009c	COX17	interacts genetically with SCO1 and SCO2 in cytochrome oxidase assembly	YLR452c	SST2	involved in desensitization to α-factor pheromone	II alls	port	raciiitation
YJR034w	PET191	involved in assembly of cytochrome	YKL213c	DOA1	involved in ubiquitin-dependent	ion chai	nnels	
YBR037c	SCO1	oxidase involved in stabilization of Cox1p and	YDL126c	CDC48	proteolysis microsomal protein of	YGR217w	CCH1	calcium channel protein
/DR375c	BCS1	Cox2p mitochondrial protein of the	YJL001w	PRE3	CDC48/PAS1/SEC18 family of ATPases	YLL052c		member of mip family transmembrane
1 DU9/90	БСЗТ	CDC48/PAS1/SEC18 (AAA) family of	TJLOUTVV	rnes	multicatalytic endopeptidase complex subunit	YJL093c	TOK1	channels outward-rectifier potassium channel
/DI 005	SEC16	ATPases	YOL038w	PRE6	multicatalytic endopeptidase complex	YPR192w		similarity to plasma membrane and wa
YPL085w YKR048c	NAP1	multidomain vesicle coat protein nucleosome assembly protein I	YBL041w	PRE7	subunit multicatalytic endopeptidase complex	YLL053c		channel proteins similarity to water channel proteins
YML102w	CAC2	p60 subunit of the chromatin assembly	YDL020c	SON1	subunit	YIL114c	POR2	voltage-dependent anion channel
/KL197c	PAS1	factor-I (CAF-I) peroxisomal assembly protein	YBR165w	UBS1	nuclear protein positive regulator of Cdc34p	YJR040w	GEF1	(YVDAC2) voltage-gated chloride channel protein
/DR265w /NL329c	PAS4 PAS8	peroxisomal assembly protein peroxisomal assembly protein	YDL007w	YTA5	probable component of 26S proteasome complex	ion tran	sporte	
YBR237w	PRP5	pre-mRNA processing RNA-helicase	YIL148w	UBI1	ribosomal protein		•	
YJL203w YER017c	PRP21 AFG3	pre-mRNA splicing factor protease of the SEC18/CDC48/PAS1	YKR094c YMR223w	UBI2	ribosomal protein similarity to human putative ubiquitin	YNR055c	HOL1	member of major facilitator superfamily multidrug-resistance protein subfamily
		family of ATPases (AAA)			carboxyl-terminal hydrolase	YIL048w		similarity to amino-phospholipids-ATPa
/PR024w	YME1	protease of the SEC18/CDC48/PAS1 family of ATPases (AAA)	YDR390c YPL003w	UBA2	similarity to Uba1p similarity to ubiquitin-activating enzymes			Drs2p
/MR089c	YTA12	protease of the SEC18/CDC48/PAS1	YPR180w		similarity to ubiquitin-activating enzymes			ters (Cu, Fe, etc.)
/PL215w	CBP3	family of ATPases (AAA) required for assembly of cytochrome bc1	YGL087c YPL074w	YTA6	similarity to ubiquitin-protein ligase similarity to Vps4p and Yta4p	YOR316c YPR124w	COT1 CTR1	cobalt accumulation protein copper transport protein
		complex	YOR261c		strong similarity to human 26S	YHR175w	CTR2	copper transport protein
/BR185c /LL008w	MBA1 DRS1	respiratory chain assembly protein RNA helicase of the DEAD box family	YOR339c		proteasome regulatory subunit, p40 strong similarity to ubiquitin conjugating	YLR411w YGL255w	CTR3 ZRT1	copper transport protein high-affinity zinc transport protein
/BR227c		similarity to E. coli ATP-binding protein			enzymes	YLR130c	ZRT2	low-affininty zinc transporter
/GR241c		clpX similarity to rat clathrin assembly protein	YPR066w		strong similarity to ubiquitin-activating enzymes	YMR319c YOL122c	FET4 SMF1	low-affinity Fe(II) iron transport protein manganese transporter
/HR161c		similarity to rat clathrin assembly protein	YML111w		strong similarity to ubiquitination protein	YBR290w	BSD2	metal homeostasis protein
/GR074w	SMD1	AP180 snRNA-associated protein	YHR027c	HRD2	Bul1p subunit of 26S proteasome	YDR270w YBR295w		probable copper-transporting ATPase P-type Cu <sup>2+</sup> -transporting ATPase
BR024w	SCO2	strong similarity to Sco1p	YKL022c	CDC16	subunit of anaphase-promoting complex	YMR243c		zinc- and cadmium resistance protein
LR327c	BAG7	strong similarity to STF2p structural homologue of Sac7p	YHR166c	CDC23	(cyclosome) subunit of anaphase-promoting complex	other cati	on transp	oorters (Na, K, Ca, NH <sub>4</sub> , etc.)
∪r 134W	SAC7	suppressor of actin mutation			(cyclosome)	YGR121c	MEP1	ammonia permease of high capacity a
/DR389w	VAM3 TFB3	syntaxin related protein TFIIH subunit (transcription/repair factor)	YBL084c	CDC27	subunit of anaphase-promoting complex (cyclosome)	YDL128w	VCX1	moderate affinity Ca <sup>2+</sup> -transport (H <sup>+</sup> /Ca <sup>2+</sup> exchange) prote
DR389w OR106w		U4/U6 snRNP 52K protein	YLL039c	UBI4 UBP7	ubiquitin	YGL006w		vacuolar
/DR389w /OR106w /DR460w /PR178w	PRP4		YIL156w	UBP9	ubiquitin carboxy terminal hydrolase ubiquitin carboxyl-terminal hydrolase	YGL167c	PMR1	Ca <sup>2+</sup> -transporting P-type ATPase Ca <sup>2+</sup> -transporting P-type ATPase
/DR389w /OR106w /DR460w /PR178w	ABC1	ubiquinol cytochrome c reductase complex assembly protein	YER098w					
YDR389w YOR106w YDR460w YPR178w YGL119w		complex assembly protein ubiquinol-cytochrome c reductase 40K	YKR098c	UBP11	ubiquitin C-terminal hydrolase	YCR024c-8		
YDR389W YOR106W YDR460W YPR178W YGL119W YPR191W	ABC1	complex assembly protein ubiquinol-cytochrome c reductase 40K subunit II ubiquinol-cytochrome c reductase	YKR098c YJL197w YGR048w	UBP11 UBP12 UFD1	ubiquitin C-terminal hydrolase ubiquitin fusion degradation protein	YCR024c-a YEL017c-a YMR054w	PMP2	H*-ATPase subunit, plasma membrane H*-ATPase subunit, plasma membrane H*-ATPase V0 domain 102K subunit,
YDR389W YOR106W YDR460W YPR178W YGL119W YPR191W YGR174c	ABC1 QCR2 CBP4	complex assembly protein ubiquinol-cytochrome c reductase 40K subunit II ubiquinol-cytochrome c reductase assembly factor	YKR098c YJL197w YGR048w YDL190c	UBP11 UBP12 UFD1 UFD2	ubiquitin C-terminal hydrolase ubiquitin fusion degradation protein ubiquitin fusion degradation protein	YEL017c-a YMR054w	PMP2 STV1	H <sup>+</sup> -ATPase subunit, plasma membrane H <sup>+</sup> -ATPase V0 domain 102K subunit, vacuolar
YOR134W YDR389W YOR106W YDR1660W YPR178W YGL119W YPR191W YGR174c YLL039c YGR133W	ABC1 QCR2	complex assembly protein ubiquinol-cytochrome c reductase 40K subunit II ubiquinol-cytochrome c reductase	YKR098c YJL197w YGR048w	UBP11 UBP12 UFD1	ubiquitin C-terminal hydrolase ubiquitin fusion degradation protein	YEL017c-a	PMP2 STV1	H <sup>+</sup> -ATPase subunit, plasma memb H <sup>+</sup> -ATPase V0 domain 102K subun

ı	YEL027w	CUP5	H <sup>+</sup> -ATPase V0 domain 17K subunit,	YCR098c	GIT1	similarity to phosphate transporter	YOR071c		similarity to allantoin or uracil transport
	YPL234c	TFP3	vacuolar H <sup>+</sup> -ATPase V0 domain 17K subunit,	YDL199c		proteins similarity to sugar transporter proteins	YOR192c		proteins similarity to allantoin or uracil transport
	YLR447c	VMA6	vacuolar H <sup>+</sup> -ATPase V0 domain 36K subunit,	YFL040w		similarity to yeast glucose transport proteins	YLR237w		proteins similarity to allantoin transport protein
	YOR270c	VPH1	vacuolar H <sup>+</sup> -ATPase V0 domain 95K subunit,	YHR096c YDL245c	HXT5 HXT15	strong similarity to hexose transporters strong similarity to Hxt17p and Haxt7p	YLL055w YBL042c		similarity to Dal5p strong similarity to allantoin and uracil
	YGR020c	VMA7	vacuolar H <sup>+</sup> -ATPase V1 domain 14K subunit,	YJR160c YDR536w	STL1	strong similarity to Mal3Tp strong similarity to members of the sugar	YAL067c	SEO1	transport proteins suppressor of sulphoxyde ethionine
	YOR332w	VMA4	vacuolar H <sup>+</sup> -ATPase V1 domain 27K subunit,	YOR271c		permease family strong similarity to <i>Rattus</i> tricarboxylate	4======	ATD	resistance
	YEL051w	VMA8	vacuolar H <sup>+</sup> -ATPase V1 domain 32K subunit,	YDL247w		carrier strong similarity to sugar transport	YGL006w		
	YKL080w	VMA5	vacuolar H*-ATPase V1 domain 42K subunit, vacuolar	YIL171w		proteins strong similarity to sugar transport proteins	YGL167c YKL016c	PMR1	Ca <sup>2+</sup> -transporting P-type ATPase Ca <sup>2+</sup> -transporting P-type ATPase F1F0-ATPase complex, F0 D subunit
	YPR036w	VMA13	H <sup>+</sup> -ATPase V1 domain 54K subunit, vacuolar	YIL170w	HXT12	strong similarity to sugar transport proteins	YBL099w		F1F0-ATPase complex, F1 α subunit F1F0-ATPase complex, F1 β subunit
	YBR127c	VMA2	H <sup>+</sup> -ATPase V1 domain 60K subunit, vacuolar	YJR158w	HXT16	strong similarity to sugar transport proteins	YDL004w YPL078c	ATP16	F1F0-ATPase complex, F1 δ subunit F1F0-ATPase complex, F1 δ subunit
	YDL185w	TFP1	H*-ATPase V1 domain 69K subunit, vacuolar	YNR072w YDL138w	HXT17 RGT2	sugar transport protein suppressor of <i>snf3</i> mutant	YPL271w YBR039w	ATP15	F1F0-ATPase complex, F1 ε subunit F1F0-ATPase complex, F1 γ subunit
	YGL008c YPL036w	PMA1 PMA2	H <sup>+</sup> -transporting P-type ATPase H <sup>+</sup> -transporting P-type ATPase 2			nsporters	YDR298c YLR295c	ATP5	F1F0-ATPase complex, OSCP subunit F1F0-ATPase complex, subunit h
	YNL142w	MEP2	high-affinity low-capacity ammonia permease	YBR068c	BAP2	amino-acid permease	YCR024c-a YEL017c-a	PMP1	H <sup>+</sup> -ATPase subunit, plasma membrane H <sup>+</sup> -ATPase subunit, plasma membrane
	YJL129c YAL026c	TRK1 DRS2	high-affinity potassium transport protein membrane-spanning P-type amino-	YEL063c YBR069c	CAN1 VAP1	amino-acid permease amino-acid permease	YMR054w	STV1	H <sup>+</sup> -ATPase V0 domain 102K subunit, vacuolar
	YKR050w	TRK2	phospholipids-ATPase moderate-affinity potassium transport	YCL025c YGL077c	AGP1 HNM1	asparagine and glutamine permease choline permease	YHR039c-a	VMA10	H <sup>+</sup> -ATPase V0 domain 13K subunit, vacuolar
	YHR026w	PPA1	protein proteolipid protein of proton-transporting	YPL265w YDL210w	DIP5 UGA4	dicarboxylic amino-acid permease GABA-specific high-affinity permease		CUP5	H <sup>+</sup> -ATPase V0 domain 17K subunit, vacuolar
	YEL031w	SPF1	ATPase P-type ATPase	YKR039w YDR508c	GNP1	general amino-acid permease high-affinity glutamine permease		TFP3	H <sup>+</sup> -ATPase V0 domain 17K subunit, vacuolar
	YLR138w YBR235w	NHA1	putative Na <sup>+</sup> /H <sup>+</sup> antiporter similarity to bumetanide-sensitive Na <sup>+</sup> -K <sup>+</sup> -	YGR055w YNL270c	MUP1 ALP1	high-affinity methionine permease high-affinity permease for basic amino	YLR447c	VMA6	H <sup>+</sup> -ATPase V0 domain 36K subunit, vacuolar
	YJL094c		Cl <sup>-</sup> cotransport protein similarity to <i>E. hirae</i> Na <sup>+</sup> /H <sup>+</sup> -antiporter	YOL020w	SCM2	acids high-affinity tryptophan transport protein		VPH1	H*-ATPase V0 domain 95K subunit, vacuolar
	YDR456w	MEDO	NapA similarity to Na <sup>+</sup> /H <sup>+</sup> antiporters		LYP1	histidine permease lysine-specific high-affinity permease		VMA7 VMA4	H <sup>+</sup> -ATPase V1 domain 14K subunit, vacuolar
	YPR138c YHL016c	MEP3 DUR3	strong similarity to ammonium transport proteins urea transport protein	YOR130c YHL036w	ARG11 MUP3	member of the mitochondrial carrier family (MCF) methionine permease		VIVIA4 VMA8	H*-ATPase V1 domain 27K subunit, vacuolar H*-ATPase V1 domain 32K subunit,
			(Cl, SO <sub>4</sub> ,PO <sub>4</sub> , etc)	YOR348c YKL174c	PUT4	proline and γ-aminobutyrate permease similarity to choline transport protein		VIVIA6 VMA5	vacuolar H*-ATPase V1 domain 42K subunit,
	YLR348c YML123c	PHO84	dicarboxylate carrier protein high-affinity inorganic phosphate/H <sup>+</sup>	YNR056c		Ctr1p similarity to choline transport protein		VMA13	vacuolar H*-ATPase V1 domain 54K subunit,
	YBR294w	SUL1	symporter high-affinity sulphate transport protein	YFL055w		Ctr1p similarity to Gap1p and other amino-acid		VMA2	vacuolar H <sup>+</sup> -ATPase V1 domain 60K subunit,
	YJL117w YCR037c	PHO86 PHO87	inorganic phospate transporter member of the phosphate permease	YDR160w		permeases similarity to lysine transport protein LYP1	YDL185w		vacuolar H <sup>+</sup> -ATPase V1 domain 69K subunit,
	YJR077c	MIR1	family phosphate transport protein,	YLL061w		strong similarity to amino-acid transport protein Gap1p		PMA1	vacuolar H <sup>+</sup> -transporting P-type ATPase
	YBR235w		mitochondrial (MCF) similarity to bumetanide-sensitive Na*-K*-	YDR046c	(PAP1)	strong similarity to amino-acid transport proteins		PMA2 DRS2	H <sup>+</sup> -transporting P-type ATPase 2 membrane-spanning P-type amino-
	YJL094c		Cl <sup>-</sup> cotransport protein similarity to <i>E. hirae</i> Na <sup>+</sup> /H <sup>+</sup> -antiporter	YBR132c YPL274w		strong similarity to amino-acid permeases strong similarity to amino-acid transport	YDR270w		phospholipids-ATPase probable copper-transporting ATPase
	YNR013c		NapA similarity to membrane protein Pho87p	limidano		proteins	YHR026w		proteolipid protein of proton-transporting ATPase
	YCR098c	GIT1	and hypothetical protein YJL198w similarity to phosphate transporter	lipid tra	•			SPF1 ENA1	P-type ATPase P-type ATPase involved in Na <sup>+</sup> and Li <sup>+</sup>
	YPR003c YER053c		proteins similarity to sulphate transporter proteins	YBR041w YKL188c YPL147w	PAT1 PXA1	fatty-acid transporter long-chain-fatty-acid transporter long-chain-fatty-acid transporter		ENA2 ENA5	efflux P-type ATPase involved in Na <sup>+</sup> efflux P-type ATPase involved in Na <sup>+</sup> efflux
	YJL198w		strong similarity to mitochondrial phosphate carrier protein strong similarity to Pho87p	YKL174c	FAAI	similarity to choline transport protein Ctr1p		PCA1	P-type Cu <sup>2+</sup> -transporting ATPase similarity to amino-phospholipids-ATPase
	YBR296c		strong similarity to Priodrp strong similarity to phosphate-repressible phosphate permease	YNR056c		similarity to choline transport protein Ctr1p	YER166w		Drs2p similarity to ATPase <i>P. falciparum</i> ATPase
	YLR092w	SEL2	strong similarity to Sul1p	YHR123w	EPT1	sn-1,2-diacylglycerol ethanolamine- and cholinephosphotransferase	YMR162c		2 similarity to ATPases
	sugar a	nd carb	ohydrate transporters	purine a	nd pyri	midine transporters	YDR093w		similarity to P. falciparum ATPase 2
	YPR021c		similarity to human citrate transporter protein	YMR056c		ADP/ATP carrier protein (MCF)	ABC trai	nsport	ers
	YKL217w YBR291c	JEN1 CTP1	carboxylic-acid transporter protein citrate transport protein, mitochondrial	YBL030c YBR085w	AAC3	ADP/ATP carrier protein (MCF) ADP/ATP carrier protein (MCF)	YDR406w		ATP-binding cassette protein family member
	YLR348c		(MCF) dicarboxylate carrier protein	YBR192w YER056c	FCY2	mitochondrial carrier protein (MCF) purine-cytosine permease	YLR188w		ATP-binding cassette transporter family member
	YLR081w YGR289c	GAL2 AGT1	galactose (and glucose) permease general α-glucoside permease	YER060w YOR222w	FCY21	purine-cytosine permease similarity to ADP/ATP carrier proteins		MDL2	ATP-binding cassette transporter family member
	YLL043w YNL318c	HXT14	glycerol channel protein hexose transport protein	YPL134c YPR011c		similarity to ADP/ATP carrier proteins similarity to ADP/ATP carrier proteins and		STE6 YOR1	ATP-binding cassette transporter protein ATP-binding cassette transporter protein
	YJL214w YJL219w	HXT8 HXT9	hexose transport protein hexose transport protein	YOR071c		Graves disease carrier protein similarity to allantoin or uracil transport	YMR301c	ATM1	required for oligomycin resistance ATP-binding cassette transporter protein,
	YFL011w YDL194w		hexose transporter high-affinity glucose transporter	YOR192c		proteins similarity to allantoin or uracil transport		ADP1	mitochondrial ATP-dependent permease
	YEL069c YMR011w YDR343c	HXT13 HXT2 HXT6	high-affinity hexose transporter high-affinity hexose transporter high-affinity hexose transporter	YGR096w		proteins similarity to bovine Graves disease carrier protein		YCF1 PAT1	glutathione S-conjugate transporter, vacuolar long-chain-fatty-acid transporter
	YDR343C YDR342C YML123C	HXT7 PHO84	high-affinity hexose transporter high-affinity inorganic phosphate/H <sup>+</sup>	YHR002w		similarity to bovine mitochondrial carrier protein/Grave's disease carrier protein	YPL147w	PXA1 PXA1 SNQ2	long-chain-fatty-acid transporter multidrug resistance protein
	1 IVIL ICOU		symporter	YGL186c		similarity to hypothetical protein YER060w and weak similarity to FCY2 protein		PDR12	multidrug resistance protein multidrug resistance transporter pleiotropic drug resistance protein
	YOL 156W	HX I 11							
	YOL156w YHR094c YDR345c	HXT11 HXT1 HXT3	low-affinity glucose transporter low-affinity hexose transporter low-affinity hexose transporter	YBL042c		strong similarity to allantoin and uracil transport proteins	YOL075c		similarity to <i>A. gambiae</i> ATP-binding- cassette protein

allantoin permease similarity to allantoate permease Dal5p

similarity to allantoate transport protein similarity to allantoate transport protein

similarity to allantoate permease transporter

YLL015w

YHL035c YKR103w

YKR104w

YLL048c YIL013c

YOR011w

YOR328w PDR10

PDR11

proteins

allantoin and allantoate transporters

strong similarity to Fcy2p uracil permease

allantoate permease

YJR152w

YIR028w YIL166c

YCR028c

YGR260w

YLR004c

YER060w-a *FCY22* YBR021w *FUR4* 

DAL4

FEN2

52

ITR1 MAL31

YHM1

HXT4

major myo-inositol permease maltose permease

transporter

proteins

member of the mitochondrial carrier family (MCF)

myo-inositol transport protein similarity to glucose transport proteins

similarity to glucose transport proteins similarity to ltr1p and ltr2p

similarity to mitochondrial citrate transport

moderate- to low-affinity glucose

YDR497c YBR298c

YDL198c

YHR092c

YGL104c

YFR045w

YOL103w ITR2 YBR241c

similarity to members of the ABC transporter family

similarity to metal resistance proteins similarity to multidrug resistance proteins

similarity to rat organic anion transporter similarity to Snq2p and other ATP-

dependent permeases strong similarity to ABC transporter

strong similarity to ATP-dependent

YDR091c  YNR070w  drug tran								
		strong similarity to human RNase L inhibitor and to M. jannaschii ABC	YCL069w		strong similarity to drug resistance protein SGE1	YOR130c	ARG11	member of the mitochondrial carrier family (MCF)
		transporter strong similarity to Snq2p	YER087c-a	SEB1	strong similarity to mammalian Sec61β subunit	YDL198c	YHM1	member of the mitochondrial carrier family (MCF)
drug tran			YKR067w		strong similarity to Sct1p	YNL064c	YDJ1	mitochondrial and ER import protein
	nsport	ers	YBL011w YBL089w	SCT1	suppresses a choline-transport mutant weak similarity to A. thaliana aminoacid	YBR192w YPR058w	RIM2 YMC1	mitochondrial carrier protein (MCF) mitochondrial carrier protein (MCF)
YML116w A	ATR1	aminotriazole and 4-nitroquinoline			permease AAP3	YBR104w	YMC2	mitochondrial carrier protein (MCF)
YGR281w )	YOR1	resistance protein ATP-binding cassette transporter protein	YIL088c		weak similarity to A. thaliana aminoacid permease AAP4	YML062c YNR017w	MFT1 MAS6	mitochondrial fusion target protein mitochondrial inner membrane import
		required for oligomycin resistance	YJR001w		weak similarity to A. thaliana aminoacid			translocase subunit
YGR197c S YEL065w	SNG1	involved in nitroguanidine resistance probably multidrug resistance protein	YER119c		permease AAP4 weak similarity to E. herbicola tyrosine	YJL143w	TIM17	mitochondrial inner membrane import translocase subunit
YMR123w F	PKR1	resistance against Pichia farinosa killer			permease	YIL022w	TIM44	mitochondrial inner membrane import
		toxin (SMK toxin) when expressed by a multicopy plasmid	YKL221w		weak similarity to human X-linked PEST- containing transporter	YNL131w	TOM22	translocase subunit mitochondrial outer membrane import
YMR088c		similarity multidrug resistance proteins	YEL064c		weak similarity to members of the major			receptor subunit
YDR119w		similarity to <i>B. subtilis</i> tetracyclin resistance	YJR106w		facilitator superfamily weak similarity to Na <sup>+</sup> /H <sup>+</sup> antiporter	YGR082w	TOM20	mitochondrial outer membrane import receptor subunit, 20K
YBR293w YGR138c		similarity to multidrug resistance proteins similarity to multidrug resistance proteins	YDL206w YKL146w		weak similarity to transporter proteins weak similarity to transporter proteins	YMR060c	TOM37	mitochondrial outer membrane import receptor subunit, 37K
YHR048w		similarity to multidrug resistance proteins	TRETTOW		weak difficulty to transporter proteins	YMR203w	TOM40	mitochondrial outer membrane import
YPR156c YNL065w		similarity to multidrug resistance proteins similarity to resistance proteins	les Acres a			YOR045w	TOM6	receptor subunit, 40K mitochondrial outer membrane import
YIL013c F	PDR11	similarity to Snq2p and other ATP-	intra	cellul	ar transport	VAII 070	TO 147	receptor subunit, 6K
YMR279c		dependent permeases strong similarity to aminotriazole	nuclear	transp	ort	YNL070w	TOM7	mitochondrial outer membrane import receptor subunit, 7K
VCD224w		resistance protein	VII 07Eo	SEN3	260 protogomo rogulator / gubunit	YNL055c	POR1	mitochondrial outer membrane porin
YGR224w		strong similarity to drug resistance protein SGE1	YIL075c YOR048c	RAT1	26S proteasome regulatory subunit 5'-3' exoribonuclease	YNL121c	TOM70	mitochondrial outer membrane specialized import receptor
YBR052c		strong similarity to <i>S. pombe</i> brefeldin A	YGL097w	SRM1	GDP/GTP exchange factor for Gsp1p/Gsp2p	YAR035w	YAT1	outer carnitine acetyltransferase, mitochondrial
YAL067c S	SEO1	resistance protein obr1 suppressor of sulphoxyde ethionine	YOR185c	GSP2	GTP-binding protein	YJR077c	MIR1	phosphate transport protein,
		resistance	YLR293c	GSP1	GTP-binding protein of the RAS superfamily	YBR091c	MRS5	mitochondrial (MCF) regulator of mitochondrial intron splicing
other tra	nspor	t-facilitators	YAL005c	SSA1	heat-shock protein of HSP70 family	YPL134c		similarity to ADP/ATP carrier proteins
YFL028c (	CAF16	ATP-binding cassette transporter protein	YOR160w YJL050w	MTR10 MTR4	involved in mRNA transport involved in nucleocytoplasmic transport of	YER024w		similarity to carnitine O-acetyltransferase Yat1p
YER019c-a 3		family member		KAP104	mRNA	YPR021c		similarity to human citrate transporter
YLR378c S	SEC61	ER protein-translocation complex subunit ER protein-translocation complex subunit	YBR017c YNL189w	SRP1	karyopherin-α or importin	YER053c		protein strong similarity to mitochondrial
	SEC62 SEC63	ER protein-translocation complex subunit ER protein-translocation complex subunit	YLR347c YKL186c	KAP95 MTR2	karyopherin-β mRNA transport protein	YLR034c		phosphate carrier protein strong similarity to SMF2 protein
YBR171w S	SEC66	ER protein-translocation complex subunit	YPL124w	NIP29	nuclear import protein	YHR117w	TOM71	strong similarity to Tom70p/Mas70p
	SEC72 SSS1	ER protein-translocation complex subunit ER protein-translocation complex subunit	YPL174c YMR129w	NIP80 POM152	nuclear import protein nuclear pore membrane glycoprotein	YHR050w	SMF2	suppressor of mitochondrial matrix mutant
YIL134w F	FLX1	FAD carrier protein, mitochondrial (MCF)	YFR002w	NIC96	nuclear pore protein	YIL114c	POR2	voltage dependent anion channel
YCR023c		member of major facilitator superfamily multidrug-resistance protein family 2	YJL041w YOR098c	NSP1 NUP1	nuclear pore protein nuclear pore protein			(YVDAC2)
YKL039w F	PTM1	member of the major facilitator superfamily	YKL068w YMR047c		nuclear pore protein nuclear pore protein	vesicul	ar trans	sport (Golgi network, etc.)
	YMC1	mitochondrial carrier protein (MCF)	YKL057c	NUP120	nuclear pore protein	YBR164c	ARL1	ADP-ribosylation factor
YNR017w /	MAS6	mitochondrial inner membrane import translocase subunit	YKR082w YGL092w		nuclear pore protein nuclear pore protein	YOR094w YGL167c	ARF3 PMR1	ADP-ribosylation factor 3 Ca <sup>2+</sup> -transporting P-type ATPase
YJL143w 7	TIM17	mitochondrial inner membrane import	YER105c	NUP157	nuclear pore protein	YGR167w	CLC1	clathrin light chain
YIL022w 7	TIM44	translocase subunit mitochondrial inner membrane import	YIL115c YBL079w	NUP159 NUP170	nuclear pore protein nuclear pore protein	YOL062c YPL259c	APM4 APM1	clathrin-associate protein YAP54 clathrin-associated protein
	TOM22	translocase subunit		NUP188	nuclear pore protein	YBR288c	APM3	clathrin-associated protein complex,
		mitochondrial outer membrane import receptor subunit	YDR192c	NUP42	nuclear pore protein nuclear pore protein	YPL010w	RET3	medium subunit coatomer complex ζ subunit
YGR082w 7	TOM20	mitochondrial outer membrane import receptor subunit, 20K	YGL172w YGR119c	NUP49 NUP57	nuclear pore protein nuclear pore protein	YDL145c	RET1	coatomer complex α subunit of secretor pathway vesicles
YMR060c 7	TOM37	mitochondrial outer membrane import	YJL061w	NUP82	nuclear pore protein	YGL137w	SEC27	coatomer complex β' subunit (β'-cop) of
YMR203w 7	ТОМ40	receptor subunit, 37K mitochondrial outer membrane import	YDL116w YJR042w	NUP84 NUP85	nuclear pore protein nuclear pore protein	YDR238c	SEC26	secretory pathway vesicles coatomer complex β subunit of secretor
		receptor subunit, 40K	YGL100w	SEH1	nuclear pore protein			pathway vesicles
YOR045w 7	I OIVI6	mitochondrial outer membrane import receptor subunit, 6K	YBR170c	NPL4	nuclear protein localization factor and ER translocation component	YFR051c YNL287w	RET2 SEC21	coatomer complex δ subunit coatomer complex γ subunit (γ-COP) of
YNL070w 7	TOM7	mitochondrial outer membrane import receptor subunit, 7K	YER009w YDR432w		nuclear transport factor nucleolar protein	YDR170c	SEC7	secretory pathway vesicles component of non-clathrin vesicle coat
	POR1	mitochondrial outer membrane porin	YDR002w	YRB1	ran-specific GTPase-activating protein	YPR181c	SEC23	component of the COPII coat of ER-Golg
YNL121c 7	TOM70	mitochondrial outer membrane specialized import receptor	YER107c	GLE2	required for nuclear pore complex structure and function	YDL195w	SEC31	vesicles component of the COPII coat of ER-Golg
YAR035w	YAT1	outer carnitine acetyltransferase,	YIR011c	STS1	required for transport of Rna15p from the			vesicles
YKR093w F	PTR2	mitochondrial peptide transporter	YDL207w	GLE1	cytoplasm to the nucleus RNA export mediator	YGL200c	EMP24	component of the COPII-coated vesicles 24K
YIL120w YIL121w		similarity to antibiotic resistance proteins similarity to antibiotic resistance proteins	YIL063c YLR119w	YRB2 SRN2	similarity to Yrp1p and Nup2p suppressor of rna1-1 mutation	YML012w	ERV25	component of the COPII-coated vesicles 25K
YCL038c		similarity to bacterial membrane	YFL049w	UTITVE	weak similarity to Npl6p	YMR017w	DBI9	Dbf2p interacting protein
YBR043c		transporter similarity to benomyl/methotrexate	mitocho	ondrial t	ransport	YKR054c YLR083c	DYN1 EMP70	dynein heavy chain, cytosolic endosomal protein
		resistance protein			•	YBL040c	ERD2	ER lumen protein-retaining receptor
YHL040c YHL047c		similarity to <i>C. carbonum</i> toxin pump similarity to <i>C. carbonum</i> toxin pump	YMR056c YBL030c	AAC1 AAC2	ADP/ATP carrier protein (MCF) ADP/ATP carrier protein (MCF)	YJR031c YEL022w	GEA1 GEA2	GDP/GTP exchange factor for ARF GDP/GTP exchange factor for ARF
YER024w		similarity to carnitine O-acetyltransferase	YBR085w	AAC3	ADP/ATP carrier protein (MCF)	YNR026c	SEC12	GDP/GTP exchange factor for Sar1p
		Yat1p similarity to cation translocating ATPases	YMR301c		ATP-binding cassette transporter protein, mitochondrial	YPR017c YDL192w	DSS4 ARF1	GDP/GTP exchange factor for Sec4p GTP-binding protein of the ARF family
YOR291w		similarity to channel proteins similarity to drug resistance proteins	YML042w YBR291c	CAT2 CTP1	carnitine O-acetyltransferase citrate transport protein, mitochondrial	YDL137w YPL218w	ARF2 SAR1	GTP-binding protein of the ARF family GTP-binding protein of the ARF family
YFL054c		similarity to Flx1p			(MCF)	YFL038c	YPT1	GTP-binding protein of the RAB family
YFL054c YBR180w YIL006w		similarity to human X-linked PEST- containing transporter	YOR316c YOR037w	COT1	cobalt accumulation protein cytochrome c mitochondrial import factor	YER031c YLR262c	YPT31 YPT6	GTP-binding protein of the RAB family GTP-binding protein of the RAB family
YFL054c YBR180w YIL006w		similarity to hypothetical protein YER064c	YLR348c		dicarboxylate carrier protein	YML001w	YPT7	GTP-binding protein of the RAB family
YFL054c YBR180w YIL006w YOR306c YIL056w	00.70		YKL016c	ATP7 ATP1	F1F0-ATPase complex, F0 D subunit F1F0-ATPase complex, F1 α subunit	YFL005w	SEC4	GTP-binding protein of the RAS superfamily
YFL054c YBR180w YIL006w YOR306c YIL056w	PET8	similarity to mitochondrial rat tricarboxylate transport protein	YBL099w			1/1/1004	0040	
YFL054c YBR180w YIL006w YOR306c YIL056w YNL003c F	PET8	similarity to mitochondrial rat tricarboxylate transport protein similarity to monocarboxylate transporter	YBL099w YJR121w	ATP2	F1F0-ATPase complex, F1 β subunit	YLL024c	SSA2	heat-shock protein of HSP70 family,
YFL054c YBR180w YIL006w YOR306c YIL056w	PET8	similarity to mitochondrial rat tricarboxylate transport protein	YBL099w	ATP2	F1F0-ATPase complex, F1 β subunit F1F0-ATPase complex, F1 δ subunit F1F0-ATPase complex, F1 δ subunit	YLL024c YLR268w	SEC22	heat-shock protein of HSP70 family, cytosolic high copy suppressor of <i>ypt1</i> null
YFL054c YBR180w YIL006w YOR306c YIL056w YNL003c YOL119c YGR065c YOL163w	PET8	similarity to mitochondrial rat tricarboxylate transport protein similarity to monocarboxylate transporter proteins similarity to <i>P. putida</i> phthalate transporter similarity to <i>P. putida</i> phthalate transporter	YBL099w YJR121w YDL004w YPL078c YPL271w	ATP2 ATP16 ATP4 ATP15	F1F0-ATPase complex, F1 δ subunit F1F0-ATPase complex, F1 δ subunit F1F0-ATPase complex, F1 ε subunit	YLR268w	SEC22	cytosolic high copy suppressor of <i>ypt1</i> null mutation
YFL054c YBR180w YIL006w YOR306c YIL056w YNL003c F YOL119c YGR065c	PET8	similarity to mitochondrial rat tricarboxylate transport protein similarity to monocarboxylate transporter proteins similarity to <i>P. putida</i> phthalate transporter	YBL099w YJR121w YDL004w YPL078c	ATP2 ATP16 ATP4 ATP15 ATP3 ATP5	F1F0-ATPase complex, F1 δ subunit F1F0-ATPase complex, F1 δ subunit		SEC22 SLY1	cytosolic high copy suppressor of <i>ypt1</i> null
YFL054c YBR180w YIL006w YOR306c YIL056w YNL003c YOL119c YGR065c YOL163w	PET8	similarity to mitochondrial rat tricarboxylate transport protein similarity to monocarboxylate transporter proteins similarity to <i>P. putida</i> phthalate transporter similarity to <i>P. putida</i> phthalate transporter similarity to peroxisomal membrane and mitochondrial carrier proteins similarity to <i>Staphylococcus</i> multidrug	YBL099w YJR121w YDL004w YPL078c YPL271w YBR039w YDR298c YLR295c	ATP2 ATP16 ATP4 ATP15 ATP3 ATP5 ATP14	F1F0-ATPase complex, F1 & subunit F1F0-ATPase complex, F1 & subunit F1F0-ATPase complex, F1 & subunit F1F0-ATPase complex, F1 y subunit F1F0-ATPase complex, OSCP subunit F1F0-ATPase complex, subunit h	YLR268W YDR189W YDL058W	SEC22 SLY1 USO1	cytosolic high copy suppressor of ypt1 null mutation hydrophilic suppressor of ypt1 and member of the Sec1p family intracellular protein transport protein
YFL054c YBR180w YIL006w YIL006w YOR306c YIL056w YNL003c F YOL119c YGR065c YOL163w YEL006w	PET8	similarity to mitochondrial rat tricarboxylate transport protein similarity to monocarboxylate transporter proteins similarity to <i>P. putida</i> phthalate transporter similarity to <i>P. putida</i> phthalate transporter similarity to peroxisomal membrane and mitochondrial carrier proteins similarity to <i>Staphylococcus</i> multidrug resistance protein similarity to YKL221w and human X-linked	YBL099W YJR121W YDL004W YPL078c YPL271W YBR039W YDR298c YLR295c YIL134W YOR232W	ATP2 ATP16 ATP4 ATP15 ATP3 ATP5 ATP14 FLX1 MGE1	F1F0-ATPase complex, F1 & subunit F1F0-ATPase complex, F1 & subunit F1F0-ATPase complex, F1 s subunit F1F0-ATPase complex, F1 y subunit F1F0-ATPase complex, SCP subunit F1F0-ATPase complex, subunit h FAD carrier protein, mitochondrial (MCF) heat-shock protein - chaperone	YLR268w YDR189w	SEC22 SLY1	cytosolic high copy suppressor of ypt1 null mutation hydrophilic suppressor of ypt1 and member of the Sec1p family intracellular protein transport protein involved in ergosterol biosynthesis involved in targeting and fusion of ER to
YFL054c YBR180w YIL006w YOR306c YIL056w YNL003c F YOL119c YGR065c YOL163w YEL006w YJR124c YNL125c	PET8	similarity to mitochondrial rat tricarboxylate transport protein similarity to monocarboxylate transporter proteins similarity to <i>P. putida</i> phthalate transporter similarity to <i>P. putida</i> phthalate transporter similarity to peroxisomal membrane and mitochondrial carrier proteins similarity to <i>Staphylococcus</i> multidrug resistance protein similarity to <i>Staphylococcus</i> multidrug resistance protein similarity to <i>Staphylococcus</i> multidrug PEST-containing transporter	YBL099w YJR121w YDL004w YPL078c YPL271w YBR039w YDR298c YLR295c YIL134w	ATP2 ATP16 ATP4 ATP15 ATP3 ATP5 ATP14 FLX1	F1F0-ATPase complex, F1 & subunit F1F0-ATPase complex, OSCP subunit F1F0-ATPase complex, Subunit F1F0-ATPase complex, Subunit F1F0-ATPase complex, Subunit F1F0-ATPase complex, Subunit FAD carrier protein, mitochondrial (MCF) heat-shock protein - chaperone heat-shock protein of HSF70 family,	YLR268w YDR189w YDL058w YPL145c YKR068c	SEC22 SLY1 USO1 KES1 BET3	cytosolic high copy suppressor of ypt1 null mutation hydrophilic suppressor of ypt1 and member of the Sec1p family intracellular protein transport protein involved in ergosterol biosynthesis involved in targeting and fusion of ER to Golgi transport vesicles
YFL054c YBR180w YIL006w YOR306c YIL056w YNL003c YOL119c YGR065c YOL163w YEL006w YJR124c	PET8	similarity to mitochondrial rat tricarboxylate transport protein similarity to monocarboxylate transporter proteins similarity to <i>P. putida</i> phthalate transporter similarity to <i>P. putida</i> phthalate transporter similarity to peroxisomal membrane and mitochondrial carrier proteins similarity to <i>Staphylococcus</i> multidrug resistance protein similarity to YKL221w and human X-linked	YBL099W YJR121W YDL004W YPL078c YPL271W YBR039W YDR298c YLR295c YIL134W YOR232W	ATP2 ATP16 ATP4 ATP15 ATP3 ATP5 ATP14 FLX1 MGE1	F1F0-ATPase complex, F1 & subunit F1F0-ATPase complex, F1 & subunit F1F0-ATPase complex, F1 s subunit F1F0-ATPase complex, F1 y subunit F1F0-ATPase complex, SCP subunit F1F0-ATPase complex, subunit h FAD carrier protein, mitochondrial (MCF) heat-shock protein - chaperone	YLR268W YDR189W YDL058W YPL145c	SEC22 SLY1 USO1 KES1	cytosolic high copy suppressor of ypt1 null mutation hydrophilic suppressor of ypt1 and member of the Sec1p family intracellular protein transport protein involved in ergosterol biosynthesis involved in targeting and fusion of ER to

YJL004c YPL085w	SYS1 SEC16	multicopy suppressor of <i>ypt6</i> multidomain vesicle coat protein	extrace	ellular tı	ransport	YNL270c	ALP1	high-affinity permease for basic amino acids
	MYO2 BST1	myosin heavy chain negative regulator of COPII vesicle	YJL085w YDR129c	EXO70 SAC6	70K exocyst component protein actin filament bundling protein, fimbrin	YJL129c YBR294w	TRK1 SUL1	high-affinity potassium transport protein high-affinity sulphate transport protein
YMR079w	SEC14	formation phosphatidylinositol/phosphatidylcholine	YKL209c YDL226c	STE6 GCS1	ATP-binding cassette transporter protein cell proliferation zinc-finger protein	YOL020w YGR191w	SCM2 HIP1	high-affinity tryptophan transport protein histidine permease
1/00000	0554	transfer protein	YER136w	GDI1	GDP dissociation inhibitor	YMR319c	FET4	low-affinity Fe(II) iron transport protein
YCR067c YIL004c	SED4 BET1	protein of the endoplasmic reticulum protein transport protein	YLL043w YJL044c	FPS1 GYP6	glycerol channel protein GTPase-activating protein	YOL156w YHR094c	HXT11 HXT1	low-affinity glucose transporter low-affinity hexose transporter
YLR208w	SEC13	protein transport protein	YLR262c	YPT6	GTP-binding protein of the RAB family	YDR345c		low-affinity hexose transporter
YNL272c	SEC2	protein transport protein	YJL205c-a	NCE1	involved in non-classical protein export	YNL268w	LYP1	lysine-specific high-affinity permease
YGR009c	SEC9	protein transport protein	VDD440	NOFO	pathway	YDR497c	ITR1	major myo-inositol permease
YGL145w YDR498c	TIP20 SEC20	required for ER to Golgi transport secretory pathway protein	YPR149w	NCE2	involved in non-classical protein export pathway	YBR298c YOL122c	MAL31 SMF1	maltose permease manganese transporter
YBR097w	VPS15	ser/thr protein kinase	YNL036w	NCE3	involved in non-classical protein export	YKR050w	TRK2	moderate-affinity potassium transport
YBR264c YKL196c		similarity to GTP-binding proteins similarity to Sec22p	YOR326w		pathway myosin heavy chain	YHR092c	HXT4	protein moderate to low-affinity glucose
YJL193w	VDTaa	similarity to Sly41p	YJL093c YMR308c	TOK1	outward-rectifier potassium channel	VOI 100	ITDO	transporter
YGL210w YKL006c-a	YPT32 SFT1	small GTP-binding protein SNARE-like protein	YDR164c	PSE1 SEC1	protein secretion enhancer protein transport protein	YOL103w YLR240w	ITR2 VPS34	myo-inositol transport protein phosphatidylinositol 3-kinase
YPL051w		strong similarity to ADP-ribosylation	YNL272c	SEC2	protein transport protein	YOR348c	PUT4	proline and γ-aminobutyrate permease
\/DD 403		factors	YIL068c	SEC6	protein transport protein	YER056c	FCY2	purine-cytosine permease
YDR107c YAL030w	SNC1	strong similarity to EMP70 protein strong similarity to synaptic vesicle-	YPR055w YGR009c	SEC8 SEC9	protein transport protein protein transport protein	YLR088w	GAA1	required for attachment of GPI anchor onto proteins
17 (2000)	01101	associated membrane protein	YKL212w	SAC1	recessive suppressor of secretory defect	YNL084c	END3	required for endocytosis and cytoskeletal
YOR327c	SNC2	strong similarity to synaptobrevin	YLR166c	SEC10	required for exocytosis			organization
YER039c		strong similarity to vanadate resistance protein Van2p	YDR166c YNR049c	SEC5 MSO1	required for exocytosis secretion protein, multicopy suppressor of	YJR090c	GRR1	required for glucose repression and for glucose and cation transport
YLR026c YOR075w	SED5 UFE1	syntaxin (T-SNARE) syntaxin (T-SNARE) of the ER	YER008c	SEC3	sec1 secretory pathway protein	YCR009c	RVS161	similarity to human amphiphysin and Rvs167p
YPL232w YBL050w	SSO1 SEC17	syntaxin-related protein	YOR307c YBR162w-a	SLY41	secretory pathway protein	YDR046c	(PAP1)	strong similarity to amino-acid transport
YLR396c	VPS33	transport vesicle fusion protein vacuolar sorting protein	YLR250w		secretory pathway protein secretory protein	YHR096c	HXT5	proteins strong similarity to hexose transporters
YML097c	VPS9	vacuolar sorting protein	YCR032w	001 120	similarity to human CDC4L protein	YIL170w	HXT12	strong similarity to sugar transport
YGL225w YGL233w	GOG5 SEC15	vanadate-resistance protein vesicular traffic control protein	YER006w		similarity to <i>P. polycephalum</i> myosin- related protein mlpA	YJR158w	HXT16	proteins strong similarity to sugar transport
YBR080c	SEC18	vesicular-fusion protein, functional homologue of NSF	YGR131w YNL325c		strong similarity to Nce2p	YNR072w	HXT17	proteins sugar transport protein
YLR093c		weak similarity to synaptobrevin	YPL232w	SSO1	suppressor of sac1 mutation syntaxin-related protein	YOR329c	SCD5	suppressor of clathrin deficiency
YLR078c	BOS1	weak similarity to synaptobrevin	YGL233w	SEC15	vesicular traffic control protein	YPR129w	SCD6	suppressor of clathrin deficiency
		(V-SNARE)	YBR080c	SEC18	vesicular-fusion protein, functional	YBR021w YMR231w	FUR4	uracil permease
peroxis	omal tr	ansport			homologue of NSF	YLR337w	PEP5 VRP1	vacuolar biogenesis protein verprolin
•		•	cellular	import		YBR080c	SEC18	vesicular-fusion protein, functional
YML042w YKL188c	CA12 PAT1	carnitine O-acetyltransferase long-chain-fatty-acid transporter	YPL195w	YKS4	α- or γ- adaptin, large subunit of the	YJR040w	GEF1	homologue of NSF voltage-gated chloride channel protein
YPL147w	PXA1	long-chain-fatty-acid transporter			clathrin-associated protein(AP) complex	YMR243c		zinc- and cadmium resistance protein
	E 4 4 0	long-chain-fatty-acid-CoA ligase	VDI 007	4 DI 0	and a making I a man an a last substantial and a last substa			
YER015w	FAA2		YBL037w	APL3	α-adaptin, large subunit of the clathrin-	- 44 :	A 11-	
YDR329c	PAS3	peroxisomal assembly protein			associated protein(AP) complex	other in	tracell	ular-transport activities
		peroxisomal assembly protein peroxisomal assembly protein	YFL039c YDR129c	APL3 ACT1 SAC6	associated protein(AP) complex actin	other in	tracello DYN1	•
YDR329c YJL210w	PAS3 PAS5	peroxisomal assembly protein peroxisomal assembly protein peroxisomal import protein peroxisomal protein involved in protein	YFL039c YDR129c YDL029w	ACT1 SAC6 ACT2	associated protein(AP) complex actin actin filament bundling protein, fimbrin actin-like protein	YKR054c YER019c-a	DYN1 SEB2	dynein heavy chain, cytosolic ER protein-translocation complex subunit
YDR329c YJL210w YDR142c YLR191w	PAS3 PAS5 PAS7 PAS20	peroxisomal assembly protein peroxisomal assembly protein peroxisomal import protein peroxisomal protein involved in protein import	YFL039c YDR129c YDL029w YCL040w	ACT1 SAC6 ACT2 GLK1	associated protein(AP) complex actin actin filament bundling protein, fimbrin actin-like protein aldohexose specific glucokinase	YKR054c YER019c-a YLR378c	DYN1 SEB2 SEC61	dynein heavy chain, cytosolic ER protein-translocation complex subunit ER protein-translocation complex subunit
YDR329c YJL210w YDR142c	PAS3 PAS5 PAS7 PAS20	peroxisomal assembly protein peroxisomal assembly protein peroxisomal import protein peroxisomal protein involved in protein	YFL039c YDR129c YDL029w	ACT1 SAC6 ACT2	associated protein(AP) complex actin actin filament bundling protein, fimbrin actin-like protein	YKR054c YER019c-a	DYN1 SEB2	dynein heavy chain, cytosolic ER protein-translocation complex subunit ER protein-translocation complex subunit ER protein-translocation complex subunit
YDR329c YJL210w YDR142c YLR191w YDR244w	PAS3 PAS5 PAS7 PAS20 PAS10	peroxisomal assembly protein peroxisomal assembly protein peroxisomal import protein peroxisomal protein involved in protein import putative peroxisomal targeting signal receptor	YFL039c YDR129c YDL029w YCL040w YJR152w YIR028w YBR068c	ACT1 SAC6 ACT2 GLK1 DAL5 DAL4 BAP2	associated protein(AP) complex actin actin filament bundling protein, fimbrin actin-like protein aldohexose specific glucokinase allantoate permease allantoin permease amino-acid permease	YKR054c YER019c-a YLR378c YPL094c YOR254c YBR171w	DYN1 SEB2 SEC61 SEC62 SEC63 SEC66	dynein heavy chain, cytosolic ER protein-translocation complex subunit
YDR329c YJL210w YDR142c YLR191w	PAS3 PAS5 PAS7 PAS20 PAS10	peroxisomal assembly protein peroxisomal assembly protein peroxisomal import protein peroxisomal protein involved in protein import putative peroxisomal targeting signal receptor	YFL039c YDR129c YDL029w YCL040w YJR152w YIR028w YBR068c YEL063c	ACT1 SAC6 ACT2 GLK1 DAL5 DAL4 BAP2 CAN1	associated protein(AP) complex actin actin filament bundling protein, fimbrin actin-like protein aldohexose specific glucokinase allantoate permease allantoin permease amino-acid permease amino-acid permease	YKR054c YER019c-a YLR378c YPL094c YOR254c YBR171w YLR292c	DYN1 SEB2 SEC61 SEC62 SEC63 SEC66 SEC72	dynein heavy chain, cytosolic ER protein-translocation complex subunit
YDR329c YJL210w YDR142c YLR191w YDR244w	PAS3 PAS5 PAS7 PAS20 PAS10	peroxisomal assembly protein peroxisomal assembly protein peroxisomal import protein peroxisomal protein involved in protein import putative peroxisomal targeting signal receptor	YFL039c YDR129c YDL029w YCL040w YJR152w YIR028w YBR068c	ACT1 SAC6 ACT2 GLK1 DAL5 DAL4 BAP2	associated protein(AP) complex actin actin filament bundling protein, fimbrin actin-like protein aldohexose specific glucokinase allantoate permease amino-acid permease amino-acid permease amino-acid permease amino-acid permease amino-acid permease	YKR054c YER019c-a YLR378c YPL094c YOR254c YBR171w YLR292c YDR086c	DYN1 SEB2 SEC61 SEC62 SEC63 SEC66	dynein heavy chain, cytosolic ER protein-translocation complex subunit
YDR329c YJL210w YDR142c YLR191w YDR244w Vacuola YDL128w	PAS3 PAS5 PAS7 PAS20 PAS10 PAS10 VCX1	peroxisomal assembly protein peroxisomal assembly protein peroxisomal import protein peroxisomal protein involved in protein import putative peroxisomal targeting signal receptor port Ca²-transport (H*/Ca²- exchange) protein, vacuolar	YFL039c YDR129c YDL029w YCL040w YJR152w YIR028w YBR068c YEL063c YBR069c YGR121c	ACT1 SAC6 ACT2 GLK1 DAL5 DAL4 BAP2 CAN1 VAP1 MEP1	associated protein(AP) complex actin actin filament bundling protein, fimbrin actin-like protein aldohexose specific glucokinase allantoate permease allantoin permease amino-acid permease amino-acid permease amino-acid permease amnona permease of high capacity and moderate affinity	YKR054c YER019c-a YLR378c YPL094c YOR254c YBR171w YLR292c	DYN1 SEB2 SEC61 SEC62 SEC63 SEC66 SEC72 SSS1	dynein heavy chain, cytosolic ER protein-translocation complex subunit intracellular protein transport protein involved in clathrin-dependent transport
YDR329c YJL210w YDR142c YLR191w YDR244w Vacuola YDL128w YGL006w	PAS3 PAS5 PAS7 PAS20 PAS10 PT trans VCX1 PMC1	peroxisomal assembly protein peroxisomal assembly protein peroxisomal import protein peroxisomal protein involved in protein import putative peroxisomal targeting signal receptor port Ca²-transport (H*/Ca²+ exchange) protein, vacuolar Ca²-transporting P-type ATPase	YFL039c YDR129c YDL029w YCL040w YJR152w YIR028w YBR068c YEL063c YBR069c YGR121c YKL135c	ACT1 SAC6 ACT2 GLK1 DAL5 DAL4 BAP2 CAN1 VAP1 MEP1	associated protein(AP) complex actin actin filament bundling protein, fimbrin actin-like protein aldohexose specific glucokinase allantoate permease allantoin permease amino-acid permease amino-acid permease amino-acid permease amino-acid permease amino-acid permease amino-acid permease amonia permease of high capacity and moderate affinity β-adaptin	YKR054c YER019c-a YLR378c YPL094c YOR254c YBR171w YLR292c YDR086c YCR075c YHL019c	DYN1 SEB2 SEC61 SEC62 SEC63 SEC66 SEC72 SSS1 ERS1 APM2	dynein heavy chain, cytosolic ER protein-translocation complex subunit intracellular protein transport protein involved in clathrin-dependent transport processes
YDR329c YJL210w YDR142c YLR191w YDR244w Vacuola YDL128w YGL006w YDR135c	PAS3 PAS5 PAS7 PAS20 PAS10 PT trans VCX1 PMC1 YCF1	peroxisomal assembly protein peroxisomal assembly protein peroxisomal import protein peroxisomal import protein inport protein inport putative peroxisomal targeting signal receptor  port  Ca²-transport (H*/Ca²+ exchange) protein, vacuolar  Ca²-transporting P-type ATPase glutathione S-conjugate transporter, vacuolar	YFL039c YDR129c YDL029w YCL040w YJR152w YJR028w YBR068c YEL063c YBR069c YGR121c YKL135c YGR261c	ACT1 SAC6 ACT2 GLK1 DAL5 DAL4 BAP2 CAN1 VAP1 MEP1 APL2 YKS5	associated protein(AP) complex actin actin filament bundling protein, fimbrin actin-like protein aldohexose specific glucokinase allantoate permease allantoin permease amino-acid permease amino-acid permease amino-acid permease ammonia permease of high capacity and moderate affinity β-adaptin, large subunit of the clathrin-associated protein(AP) complex	YKR054c YER019c-a YLR378c YPL094c YOR254c YBR171w YLR292c YDR086c YCR075c	DYN1 SEB2 SEC61 SEC62 SEC63 SEC66 SEC72 SSS1 ERS1	dynein heavy chain, cytosolic ER protein-translocation complex subunit intracellular protein transport protein involved in clathrin-dependent transport processes nuclear fusion protein nuclear protein localization factor and ER
YDR329c YJL210w YDR142c YLR191w YDR244w YDL128w YGL006w YDR135c YOR089c	PAS3 PAS5 PAS7 PAS70 PAS10 VCX1 PMC1 YCF1 VPS21	peroxisomal assembly protein peroxisomal assembly protein peroxisomal import protein peroxisomal protein import import putative peroxisomal targeting signal receptor  Ca²-transport (H¹/Ca²- exchange) protein, vacuolar Ca²-transporting P-type ATPase glutathione S-conjugate transporter, vacuolar GTP-binding protein	YFL039c YDR129c YDL029w YCL040w YJR152w YJR028w YBR068c YEL063c YBR069c YGR121c YKL135c YGR261c YBR109c	ACT1 SAC6 ACT2 GLK1 DAL5 DAL4 BAP2 CAN1 WAP1 MEP1 APL2 YKS5 CMD1	associated protein(AP) complex actin actin filament bundling protein, fimbrin actin-like protein aldohexose specific glucokinase allantoate permease allantoin permease amino-acid permease amino-acid permease amino-acid permease amino-acid permease amino-acid permease amino-acid permease amonaci permease of high capacity and moderate affinity  B-adaptin  B-adaptin, large subunit of the clathrin-associated protein(AP) complex calmodulin	YKR054c YER019c-a YLR378c YPL094c YPL094c YDR254c YBR171w YLR292c YDR086c YCR075c YHL019c YJL034w YBR170c	DYN1 SEB2 SEC61 SEC62 SEC63 SEC66 SEC72 SSS1 ERS1 APM2 KAR2 NPL4	dynein heavy chain, cytosolic ER protein-translocation complex subunit intracellular protein transport protein involved in clathrin-dependent transport processes nuclear fusion protein nuclear protein localization factor and ER translocation component
YDR329c YJL210w YDR142c YLR191w YDR244w Vacuola YDL128w YGL006w YDR135c YOR089c YER031c	PAS3 PAS5 PAS5 PAS10 PAS10 VCX1 PMC1 YCF1 VPS21 YPT31	peroxisomal assembly protein peroxisomal assembly protein peroxisomal import protein peroxisomal import protein import protein import putative peroxisomal targeting signal receptor  **Port**  Ca²-transport (H*/Ca²- exchange) protein, vacuolar Ca²-transporting P-type ATPase glutathione S-conjugate transporter, vacuolar GTP-binding protein of the RAB family	YFL039c YDR129c YDL029w YCL040w YJR152w YJR028w YBR068c YEL063c YBR069c YGR121c YKL135c YGR261c	ACT1 SAC6 ACT2 GLK1 DAL5 BAP2 CAN1 VAP1 MEP1 APL2 YKS5 CMD1 GCS1	associated protein(AP) complex actin actin filament bundling protein, fimbrin actin-like protein aldohexose specific glucokinase allantoate permease allantoin permease amino-acid permease amino-acid permease amino-acid permease amore amore amore amore acting permease amore amore acting permease acting a	YKR054c YER019c-a YLR378c YPL094c YOR254c YBR171w YLR292c YDR086c YCR075c YHL019c YJL034w YBR170c YKR093w	DYN1 SEB2 SEC61 SEC62 SEC63 SEC66 SEC72 SSS1 ERS1 APM2 KAR2 NPL4 PTR2	dynein heavy chain, cytosolic ER protein-translocation complex subunit intracellular protein transport protein involved in clathrin-dependent transport processes nuclear fusion protein nuclear protein localization factor and ER translocation component peptide transporter
YDR329c YJL210w YDR142c YLR191w YDR244w YDL128w YGL006w YDR135c YOR089c	PAS3 PAS5 PAS7 PAS70 PAS10 VCX1 PMC1 YCF1 VPS21	peroxisomal assembly protein peroxisomal assembly protein peroxisomal import protein peroxisomal protein import protein import putative peroxisomal targeting signal receptor  **Port**  Ca²-transport (H¹/Ca²- exchange) protein, vacuolar Ca²-transporting P-type ATPase glutathione S-conjugate transporter, vacuolar GTP-binding protein of the RAB family	YFL039c YDR129c YDL029w YCL040w YJR152w YJR028w YBR068c YEL063c YBR069c YGR121c YKL135c YGR261c YBR109c YDL226c YMR058w YGL077c	ACT1 SAC6 ACT2 GLK1 DAL5 DAL4 BAP2 CAN1 VAP1 MEP1 APL2 YKS5 CMD1 GCS1 FET3 HNM1	associated protein(AP) complex actin actin filament bundling protein, fimbrin actin-like protein aldohexose specific glucokinase allantoate permease allantoin permease amino-acid permease filip had patring permease of high capacity and moderate affinity β-adaptin β-adaptin, large subunit of the clathrin-associated protein(AP) complex calmodulin cell proliferation zinc-finger protein cell-surface ferroxidase choline permease	YKR054c YER019c-a YLR378c YPL094c YPL094c YDR254c YBR171w YLR292c YDR086c YCR075c YHL019c YJL034w YBR170c	DYN1 SEB2 SEC61 SEC62 SEC63 SEC66 SEC72 SSS1 ERS1 APM2 KAR2 NPL4	dynein heavy chain, cytosolic ER protein-translocation complex subunit intracellular protein transport protein involved in clathrin-dependent transport processes nuclear fusion protein nuclear protein localization factor and ER translocation component peptide transporter polyamine transport enhancing protein P-type ATPase involved in Na* and Li*
YDR329c YJL210w YDR142c YLR191w YDR244w YDL128w YGL006w YDR135c YOR089c YER031c YKR014c YNL093w	PAS3 PAS5 PAS7 PAS7 PAS20  PAS10  Trans  VCX1  PMC1 YCF1  VPS21 YPT31 YPT52 YPT53	peroxisomal assembly protein peroxisomal assembly protein peroxisomal import protein peroxisomal import protein inport protein peroxisomal protein involved in protein import putative peroxisomal targeting signal receptor  **Port**  Ca²-transport (H*/Ca²- exchange) protein, vacuolar  Ca²-transporting P-type ATPase glutathione S-conjugate transporter, vacuolar  GTP-binding protein GTP-binding protein of the RAB family  (RAS superfamily)	YFL039c YDR129c YDL029w YCL040w YIR152w YIR028w YBR068c YEL063c YBR069c YGR121c YKL135c YGR261c YBR109c YDL226c YMR058w YGL070c YGL206c	ACT1 SAC6 ACT2 GLK1 DAL5 DAL4 BAP2 CAN1 MEP1 APL2 YKS5 CMD1 GCS1 FET3 HNM1 CHC1	associated protein(AP) complex actin actin illament bundling protein, fimbrin actin-like protein aldohexose specific glucokinase allantoate permease allantoate permease amino-acid permease amino-acid permease amino-acid permease amino-acid permease ammonia permease of high capacity and moderate affinity β-adaptin, large subunit of the clathrinassociated protein(AP) complex calmodulin cell proliferation zinc-finger protein cell-surface ferroxidase choline permease clathrin heavy chain	YKR054c YER019c-a YLR378c YPL094c YOR254c YBR171w YLR292c YDR086c YCR075c YHL019c YJL034w YBR170c YKR093w YKL198c YDR040c	DYN1 SEB2 SEC61 SEC62 SEC63 SEC66 SEC72 SSS1 ERS1 APM2 KAR2 NPL4 PTR2 PTK1 ENA1	dynein heavy chain, cytosolic ER protein-translocation complex subunit intracellular protein transport protein involved in clathrin-dependent transport processes nuclear fusion protein nuclear protein localization factor and ER translocation component peptide transporter polyamine transport enhancing protein
YDR329c YJL210w YDR142c YLR191w YDR244w YDL128w YGL006w YDR135c YOR089c YER031c YKR014c YNL093w YMR054w	PAS3 PAS5 PAS7 PAS70 PAS10  PAS10  PT Trans VCX1 PMC1 YCF1  VPS21 YPT52 YPT53  STV1	peroxisomal assembly protein peroxisomal assembly protein peroxisomal import protein peroxisomal import protein protein protein import protei	YFL039c YDR129c YDL029w YCL040w YJR152w YJR028w YBR068c YEL063c YBR069c YGR121c YKL135c YGR261c YBR109c YDL226c YMR058w YGL077c	ACT1 SAC6 ACT2 GLK1 DAL5 DAL4 BAP2 CAN1 MEP1 APL2 YKS5 CMD1 GCS1 FET3 HNM1 CHC1	associated protein(AP) complex actin actin filament bundling protein, fimbrin actin-like protein aldohexose specific glucokinase allantoate permease allantoin permease amino-acid permease amino-acid permease amino-acid permease amino-acid permease amino-acid permease amino-acid permease amore approved permease amore actinity β-adaptin β-adaptin, large subunit of the clathrin-associated protein(AP) complex calmodulin cell proliferation zinc-finger protein cell-surface ferroxidase clathrin heavy chain clathrin-associated protein (AP) complex, clathrin-associated protein (AP) complex, clathrin-associated protein (AP) complex,	YKR054c YER019c-a YLR378c YPL094c YOR254c YBR171w YLR292c YDR066c YCR075c YHL019c YIL034w YBR170c YKR093w YKL1980 YPB040c YER060w YNL183c	DYN1 SEB2 SEC61 SEC62 SEC63 SEC66 SEC72 SSS1 ERS1 APM2 KAR2 NPL4 PTR2 PTK1 ENA1	dynein heavy chain, cytosolic ER protein-translocation complex subunit intracellular protein transport protein involved in clathrin-dependent transport processes nuclear fusion protein nuclear protein localization factor and ER translocation component peptide transporter polyamine transport enhancing protein P-type ATPase involved in Na' and Li' efflux purine-cytosine permease ser/thr protein kinase
YDR329c YJL210w YDR142c YLR191w YDR244w YDR244w YDL128w YGL006w YDR135c YOR089c YER031c YKR014c YNL093w YMR054w YHR039c-a	PAS3 PAS5 PAS7 PAS70 PAS10  PAS10  PMC1 YCK1  VPS21 YPT52 YPT53  STV1  VMA10	peroxisomal assembly protein peroxisomal assembly protein peroxisomal import protein peroxisomal import protein import import putative peroxisomal targeting signal receptor  **Ca²-transport (H¹/Ca²- exchange) protein, vacuolar Ca²-transporting P-type ATPase glutathione S-conjugate transporter, vacuolar GTP-binding protein of the RAB family (RAS superfamily) H¹-ATPase V0 domain 102K subunit, vacuolar H²-ATPase V0 domain 13K subunit, vacuolar had superfamily (RAS superfamily) H²-ATPase V0 domain 13K subunit, vacuolar had superfamily vacuolar had subunit vacuolar had superfamily	YFL039c YDR129c YDL029w YCL040w YJR1628w YJR028w YBR068c YBR069c YGR121c YKL135c YGR261c YBR109c YDL226c YMR058w YGL077c YGL106c YGR167w YGL167f	ACT1 SAC6 ACT2 GLK1 DAL5 DAL4 BAP2 CAN1 VAP1 MEP1 APL2 YKS5 CMD1 GCS1 HNM1 CHC1 CHC1	associated protein(AP) complex actin actin filament bundling protein, fimbrin actin-like protein aldohexose specific glucokinase allantoate permease allantoin permease amino-acid permease and permease affinity B-adaptin B-adaptin Iarge subunit of the clathrin-associated protein(AP) complex calmodulin cell proliferation zinc-finger protein cell-surface ferroxidase choline permease clathrin heavy chain clathrin-associated protein (AP) complex, small subunit AP19 clathrin-associated protein 17, small	YKR054c YER019c-a YLR378c YPL094c YPL094c YOR254c YBR171w YLR292c YOR075c YHL019c YKL0934w YBR170c YKR0934w YKL198c YDR040c YER060w YML183c YOR100c	DYN1 SEB2 SEC61 SEC62 SEC63 SEC66 SEC72 SSS1 APM2 KAR2 NPL4 PTR2 PTK1 ENA1 FCY21	dynein heavy chain, cytosolic ER protein-translocation complex subunit intracellular protein transport protein involved in clathrin-dependent transport processes nuclear fusion protein nuclear protein localization factor and ER translocation component peptide transporter polyamine transport enhancing protein P-type ATPase involved in Na* and Li* efflux purine-cytosine permease ser/thr protein kinase similarity to mitochondrial carrier protein YMC1
YDR329c YJL210w YDR142c YLR191w YDR244w YDL128w YDL128w YGL006w YDR135c YOR089c YER031c YKR014c YNL093w YMR054w YHR039c-6	PAS3 PAS5 PAS7 PAS7 PAS10 PAS10 PAS10 VCX1 PMC1 YCF1 VPS21 YPT31 YPT52 YPT53 STV1 VMA10 CUP5	peroxisomal assembly protein peroxisomal assembly protein peroxisomal import protein peroxisomal import protein import protein peroxisomal protein involved in protein import putative peroxisomal targeting signal receptor  **Port**  Ca²-transport (H*/Ca²- exchange) protein, vacuolar  Ca²-transporting P-type ATPase glutathione S-conjugate transporter, vacuolar  GTP-binding protein of the RAB family  GTP-bin	YFL039c YDR129c YDL029w YCL040w YJR152w YBR068c YEL063c YBR069c YGR121c YKL135c YGR261c YBR109c YDL226c YMR058w YGL076 YGL206c YGR167w YL170c	ACT1 SAC6 ACT2 GLK1 DAL5 DAL4 BAP2 CAN1 VAP1 MEP1 APL2 YKS5 CMD1 GCS1 FET3 HNM1 CHC1 CLC1 APS1	associated protein(AP) complex actin actin filament bundling protein, fimbrin actin-like protein aldohexose specific glucokinase allantoate permease allantoate permease amino-acid permease amore appeared permease amore appeared permease amore appeared permease of high capacity and moderate affinity \$\textit{B}\$-adaptin, large subunit of the clathrin-associated protein(AP) complex calmodulin cell proliferation zinc-finger protein cell-surface ferroxidase choline permease clathrin heavy chain clathrin-associated protein (AP) complex, small subunit AP19 clathrin-associated protein 17, small subunit clathrin-associated protein complex,	YKR054c YER019c-a YLR378c YPL094c YOR254c YBR171w YLR292c YDR086c YCR075c YHL019c YJL034w YKR198c YDR040c YER060w YNL183c YOR100c YGL216w	DYN1 SEB2 SEC61 SEC62 SEC63 SEC66 SEC72 SSS1 APM2 KAR2 NPL4 PTR2 PTK1 ENA1 FCY21	dynein heavy chain, cytosolic ER protein-translocation complex subunit intracellular protein transport protein involved in clathrin-dependent transport processes nuclear fusion protein nuclear protein localization factor and ER translocation component peptide transporter polyamine transport enhancing protein P-type ATPase involved in Na' and Li' efflux purine-cytosine permease ser/fthr protein kinase similarity to mitochondrial carrier protein YMC1 similarity to mouse kinesin-related protein KIF3
YDR329c YJL210w YDR142c YLR191w YDR244w YDR244w YDL128w YGL006w YDR135c YOR089c YER031c YKR014c YNL093w YMR054w YHR039c-a	PAS3 PAS5 PAS7 PAS70 PAS10  PAS10  PMC1 YCK1  VPS21 YPT52 YPT53  STV1  VMA10	peroxisomal assembly protein peroxisomal assembly protein peroxisomal import protein peroxisomal import protein protein protein protein import protein impor	YFL039c YDR129c YDL029w YCL040w YJR152w YBR068c YEL063c YBR068c YGR261c YKL135c YGR261c YBR109c YDL226c YMR058w YGL077c YGL206c YGR167w YLR170c YJR058c	ACT1 SAC6 ACT2 GLK1 DAL5 DAL4 BAP2 CAN1 VAP1 MEP1 APL2 YKS5 CMD1 GCS1 FET3 HNM1 CHC1 CLC1 APS1	associated protein(AP) complex actin actin filament bundling protein, fimbrin actin-like protein actin-like protein actin-like protein aldohexose specific glucokinase allantoate permease allantoin permease amino-acid permease amino-acid permease amino-acid permease ammonia permease of high capacity and moderate affinity β-adaptin β-adaptin, large subunit of the clathrin-associated protein(AP) complex calmodulin cell proliferation zinc-finger protein cell-surface ferroxidase choline permease clathrin heavy chain clathrin-associated protein (AP) complex, small subunit AP19 clathrin-associated protein 17, small subunit actin in sasociated protein 17, small subunit subunit actin in sasociated protein 17, small subunit actin in sasociated protein 18, small sasociated p	YKR054c YER019c-a YLR378c YPL094c YPL094c YOR254c YBR171w YLR292c YOR075c YHL019c YKL0934w YBR170c YKR0934w YKL198c YDR040c YER060w YML183c YOR100c	DYN1 SEB2 SEC61 SEC61 SEC63 SEC63 SEC66 SEC72 SSS1 ERS1 APM2 KAR2 NPL4 PTR2 PTR1 ENA1 FCY21 NPR1	dynein heavy chain, cytosolic ER protein-translocation complex subunit intracellular protein transport protein involved in clathrin-dependent transport processes nuclear fusion protein nuclear protein localization factor and ER translocation component peptide transporter polyamine transport enhancing protein P-type ATPase involved in Na* and Li* efflux purine-cytosine permease ser/thr protein kinase similarity to mitochondrial carrier protein YMC1 similarity to mouse kinesin-related protein KIF3 similarity to sterol uptake protein Sut1p sin-1,2-diacy/glycerol ethanolamine- and
YDR329c YJL210w YDR142c YLR191w YDR244w YDL128w YDL128w YGL006w YDR135c YOR089c YER031c YKR014c YNL093w YMR054w YHR039c-6	PAS3 PAS5 PAS7 PAS7 PAS10 PAS10 PAS10 VCX1 PMC1 YCF1 VPS21 YPT31 YPT52 YPT53 STV1 VMA10 CUP5	peroxisomal assembly protein peroxisomal assembly protein peroxisomal import protein peroxisomal import protein import protein peroxisomal protein involved in protein import putative peroxisomal targeting signal receptor  **Port**  Ca²-transport (H*/Ca²- exchange) protein, vacuolar  Ca²-transporting P-type ATPase glutathione S-conjugate transporter, vacuolar  GTP-binding protein of the RAB family  H-ATPase V0 domain 102K subunit, vacuolar  H-ATPase V0 domain 17K subunit, vacuolar  H-ATPase V0 domain 36K subunit,	YFL039c YDR129c YDL029w YCL040w YJR152w YIR028w YBR069c YEL063c YBR069c YGR121c YBK109c YDL226c YMR058w YGL077c YGL206c YGR167w YLR170c YJR058c YJR005w YJL024c	ACT1 SAC6 ACT2 GLK1 DAL5 DAL4 BAP2 CAN1 VAP1 VAP1 APL2 YKS5 CMD1 GCS1 FET3 HNM1 CHC1 CLC1 APS1 APS2 YAP80	associated protein(AP) complex actin actin filament bundling protein, fimbrin actin-like protein aldohexose specific glucokinase allantoate permease allantoate permease amino-acid permease amino-acid permease amino-acid permease amino-acid permease amino-acid permease amino-acid permease amona permease of high capacity and moderate affinity β-adaptin β-adaptin, large subunit of the clathrin-associated protein(AP) complex calmodulin cell proliferation zinc-finger protein cell-surface ferroxidase choline permease clathrin heavy chain clathrin-associated protein (AP) complex, small subunit AP19 clathrin-associated protein 17, small subunit clathrin-associated protein complex, β subunit clathrin-associated protein complex, small subunit clathrin-associated protein (AP) complex, small subunit	YKR054c YER019c-a YLR378c YPL094c YOR254c YOR254c YOR075c YJR098c YCR075c YHL0192 YJL034w YKR198c YDR040c YKR093w YKL198c YDR040c YER060w YML183c YOR100c YGL216w YPR094w YHR123w	DYN1 SEB2 SEC61 SEC62 SEC63 SEC66 SEC7 SEC7 SEC7 SEC7 SEC7 SEC7 SEC7 SEC7	dynein heavy chain, cytosolic ER protein-translocation complex subunit intracellular protein transport protein involved in clathrin-dependent transport processes nuclear fusion protein nuclear protein localization factor and ER translocation component peptide transporter polyamine transport enhancing protein P-type ATPase involved in Na* and Li* efflux purine-cytosine permease ser/thr protein kinase similarity to mitochondrial carrier protein YMC1 similarity to mouse kinesin-related protein KIF3 similarity to sterol uptake protein Sut1p similarity to sterol uptake protein Sut1p sn-1,2-diacylglycerol ethanolamine- and cholinephosphotransferase
YDR329c YJL210w YDR142c YLR191w YDR244w YDR244w YDL128w YGL006w YDR135c YOR089c YER031c YKR014c YNL093w YMR054w YHR039c-a YEL027w YPL234c	PAS3 PAS5 PAS7 PAS7 PAS20  PAS10  Transi  VCX1  PMC1 YCF1  VPS21 YPT31 YPT52 YPT53  STV1  VMA10  CUP5  TFP3	peroxisomal assembly protein peroxisomal assembly protein peroxisomal import protein peroxisomal import protein import protein peroxisomal protein involved in protein import putative peroxisomal targeting signal receptor  **Port**  Ca²-transport (H*/Ca²- exchange) protein, vacuolar Ca²-transporting P-type ATPase glutathione S-conjugate transporter, vacuolar GTP-binding protein GTP-binding protein of the RAB family (RAS superfamily) H-ATPase V0 domain 102K subunit, vacuolar H-ATPase V0 domain 17K subunit, vacuolar H-ATPase V0 domain 17K subunit, vacuolar H-ATPase V0 domain 17K subunit, vacuolar H-ATPase V0 domain 36K subunit, vacuolar H-ATPase V0 domain 95K subunit, Vacuolar H-ATPase V0 domain 95K subunit, Vacuolar H-ATPase V0 domain 95K subunit,	YFL039c YDR129c YDR129c YDL029w YCL040w YIR152w YIR028w YBR068c YEL063c YBR069c YGR121c YKL135c YGR261c YMR109c YDL226c YMR058w YGL276c YGL276c YGR167W YLR170c YJR058c YJR005w YJL024c YPR124w YHR175w	ACT1 SAC6 ACT2 GLK1 DAL5 DAL4 BAP2 CAN1 VAP1 MEP1 APL2 YKS5 CMD1 GCS1 FET3 HNM1 CHC1 CLC1 APS1 APS2 YAP80 APS3 CTR1 CTR2	associated protein(AP) complex actin actin filament bundling protein, fimbrin actin-like protein aldohexose specific glucokinase allantoate permease allantoate permease amino-acid permease amino-acid permease amino-acid permease ammonia permease of high capacity and moderate affinity β-adaptin, large subunit of the clathrin-associated protein(AP) complex calmodulin cell proliferation zinc-finger protein cell-surface ferroxidase choline permease clathrin heavy chain clathrin-associated protein (AP) complex, small subunit AP19 clathrin-associated protein (AP) complex, small subunit clathrin-associated protein complex, β subunit clathrin-associated protein (AP) complex, small subunit copper transport protein copper transport protein copper transport protein	YKR054c YER019c-a YLR378c YPL094c YPL094c YOR254c YBR171w YLR292c YCR075c YHL019c YKL093w YKL198c YDR040c YER060w YML183c YOR100c YGL216w YPR009w	DYN1 SEB2 SEC61 SEC62 SEC61 SEC62 SEC63 SEC66 SEC72 SSS1 ERS1 APM2 KAR2 NPL4 PTR2 PTR1 ENA1 FCY21 NPR1	dynein heavy chain, cytosolic ER protein-translocation complex subunit intracellular protein transport protein involved in clathrin-dependent transport processes nuclear fusion protein nuclear protein localization factor and ER translocation component peptide transporter polyamine transport enhancing protein P-type ATPase involved in Na* and Li* efflux purine-cytosine permease ser/thr protein kinase similarity to mitochondrial carrier protein YMC1 similarity to mouse kinesin-related protein KIF3 similarity to sterol uptake protein Sut1p sn-1,2-diacylglycerol ethanolamine- and cholinephosphotransferase strong similarity to Fcy2p strong similarity to mammalian Sec61β
YDR329c YJL210w YDR142c YLR191w YDR244w YDR1244w YDL128w YGL006w YDR135c YCR031c YKR014c YNL093w YMR054w YHR039c-2 YEL027w YPL234c YLR447c	PAS3 PAS4 PAS7 PAS7 PAS20  PAS10  Trans  VCX1  PMC1 YCF1  VPS21 YPT31 YPT52 YPT53  STV1  CUP5  TFP3  VMA6	peroxisomal assembly protein peroxisomal assembly protein peroxisomal import protein peroxisomal import protein import protein peroxisomal protein involved in protein import putative peroxisomal targeting signal receptor  PORT  Ca²-transport (H¹/Ca²- exchange) protein, vacuolar Ca²-transporting P-type ATPase glutathione S-conjugate transporter, vacuolar GTP-binding protein of the RAB family GTP-binding protein of the RAB family GTP-binding protein of the RAB family (RAS superfamily) H¹-ATPase V0 domain 102K subunit, vacuolar H¹-ATPase V0 domain 17K subunit, vacuolar H¹-ATPase V0 domain 17K subunit, vacuolar H¹-ATPase V0 domain 36K subunit, vacuolar H¹-ATPase V0 domain 95K subunit, vacuolar H¹-ATPase V0 domain 95K subunit, vacuolar H¹-ATPase V0 domain 95K subunit, vacuolar	YFL039c YDR129c YDR129c YDL029w YCL040w YJR152w YJR028w YBR068c YEL063c YBR068c YGR121c YKL135c YGR261c YKL135c YGR261c YKL135c YGR261c YKL135c YGR261c YKL135c YGR261c YKL135c YGR261c YKL135c YJR026c YMR058w YGL077c YGL206c YGR167w YLR170c YJR005w YJR005w YJL024c YPR124w YHR175w YNL243w YNL243w YLL001w	ACT1 SAC6 ACT2 GLK1 DAL5 DAL4 BAP2 CAN1 VAP1 APL2 YKS5 CMD1 GCS1 FET3 HNM1 CHC1 CLC1 APS2 YAP80 APS3 CTR1 CTR2 SLA2 DNM1	associated protein(AP) complex actin actin filament bundling protein, filmbrin actin-like protein aldohexose specific glucokinase allantoate permease allantoate permease amino-acid permease allanto activation activati	YKR054c YER019c-a YLR378c YPL094c YPL094c YDR0254c YBR171w YLR292c YDR008c YCR075c YHL019c YKR093w YKL198c YDR040c YER060w YML183c YOR100c YGL216w YPR009w YHR123w YER060w-1	DYN1 SEB2 SEC61 SEC62 SEC61 SEC62 SEC63 SEC66 SEC72 SSS1 ERS1 APM2 KAR2 NPL4 PTR2 PTR1 ENA1 FCY21 NPR1	dynein heavy chain, cytosolic ER protein-translocation complex subunit intracellular protein transport protein involved in clathrin-dependent transport processes nuclear fusion protein nuclear protein localization factor and ER translocation component peptide transporter polyamine transport enhancing protein P-type ATPase involved in Na* and Li* efflux purine-cytosine permease ser/thr protein kinase similarity to mitochondrial carrier protein YMC1 similarity to mouse kinesin-related protein KIF3 similarity to sterol uptake protein Sut1p sn-12-diacylglycerol ethanolamine- and cholinephosphotransferase strong similarity to Fcy2p
YDR329c YJL210w YDR142c YLR191w YDR244w YDR128w YDL128w YGL006w YDR135c YOR089c YER031c YKR014c YNL093w YHR039c-a YEL027w YPL234c YLR447c YOR270c	PASS PASS PASS PASS PASS PASS PASS PASS	peroxisomal assembly protein peroxisomal assembly protein peroxisomal import protein peroxisomal import protein import protein peroxisomal protein involved in protein import putative peroxisomal targeting signal receptor  **Ca2**-transport (H*/Ca2** exchange) protein, vacuolar Ca2**-transporting P-type ATPase glutathione S-conjugate transporter, vacuolar GTP-binding protein of the RAB family GTP-binding protein of the RAB family GTP-binding protein of the RAB family (RAS superfamily) H*-ATPase V0 domain 102K subunit, vacuolar H*-ATPase V0 domain 17K subunit, vacuolar H*-ATPase V0 domain 17K subunit, vacuolar H*-ATPase V0 domain 36K subunit, vacuolar H*-ATPase V0 domain 36K subunit, vacuolar H*-ATPase V0 domain 95K subunit, vacuolar H*-ATPase V0 domain 95K subunit, vacuolar H*-ATPase V1 domain 95K subunit, vacuolar H*-ATPase V1 domain 14K subunit, vacuolar H*-ATPase V1 domain 14K subunit, vacuolar H*-ATPase V1 domain 14K subunit, vacuolar H*-ATPase V1 domain 27K subunit, Vacuolar H*	YFL039c YDR129c YDR129c YDL029w YCL040w YJR152w YJR068c YEL063c YBR068c YEL063c YGR261c YKL135c YGR261c YMR068w YGL027c YJR058w YJR058c YJR058c YJR058c YJR054c YJR054	ACT1 SAC6 ACT2 GLK1 DAL5 DAL4 BAP2 CAN1 VAP1 APL2 YKS5 CMD1 GCS1 FET3 HNM1 CHC1 CLC1 APS1 APS2 YAP80 APS3 CTR1 CTR2 SLA2	associated protein(AP) complex actin actin filament bundling protein, fimbrin actin-like protein actin-like protein aldohexose specific glucokinase allantoate permease allantoate permease amino-acid permease albatin, large subunit of the clathrin-associated protein(AP) complex calmodulin cell proliferation zinc-finger protein cell-surface ferroxidase choline permease clathrin heavy chain clathrin light chain clathrin-associated protein (AP) complex, small subunit AP19 clathrin-associated protein complex, β subunit clathrin-associated protein complex, β subunit copper transport protein copper transport protein copper transport protein dynamin-related protein the clathrin-	YKR054c YER019c-a YLR378c YPL034c YOR254c YBR171w YLR292c YDR086c YCR075c YHL019c YKR093w YKL198c YDR040c YER060w YKL198c YDR040c YGR100c YGL216w YPR009w YHR123w YER087c-a	DYN1 SEB2 SEC61 SEC62 SEC63 SEC63 SEC66 SEC72 SSS1 ERS1 APM2 KAR2 NPL4 PTR2 PTK1 ENA1 FCY21 NPR1	dynein heavy chain, cytosolic ER protein-translocation complex subunit intracellular protein transport protein involved in clathrin-dependent transport processes nuclear fusion protein nuclear protein localization factor and ER translocation component peptide transporter polyamine transport enhancing protein P-type ATPase involved in Na* and Li* efflux purine-cytosine permease ser/thr protein kinase similarity to mitochondrial carrier protein YMC1 similarity to mouse kinesin-related protein KIF3 similarity to sterol uptake protein Sut1p similarity to mammalian Sec61β subunit
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YDR329c YJL210w YDR142c YLR191w YDR244w YDR142c YLR191w YDL128w YGL006w YDR135c YCR031c YKR014c YNL093w YMR054w YHR039c-2 YEL027w YPL234c YLR447c YOR270c YGR020c YOR332w YEL051w	PAS3 PAS5 PAS7 PAS20 PAS10  PAS10  Trans VCX1  PMC1 YCF1  VPS21 YPT31 YPT53  STV1  VMA10  CUP5  TFP3  VMA6  VPH1  VMA7  VMA4  VMA8	peroxisomal assembly protein peroxisomal assembly protein peroxisomal import protein peroxisomal import protein import protein peroxisomal protein involved in protein import putative peroxisomal targeting signal receptor  PORT  Ca²-transport (H¹/Ca²- exchange) protein, vacuolar Ca²-transporting P-type ATPase glutathione S-conjugate transporter, vacuolar GTP-binding protein of the RAB family (RAS superfamily) H¹-ATPase V0 domain 102K subunit, vacuolar H²-ATPase V0 domain 17K subunit, vacuolar H²-ATPase V0 domain 17K subunit, vacuolar H²-ATPase V0 domain 36K subunit, vacuolar H²-ATPase V0 domain 95K subunit, vacuolar H²-ATPase V1 domain 95K subunit, vacuolar H²-ATPase V1 domain 27K subunit, vacuolar H²-ATPase V1 domain 54K subunit, vacuolar H²-ATPase V1 domain 54K subunit, vacuolar	YFL039c YDR129c YDR129c YDL029w YCL040w YJR152w YJR028w YBR088c YEL063c YBR088c YGR121c YKL135c YGR261c YMR058w YGL07c YGL206c YMR058w YGL07c	ACT1 SAC6 ACT2 GLK1 DAL5 DAL4 BAP2 CAN1 VAP1  APL2 YKS5  CMD1 GCS1 FET3 HNM1 CHC1 CLC1 CLC1 APS1 APS2 YAP80  APS3  CTR1 CTR2 SLA2 DNM1 UGA4 APL4 SEC12 GAP1 FPS1	associated protein(AP) complex actin actin filament bundling protein, filmbrin actin-like protein actin-like protein actin-like protein actin-like protein aldohexose specific glucokinase allantoate permease allantoate permease amino-acid permease of high capacity and moderate affinity β-adaptin β-adaptin, large subunit of the clathrin-associated protein(AP) complex calmodulin cell proliferation zinc-finger protein cell-surface ferroxidase clothine permease clathrin heavy chain clathrin light chain clathrin-associated protein (AP) complex, small subunit AP19 clathrin-associated protein complex, β subunit clathrin-associated protein complex, β subunit clathrin-associated protein complex, small subunit copper transport protein copper transport protein copper transport protein gABA-specific high-affinity permease gadaptin, large subunit of the clathrin-associated protein(AP) complex galactose (and glucose) permease GDP/GTP exchange factor for Sar1p general amino-acid permease glycerol channel protein GTP-binding protein	YKR054c YER019c-a YLR378c YPL094c YOR254c YBR171w YLR292c YDR086c YCR075c YHL019c YJL034w YBR170c YKR093w YKL198c YDR040c YER060w YNL183c YOR100c YFR009w YHR123w YER060w-1 YER060w-1 YER087c-a	DYN1 SEB2 SEC61 SEC62 SEC63 SEC66 SEC72 SSS1 ERS1 APM2 NPL4 PTR2 PTK1 ENA1 FCY21 NPR1  EPT1  EPT1 FCY22 SEB1	dynein heavy chain, cytosolic ER protein-translocation complex subunit intracellular protein transport protein involved in clathrin-dependent transport processes nuclear fusion protein nuclear protein localization factor and ER translocation component peptide transporter polyamine transport enhancing protein P-type ATPase involved in Na* and Li* efflux purine-cytosine permease ser/thr protein kinase similarity to mitochondrial carrier protein YMC1 similarity to mouse kinesin-related protein KIF3 similarity to sterol uptake protein Sut1p sn-1,2-diacylglycerol ethanolamine- and cholinephosphotransferase strong similarity to Fcy2p strong similarity to mammalian Sec61β subunit
YDR329c YJL210w YDR142c YLR191w YDR142c YLR191w YDR244w  Vacuola YDL128w YGL006w YDR135c YOR089c YER031c YKR014c YKR014c YKL039w YMR054w YHR039c-a YEL027w YPL234c YLR447c YOR270c YGR020c YOR332w YEL051w YKL080w	PASS PASS PASS PASS PASS PASS PASS PASS	peroxisomal assembly protein peroxisomal assembly protein peroxisomal import protein peroxisomal import protein import protein peroxisomal protein involved in protein import putative peroxisomal targeting signal receptor  **Ca2*-transport (H*/Ca2* exchange) protein, vacuolar Ca2*-transporting P-type ATPase glutathione S-conjugate transporter, vacuolar GTP-binding protein of the RAB family (RAS superfamily) H*-ATPase V0 domain 102K subunit, vacuolar H*-ATPase V0 domain 17K subunit, vacuolar H*-ATPase V0 domain 17K subunit, vacuolar H*-ATPase V0 domain 36K subunit, vacuolar H*-ATPase V0 domain 36K subunit, vacuolar H*-ATPase V1 domain 36K subunit, vacuolar H*-ATPase V1 domain 27K subunit, vacuolar H*-ATPase V1 domain 32K subunit, vacuolar H*-ATPase V1 domain 32K subunit, vacuolar H*-ATPase V1 domain 32K subunit, vacuolar	YFL039c YDR129c YDR129c YDL029w YCL040w YIR152w YIR152w YIR028w YBR068c YEL063c YBR069c YGR121c YKL135c YGR261c YBR109c YGR261c YBR109c YGR261c YBR109c YGR261c YBR109c YJR058w YJL024c YPR124w YHR175w YNL021ow YDL210w YPR029c YLR031w YNR026c YRR039w YLL043w YNR026c YKR039w YLL043w YNR026c YKR039w YLL043w YNR026c YKR039w YLL043w YOR039c YLR031w YOR036c	ACT1 SAC6 ACT2 GLK1 DAL5 DAL4 BAP2 CAN1 VAP1 APL2 YKS5  CMD1 GCS1 FET3 HNM1 CHC1 CLC1 APS1 APS2 YAP80 APS3 CTR1 CTR2 DNM1 UGA4 GAL2 SEC12 GAP1 FPS1	associated protein(AP) complex actin actin-filament bundling protein, fimbrin actin-filke protein actin-filke protein aldohexose specific glucokinase allantoate permease allantoate permease amino-acid permease and selection action acti	YKR054c YER019c-a YLR378c YPL094c YPL094c YDR254c YDR086c YCR075c YHL0192 YJL034w YSR170c YKR033w YKL198c YDR040c YER060w YNL183c YOR100c YFR009w YHR123w YER060w-3	DYN1 SEB2 SEC61 SEC62 SEC63 SEC66 SEC66 SEC7 SSS1 ERS1 ERS1 ERS1 FOY21 NPR1  FOY21 NPR1  EPT1 A FCY22 SEB1  Lar or  Pnesi: ation alimembr	dynein heavy chain, cytosolic ER protein-translocation complex subunit intracellular protein ransport protein involved in clathrin-dependent transport processes nuclear fusion protein nuclear protein localization factor and ER translocation component peptide transporter polyamine transport enhancing protein P-type ATPase involved in Na* and Li* efflux purine-cytosine permease ser/thr protein kinase similarity to mitochondrial carrier protein YMC1 similarity to mouse kinesin-related protein KIF3 similarity to sterol uptake protein Sut1p sn-12-diacylglycerol ethanolamine- and cholinephosphotransferase strong similarity to mammalian Sec61β subunit  rganization and S  and biogenesis of cell wall and ane
YDR329c YJL210w YDR142c YLR191w YDR142c YLR191w YDR244w  Vacuola YDL128w YGL006w YDR135c YOR089c YER031c YKR014c YNL093w YMR054w YHR039c-a YEL027w YPL234c YLR447c YOR270c YGR020c YOR332w YEL051w YKL080w YPR036w YPR036w YBR127c	PAS3 PAS5 PAS7 PAS7 PAS70 PAS10  PAS10  VCX1 PMC1 YCF1  VPS21 YPT31 YPT52 YPT53 STV1  VMA10 CUP5 TFP3 VMA6 VPH1 VMA7 VMA4 VMA8 VMA5 VMA5 VMA13 VMA2	peroxisomal assembly protein peroxisomal assembly protein peroxisomal import protein peroxisomal import protein import protein peroxisomal protein involved in protein import putative peroxisomal targeting signal receptor  PORT  Ca²-transport (H¹/Ca²- exchange) protein, vacuolar Ca²-transporting P-type ATPase glutathione S-conjugate transporter, vacuolar GTP-binding protein GTP-binding protein of the RAB family (RAS superfamily) H²-ATPase V0 domain 102K subunit, vacuolar H²-ATPase V0 domain 17K subunit, vacuolar H²-ATPase V0 domain 17K subunit, vacuolar H²-ATPase V0 domain 36K subunit, vacuolar H²-ATPase V0 domain 95K subunit, vacuolar H²-ATPase V1 domain 95K subunit, vacuolar H²-ATPase V1 domain 27K subunit, vacuolar H²-ATPase V1 domain 54K subunit, vacuolar	YFL039c YDR129c YDR129c YDL029w YCL040w YJR152w YJR028w YBR068c YEL063c YBR068c YEL063c YBR069c YGR121c YKL135c YGR261c YKL135c YGR261c YKL135c YGR261c YKL135c YGR261c YKL135c YGR261c YKL135c YJR005w YJL024c YPR124w YHR175w YJL0210w YPR029c YR029c YLR031c YKR039w YLL043w YLL043w YLL043w YLL043w YLL043w YLL043w YLL043w YC07689c YER031c YKR013c	ACT1 SAC6 ACT2 GLK1 DAL5 DAL4 BAP2 CAN1 VAP1  APL2 YKS5  CMD1 GCS1 FET3 HNM1 CHC1 CLC1 APS1 APS2 YAP80  APS3  CTR1 CTR2 SLA2 SLA2 GAP1 FPS1 VPT52 YPT51	associated protein(AP) complex actin actin filament bundling protein, filmbrin actin-like protein actin-like protein actin-like protein aldohexose specific glucokinase allantoate permease allantoate permease allantoate permease amino-acid permease of high capacity and moderate affinity β-adaptin β-adaptin, large subunit of the clathrin-associated protein(AP) complex calmodulin cell proliferation zinc-finger protein cell-surface ferroxidase choline permease clathrin light chain clathrin-associated protein (AP) complex, small subunit AP19 clathrin-associated protein complex, β subunit clathrin-associated protein complex, β subunit clathrin-associated protein complex, small subunit copper transport protein copper transport protein copper transport protein GABA-specific high-affinity permease γ-adaptin, large subunit of the clathrin-associated protein(AP) complex galactose (and glucose) permease GDP/GTP exchange factor for Sar1p general amino-acid permease glycerol channel protein GTP-binding protein of the RAB family	YKR054c YER019c-a YLR378c YPL034c YOR254c YBR171w YLR292c YDR086c YCR076c YKR093w YKL198c YDR040c YER060w YKL198c YPR009w YHR123w YER060w-a YER087c-a	DYN1 SEB2 SEC61 SEC62 SEC63 SEC66 SEC72 SSS1 ERS1 APM2 KAR2 NPL4 PTR2 PTK1 ENA1 FCY21 NPR1  EPT1  A FCY22 SEB1  EPT1  EPT1  EPT1  EPT1  FCY22 SEB1  FCY22 SEB1  FCY22 SEB1	dynein heavy chain, cytosolic ER protein-translocation complex subunit intracellular protein transport protein involved in clathrin-dependent transport processes nuclear fusion protein nuclear protein localization factor and ER translocation component peptide transporter polyamine transport enhancing protein P-type ATPase involved in Na' and Li' efflux purine-cytosine permease ser/thr protein kinase similarity to mitochondrial carrier protein YMC1 similarity to mouse kinesin-related protein KIF3 similarity to sterol uptake protein Sut1p sn-1,2-diacylglycerol ethanolamine- and cholinephosphotransferase strong similarity to mammalian Sec61β subunit  Tganization and  I,3-D-glucan synthase, catalytic subunit 1,3-D-glucan synthase, subunit
YDR329c YJL210w YDR142c YLR191w YDR142c YLR191w YDR244w  Vacuola YDL128w YGL006w YDR135c YOR089c YER031c YKR014c YNL093w YMR054w YHR039c-a YEL027w YPL234c YLR447c YOR270c YGR020c YOR322w YEL051w YKL080w YPR036w YBR127c YDL185w	PAS3 PAS5 PAS7 PAS7 PAS20  PAS10  IT Trans VCX1  PMC1 YCF1  VPS21 YPT31 YPT53  STV1  VMA10  CUP5  TFP3  VMA6  VPH1  VMA7  VMA4  VMA8  VMA6  VMA13  VMA2  TFP1	peroxisomal assembly protein peroxisomal assembly protein peroxisomal import protein peroxisomal import protein import protein peroxisomal protein involved in protein import putative peroxisomal targeting signal receptor  **Port**  Ca²-transport (H*/Ca²- exchange) protein, vacuolar Ca²-transporting P-type ATPase glutathione S-conjugate transporter, vacuolar GTP-binding protein of the RAB family GTP-binding protein of the RAB family GTP-binding protein of the RAB family (RAS superfamily) H*-ATPase V0 domain 102K subunit, vacuolar H*-ATPase V0 domain 17K subunit, vacuolar H*-ATPase V0 domain 17K subunit, vacuolar H*-ATPase V0 domain 36K subunit, vacuolar H*-ATPase V0 domain 36K subunit, vacuolar H*-ATPase V1 domain 36K subunit, vacuolar H*-ATPase V1 domain 27K subunit, vacuolar H*-ATPase V1 domain 32K subunit, vacuolar H*-ATPase V1 domain 34K subunit, vacuolar H*-ATPase V1 domain 54K subunit, vacuolar H*-ATPase V1 domain 64K subunit, vacuolar	YFL039c YDR129c YDR129c YDL029w YCL040w YJR152w YJR152w YJR058c YEL063c YBR068c YEL063c YBR068c YGR121c YKL135c YGR121c YKL135c YGR261c YMR058w YJL0226c YMR058w YJL024c YJR005w YJL024c YPR124w YHR175w YHL240w YHR029c YKR039w YLL043w YOR089c YER031c YKR014c YML001w YNL093w	ACT1 SAC6 ACT2 SAC6 ACT2 GLK1 DAL5 DAL4 BAP2 CAN1 VAP1  APL2 YKS5  CMD1 GCS1 FET3 HNM1 CHC1 CLC1 APS1  APS2 YAP80  APS3  CTR1 CTR2 SLA2 DNM1 UGA4 APL4 GAL2 SEC12 GAP1 FPS1 VPS21 YPT51 YPT53	associated protein(AP) complex actin actin filament bundling protein, fimbrin actin-like protein actin-like protein actin-like protein aldohexose specific glucokinase allantoate permease allantoate permease amino-acid permease allantoin permease of high capacity and moderate affinity β-adaptin, large subunit of the clathrin-associated protein(AP) complex calmodulin cell proliferation zinc-finger protein cell-surface ferroxidase choline permease clathrin heavy chain clathrin light chain clathrin-associated protein (AP) complex, small subunit AP19 clathrin-associated protein complex, β subunit clathrin-associated protein complex, small subunit copper transport protein copper transport protein copper transport protein dynamin-related protein dABA-specific high-affinity permease γadaptin, large subunit of the clathrin-associated protein(AP) complex galactose (and glucose) permease GDP/GTP exchange factor for Sar1p general amino-acid permease glycerol channel protein of the RAB family GTP-binding pr	YKR054c YER019c-a YLR378c YPL034c YOR254c YBR171w YLR292c YDR086c YCR075c YKR093w YKL198c YDR040c YER060w-3 YER060w-3 YER060w-3 YER060w-3 YER060w-3 YER087c-a  Cellu bioge organiz plasma  YLR342w YOR32c YUR032c YUR032c YUR032c YUR032c YER080c-a	DYN1 SEB2 SEC61 SEC62 SEC63 SEC63 SEC662 SEC72 SSS1 ERS1 APM2 KAR2 NPL4 PTR2 PTK1 ENA1 FCY21 NPR1  A FCY22 SEB1  EPT1 A FCY22 SEB1  EPT1 A FCY22 SEB1  FCS1 GSC2 PRE10 SAG1	dynein heavy chain, cytosolic ER protein-translocation complex subunit intracellular protein transport protein involved in clathrin-dependent transport processes nuclear fusion protein nuclear protein localization factor and ER translocation component peptide transporter polyamine transport enhancing protein P-type ATPase involved in Na* and Li* efflux purine-cytosine permease ser/thr protein kinase similarity to mitochondrial carrier protein YMC1 similarity to mouse kinesin-related protein KIF3 similarity to mouse kinesin-related protein KIF3 similarity to sterol uptake protein Sut1p sn-1,2-diacylglycerol ethanolamine- and cholinephosphotransferase strong similarity to Tecy2p strong similarity to mammalian Sec61β subunit  Tganization and  s  nd biogenesis of cell wall and ane  1,3—D-glucan synthase, catalytic subunit 1,3—D-glucan synthase, subunit 26S proteasome subunit C1 α-agglutinin
YDR329c YJL210w YDR142c YLR191w YDR142c YLR191w YDR244w  Vacuola YDL128w YGL006w YDR135c YOR089c YER031c YKR014c YNL093w YMR054w YHR039c-a YEL027w YPL234c YLR447c YOR270c YGR020c YOR332w YEL051w YKL080w YPR036w YPR036w YBR127c	PAS3 PAS5 PAS7 PAS7 PAS70 PAS10  PAS10  VCX1 PMC1 YCF1  VPS21 YPT31 YPT52 YPT63  STV1  VMA10  CUP5  TFP3  VMA6 VPH1  VMA7  VMA4  VMA8  VMA6  VMA13  VMA2  TFP1  VPS28	peroxisomal assembly protein peroxisomal assembly protein peroxisomal import protein peroxisomal import protein import protein peroxisomal protein involved in protein import putative peroxisomal targeting signal receptor  **Ca²*-transport (H*/Ca²* exchange) protein, vacuolar Ca²*-transporting P-type ATPase glutathione S-conjugate transporter, vacuolar GTP-binding protein of the RAB family (RAS superfamily) H*-ATPase V0 domain 102K subunit, vacuolar H*-ATPase V0 domain 17K subunit, vacuolar H*-ATPase V0 domain 17K subunit, vacuolar H*-ATPase V0 domain 36K subunit, vacuolar H*-ATPase V0 domain 36K subunit, vacuolar H*-ATPase V1 domain 36K subunit, vacuolar H*-ATPase V1 domain 27K subunit, vacuolar H*-ATPase V1 domain 27K subunit, vacuolar H*-ATPase V1 domain 27K subunit, vacuolar H*-ATPase V1 domain 32K subunit, vacuolar H*-ATPase V1 domain 42K subunit, vacuolar H*-ATPase V1 domain 42K subunit, vacuolar H*-ATPase V1 domain 54K subunit, vacuolar H*-ATPase V1 domain 60K subunit, vacuolar H*-ATPase	YFL039c YDR129c YDR129c YDL029w YCL040w YJR152w YJR028w YBR068c YEL063c YBR068c YEL063c YBR069c YGR121c YKL135c YGR261c YKL135c YGR261c YKL135c YGR261c YKL135c YGR261c YKL135c YGR261c YKL135c YJR005w YJL024c YPR124w YHR175w YJL0210w YPR029c YR029c YLR031c YKR039w YLL043w YLL043w YLL043w YLL043w YLL043w YLL043w YLL043w YC07689c YER031c YKR013c	ACT1 SAC6 ACT2 GLK1 DAL5 DAL4 BAP2 CAN1 VAP1  APL2 YKS5  CMD1 GCS1 FET3 HNM1 CHC1 CLC1 APS1 APS2 YAP80  APS3  CTR1 CTR2 SLA2 SLA2 GAP1 FPS1 VPT52 YPT51	associated protein(AP) complex actin actin-filament bundling protein, fimbrin actin-filke protein actin-filke protein actin-filke protein aldohexose specific glucokinase allantoate permease allantoin permease amino-acid permease and moderate affinity β-adaptin β-adaptin β-adaptin large subunit of the clathrin-associated protein(AP) complex calmodulin cell proliferation zinc-finger protein cell-surface ferroxidase choline permease clathrin heavy chain clathrin-fight chain clathrin-associated protein (AP) complex, small subunit AP19 clathrin-associated protein (AP) complex, subunit clathrin-associated protein complex, β subunit copper transport protein complex transport protein copper tra	YKR054c YER019c-a YLR378c YPL094c YPL094c YPL094c YDR254c YDR056c YCR075c YHL019c YKR093w YKL198c YDR040c YFR060w YRL183c YOR100c YFR060w-1 YFR060	DYN1 SEB2 SEC61 SEC62 SEC63 SEC63 SEC662 SEC72 SSS1 ERS1 APM2 KAR2 NPL4 PTR2 PTK1 ENA1 FCY21 NPR1  A FCY22 SEB1  EPT1 A FCY22 SEB1  EPT1 A FCY22 SEB1  FCS1 GSC2 PRE10 SAG1	dynein heavy chain, cytosolic ER protein-translocation complex subunit intracellular protein transport protein involved in clathrin-dependent transport processes nuclear fusion protein nuclear protein localization factor and ER translocation component peptide transporter polyamine transport enhancing protein P-type ATPase involved in Na' and Li' efflux purine-cytosine permease ser/thr protein kinase similarity to mitochondrial carrier protein YMC1 similarity to mouse kinesin-related protein KIF3 similarity to sterol uptake protein Sut1p sn-12-diacylglycerol ethanolamine- and cholinephosphotransferase strong similarity to Fcy2p strong similarity to mammalian Sec61β subunit  Tganization and  S  and biogenesis of cell wall and tane  1.3—D-glucan synthase, catalytic subunit 1.3—D-glucan synthase, subunit 26S proteasome subunit C1

plasma	membr	ane
YLR342w YGR032w YOR362c YJR004c	FKS1 GSC2 PRE10 SAG1	1,3—D-glucan synthase, catalytic subunit 1,3—D-glucan synthase, subunit 26S proteasome subunit C1 α-agglutinin
YNR044w	AGA1	α-agglutinin anchor subunit
YGL032c	AGA2	α-agglutinin binding subunit
YDR077w	SED1	abundant cell-surface glycoprotein
YJL005w	CYR1	adenylate cyclase
YCL007c	CWH36	affects the mannoprotein layer of the cell wall
YOR335c	ALA1	alanyl-tRNA synthetase, cytosolic
YPL061w	ALD6	aldehyde dehydrogenase, cytosolic
YJR152w	DAL5	allantoate permease
YIR028w	DAL4	allantoin permease
YBR068c	BAP2	amino-acid permease
YEL063c	CAN1	amino-acid permease
YRR069c	VAP1	amino-acid nermease

YJL222w

YOR036w

YNR006w

YGL095c

YDR323c YPL045w YPR173c

YAL002w

YML097c

YMR004w *MVP1* YBR097w *VPS15* 

VPS27

VPS45

PFP7

VPS16 VPS4

VPS8

VPS9

required for vacuolar protein sorting ser/thr protein kinase

vacuolar protein sorting-associated

vacuolar protein sorting-associated protein

vacuolar segregation protein vacuolar sorting protein

vacuolar sorting protein vacuolar sorting protein

vacuolar sorting protein

strong similarity to Pep1p syntaxin (T-SNARE)

protein

YJL214w YJL219w

YFL011w YDL194w YEL069c

YMR011w

YDR343c YDR342c

YML123c

YNL142w MEP2

YGR055w MUP1

HXT8 HXT9

HXT10 SNF3 HXT13

HXT2

HXT6 HXT7

PHO84

hexose transport protein hexose transport protein

permease

hexose transporter high-affinity glucose transporter high-affinity hexose transporter high-affinity hexose transporter

high-affinity hexose transporter high-affinity hexose transporter

high-affinity inorganic phosphate/H<sup>+</sup> symporter

high-affinity low capacity ammonia

high-affinity methionine permease

I YML116w	ATD1	aminatriazala and 4 nitraguinalina	I VLIDOOO	LIVTA	madarata ta law affinity alugana	L VMD100	CINIA	CTR binding protoin
YIVILII6W	AIRI	aminotriazole and 4-nitroquinoline resistance protein	YHR092c	HX14	moderate- to low-affinity glucose transporter	YMR138w YOR156c	NFI1	GTP-binding protein interacts with Cdc12p in 2-hybrid assay
YGR121c	MEP1	ammonia permease of high capacity and	YGR014w	MSB2	multicopy suppressor of a cdc24 bud	YML104c		intermediate filament protein
1 0111210		moderate affinity		WODE	emergence defect	YLL021w	SPA2	involved in cell polarity
YDR144c	MKC7	aspartyl protease of the periplasmic	YDR011w	SNQ2	multidrug resistance protein	YPL241c	CIN2	involved in chromosome segregation
		space	YOL103w	ITR2	myo-inositol transport protein	YDR085c	AFR1	involved in morphogenesis of the mating
YLR120c	YAP3	aspergillopepsin	YJL093c	TOK1	outward-rectifier potassium channel			projection
YKL209c	STE6	ATP-binding cassette transporter protein	YKR093w		peptide transporter	YEL061c	CIN8	kinesin-related protein
YGR281w	YOR1	ATP-binding cassette transporter protein	YFL026w YKL178c	STE2 STE3	pheromone α-factor receptor	YPR141c YBL063w	KAR3 KIP1	kinesin-related protein
YCR011c	ADP1	required for oligomycin resistance ATP-dependent permease	YMR008c		pheromone a-factor receptor phospholipase B (lysophospholipase)	YPL155c	KIP1 KIP2	kinesin-related protein kinesin-related protein
YER123w		casein kinase, isoform 3	YOR153w		pleiotropic drug resistance protein	YKL079w	SMY1	kinesin-related protein
YCL027w		cell fusion protein	YCR034w	GNS1	probable 1,3—glucan synthase subunit	YBR172c	SMY2	kinesin-related protein
YMR058w		cell-surface ferroxidase	YOR348c	PUT4	proline and γ-aminobutyrate permease	YOR058c	ASE1	microtubule-associated protein
YKL096w		cell-wall mannoprotein	YPL140c	MKK2	protein kinase of the MAP kinase kinase	YJL042w	MHP1	microtubule-associated protein
YKL096w-		cell-wall mannoprotein			(MEK) family	YMR294w	JNM1	mitosis protein, involved in nuclear
YNL322c		cell-wall protein	YGR009c	SEC9 FCY2	protein transport protein	YBL034c	STU1	migration
YAR050w YNL192w		cell-wall protein involved in flocculation chitin synthase I	YER056c YIL140w	SRO4	purine-cytosine permease required for axial pattern of budding		MY02	mitotic spindle protein myosin heavy chain
YBR038w		chitin synthase II	YCR089w		required for efficient mating	YAL029c	MYO4	myosin heavy chain, unconventional
YBR023c	CHS3	chitin synthase III	YDR122w		ser/thr protein kinase	17 120200		(class V) isoform
YGL077c	HNM1	choline permease	YLR096w	KIN2	ser/thr protein kinase	YMR109w	MYO5	myosin Í
YOR010c	TIR2	cold-shock induced protein	YPL176c		similarity to chinese hamster transferrin	YKL129c	MYO3	myosin type I
YER011w	TIR1	cold-shock induced protein of the Tir1p,	VICEAGO		receptor protein	YHR023w	MYO1	myosin-1 isoform (type II myosin) heavy
YPR124w	CTR1	Tip1p family	YKR102w YHL028w		similarity to Flo1p similarity to mucin and other ser-thr rich	YCL029c	BIK1	chain nuclear fusion protein
YGR282c	BGL2	copper transport protein endo-1,3glucanase of the cell wall	TTTLUZOV		proteins	YOR122c	PFY1	profilin
YOR190w		exo-1,3glucanase	YJR151c		similarity to mucin proteins	YDR164c	SEC1	protein transport protein
YDR261c	EXG2	exo-1,3glucanase minor isoform	YMR317w		similarity to mucins, glucan 1,4	YDR388w	RVS167	reduced viability upon starvation protein
YLR214w	FRE1	ferric (and cupric) reductase			glucosidase and exo-sialidase	YNL084c	END3	required for endocytosis and cytoskeletal
YKL220c	FRE2	ferric (and cupric) reductase	YCR098c	GIT1	similarity to phosphate transporter			organization
YDL210w	UGA4	GABA-specific high-affinity permease	VII 010-	DDD11	proteins	YBR130c	SHE3	required for mother cell-specific
YLR081w YLL016w	GAL2 SDC25	galactose (and glucose) permease GDP/GTP exchange factor	YIL013c	PDR11	similarity to Snq2p and other ATP- dependent permeases	YGR078c	PAC10	expression of HO required in the absence of Cin8p
YLR310c	CDC25	GDP/GTP exchange factor for Ras1p and	YIL063c	YRB2	similarity to Yrp1p and Nup2p	YDR488c	PAC11	required in the absence of Cin8p
		Ras2p	YNL126w	SPC98	spindle pole body component	YER007w	PAC2	required in the absence of Cin8p
YCR038c	BUD5	GDP/GTP exchange factor for	YHR139c	SPS100	sporulation-specific wall maturation	YJR076c	CDC11	septin
1	045:	Rsr1p/Bud1p	VORCCO	000:0	protein	YHR107c	CDC12	septin
YKR039w YMR307w		general amino-acid permease glycophospholipid-anchored surface	YOR328w	PDR10	strong similarity to ABC transporter	YDR218c YNL059c	SPR28	septin-related sporulation protein similarity to actin
YIVIR3U/W	GASI	glycoprotein	YDR046c	(PAP1)	proteins strong similarity to amino-acid transport	YLR085c		similarity to actin and actin-related
YOL081w	IRA2	GTPase-activating protein for RAS	12110400	(1 171 1)	proteins	1 =110000		proteins
10200111		proteins	YDR134c		strong similarity to Flo1p	YLR429w		similarity to actin binding protein coronin
YOR101w	RAS1	GTP-binding protein	YAL063c	FLO9	strong similarity to Flo1p	YPR034w		similarity to actins
YNL098c	RAS2	GTP-binding protein	YLR343w		strong similarity to Gas1p and C. albicans	YGL003c		similarity to C. elegans CDC20 protein
YHR005c	GPA1	GTP-binding protein α subunit of the	VOI 000		pH responsive protein	VODOOO.	DI /0404	and human p55CDC
YOR212w	STE4	pheromone pathway	YOL030w YHR096c	HXT5	strong similarity to glycoprotein GAS1	YCR009c	RVS161	similarity to human amphiphysin and
TUNZIZW	31E4	GTP-binding protein β subunit of the pheromone pathway	YDR536w	STL1	strong similarity to hexose transporters strong similarity to members of the sugar	YER018c		Rvs167p similarity to lamins
YJR086w	STE18	GTP-binding protein γ subunit of the	I DITOGOV	OILI	permease family	YOR367w		similarity to mammalian smooth muscle
		pheromone pathway	YIL170w	HXT12	strong similarity to sugar transport			protein SM22
YLR229c		GTP-binding protein of RAS superfamily	VIDATO	LINGTAG	proteins	YIL149c		similarity to Mlp1p and myosin heavy
YCR024c-a YEL017c-a		H <sup>+</sup> -ATPase subunit, plasma membrane H <sup>+</sup> -ATPase subunit, plasma membrane	YJR158w	HXT16	strong similarity to sugar transport proteins	YGL216w		chains similarity to mouse kinesin-related protein
			l			IGLLIOW		
I YGLUU8C	PMA1	H'-transporting P-type Al Pase	I YNR072w	HXT17	sugar transport protein			KIF3
YGL008c YPL036w	PMA2	H*-transporting P-type ATPase H*-transporting P-type ATPase 2	YNR072w YPL232w	HXT17 SSO1	sugar transport protein syntaxin-related protein	YKL179c		KIF3 similarity to Nuf1p
	PMA2	H <sup>+</sup> -transporting P-type ATPase 2  Hansenula Mrakll k9 killer toxin-resistance			syntaxin-related protein temp.shock induced protein of the	YJR134c		similarity to Nuf1p similarity to paramyosin, myosin
YPL036w YDR420w	PMA2 HKR1	H*-transporting P-type ATPase 2  Hansenula Mrakll k9 killer toxin-resistance protein	YPL232w YBR067c	SSO1 TIP1	syntaxin-related protein temp.shock induced protein of the Srp1p/Tip1p family	YJR134c YPL105c	NII IE1	similarity to Nuf1p similarity to paramyosin, myosin similarity to Smy2p
YPL036w	PMA2	H*-transporting P-type ATPase 2 Hansenula MrakII k9 killer toxin-resistance protein heat-shock protein of HSP70 family,	YPL232w YBR067c YJR007w	SSO1 TIP1 SUI2	syntaxin-related protein temp.shock induced protein of the Srp1p/Tip1p family translation initiation factor eIF2, $\alpha$ subunit	YJR134c YPL105c YDR356w		similarity to Nuf1p similarity to paramyosin, myosin similarity to Smy2p spindle pole body component
YPL036w YDR420w YLL024c YNL318c	PMA2 HKR1 SSA2 HXT14	H'-transporting P-type ATPase 2 Hansenula Mrakll k9 killer toxin-resistance protein heat-shock protein of HSP70 family, cytosolic hexose transport protein	YPL232w YBR067c YJR007w YIL147c YER125w	SSO1 TIP1 SUI2 SLN1 RSP5	syntaxin-related protein temp.shock induced protein of the Srp1p/Tip1p family translation initiation factor eIF2, $\alpha$ subunit two-component signal transducer ubiquitin-protein ligase	YJR134c YPL105c YDR356w YNL126w YOL069w	SPC98 NUF2	similarity to Nuf1p similarity to paranyosin, myosin similarity to Smy2p spindle pole body component spindle pole body component spindle pole body protein
YPL036w YDR420w YLL024c YNL318c YJL214w	PMA2 HKR1 SSA2 HXT14 HXT8	H*-transporting P-type ATPase 2 Hansenula Mrakll k9 killer toxin-resistance protein heat-shock protein of HSP70 family, cytosolic hexose transport protein hexose transport protein	YPL232w YBR067c YJR007w YIL147c YER125w YBR021w	SSO1 TIP1 SUI2 SLN1 RSP5 FUR4	syntaxin-related protein temp.shock induced protein of the Srp1p/Tip1p family translation initiation factor eIF2, α subunit two-component signal transducer ubiquitin-protein ligase uracil permease	YJR134c YPL105c YDR356w YNL126w YOL069w YGR059w	SPC98	similarity to Nuf1p similarity to paramyosin, myosin similarity to Smy2p spindle pole body component spindle pole body component spindle pole body protein sporulation-specific septin
YPL036w YDR420w YLL024c YNL318c YJL214w YJL219w	PMA2 HKR1 SSA2 HXT14 HXT8 HXT9	H*-transporting P-type ATPase 2 Hansenula Mrakll k9 killer toxin-resistance protein heat-shock protein of HSP70 family, cytosolic hexose transport protein hexose transport protein hexose transport protein	YPL232W YBR067c YJR007W YIL147c YER125W YBR021W YHL016c	SSO1 TIP1 SUI2 SLN1 RSP5 FUR4 DUR3	syntaxin-related protein temp.shock induced protein of the Srp1p/Πip1p family translation initiation factor eIF2, α subunit two-component signal transducer ubiquitin-protein ligase uracil permease urea transport protein	YJR134c YPL105c YDR356w YNL126w YOL069w YGR059w YEL071w	SPC98 NUF2 SPR3	similarity to Nuf1p similarity to paramyosin, myosin similarity to Smy2p spindle pole body component spindle pole body component spindle pole body protein sporulation-specific septin strong similarity to Aip2p
YPL036w YDR420w YLL024c YNL318c YJL214w YJL219w YFL011w	PMA2 HKR1 SSA2 HXT14 HXT8 HXT9 HXT10	H'-transporting P-type ATPase 2 Hansenula Mrakll k9 killer toxin-resistance protein heat-shock protein of HSP70 family, cytosolic hexose transport protein hexose transport protein hexose transport protein hexose transport	YPL232W YBR067c YJR007W YIL147c YER125W YBR021W YHL016c YGL233W	SSO1 TIP1 SUI2 SLN1 RSP5 FUR4 DUR3 SEC15	syntaxin-related protein temp.shock induced protein of the Srp1ρ/Tip1p family translation initiation factor eIF2, α subunit two-component signal transducer ubiquitin-protein ligase uracil permease urea transport protein vesicular traffic control protein	YJR134c YPL105c YDR356w YNL126w YOL069w YGR059w YEL071w YOR134w	SPC98 NUF2 SPR3 BAG7	similarity to Nuf1p similarity to paranyosin, myosin similarity to Smy2p spindle pole body component spindle pole body component spindle pole body protein sporulation-specific septin strong similarity to Aip2p structural homologue of Sac7p
YPL036w YDR420w YLL024c YNL318c YJL214w YJL219w YFL011w YDL194w	PMA2 HKR1 SSA2 HXT14 HXT8 HXT9 HXT10 SNF3	H'-transporting P-type ATPase 2 Hansenula Mrakll k9 killer toxin-resistance protein heat-shock protein of HSP70 family, cytosolic hexose transport protein hexose transport protein hexose transport protein hexose transporter	YPL232W YBR067c YJR007W YIL147c YER125W YBR021W YHL016c YGL233W YJR040W	SSO1 TIP1 SUI2 SLN1 RSP5 FUR4 DUR3 SEC15 GEF1	syntaxin-related protein temp.shock induced protein of the Srp1p/Tip1p family translation initiation factor eIF2, α subunit two-component signal transducer ubiquitin-protein ligase uracil permease urea transport protein vesicular traffic control protein voltage-gated chloride channel protein	YJR134c YPL105c YDR356w YNL126w YOL069w YGR059w YEL071w YOR134w YAL047c	SPC98 NUF2 SPR3 BAG7 SPI6	similarity to Nuf1p similarity to paranyosin, myosin similarity to Smy2p spindle pole body component spindle pole body component spindle pole body protein sporulation-specific septin strong similarity to Aip2p structural homologue of Sac7p Stu2p Interactant
YPL036w YDR420w YLL024c YNL318c YJL214w YJL219w YFL011w	PMA2 HKR1 SSA2 HXT14 HXT8 HXT9 HXT10 SNF3 HXT13	H'-transporting P-type ATPase 2 Hansenula Mrakll k9 killer toxin-resistance protein heat-shock protein of HSP70 family, cytosolic hexose transport protein hexose transport protein hexose transport protein hexose transport	YPL232W YBR067c YJR007W YIL147c YER125W YBR021W YHL016c YGL233W YJR040W YMR243c	SSO1 TIP1 SUI2 SLN1 RSP5 FUR4 DUR3 SEC15 GEF1 ZRC1	syntaxin-related protein temp.shock induced protein of the Srp1p/Tip1p family translation initiation factor eIF2, α subunit two-component signal transducer ubiquitin-protein ligase uracil permease urea transport protein vesicular traffic control protein voltage-gated chloride channel protein zinc- and cadmium resistance protein	YJR134c YPL105c YDR356w YNL126w YOL069w YGR059w YEL071w YOR134w	SPC98 NUF2 SPR3 BAG7	similarity to Nuf1p similarity to paranyosin, myosin similarity to Smy2p spindle pole body component spindle pole body component spindle pole body protein sporulation-specific septin strong similarity to Aip2p structural homologue of Sac7p Stu2p Interactant subunit of anaphase-promoting complex (cyclosome)
YPL036W YDR420W YLL024c YNL318c YJL214W YJL219W YFL011W YDL194W YEL069c	PMA2 HKR1 SSA2 HXT14 HXT8 HXT9 HXT10 SNF3 HXT13 HXT2	H'-transporting P-type ATPase 2 Hansenula Mrakll k9 killer toxin-resistance protein heat-shock protein of HSP70 family, cytosolic hexose transport protein hexose transport protein hexose transporter high-affinity glucose transporter high-affinity hexose transporter	YPL232W YBR067c YJR007W YIL147c YER125W YBR021W YHL016c YGL233W YJR040W YMR243c	SSO1 TIP1 SUI2 SLN1 RSP5 FUR4 DUR3 SEC15 GEF1 ZRC1	syntaxin-related protein temp.shock induced protein of the Srp1p/Tip1p family translation initiation factor eIF2, α subunit two-component signal transducer ubiquitin-protein ligase uracil permease urea transport protein vesicular traffic control protein voltage-gated chloride channel protein	YJR134c YPL105c YDR356w YNL126w YOL069w YGR059w YEL071w YOR134w YAL047c	SPC98 NUF2 SPR3 BAG7 SPI6	similarity to Nuf1p similarity to paramyosin, myosin similarity to Smy2p spindle pole body component spindle pole body component spindle pole body protein sporulation-specific septin strong similarity to Aip2p structural homologue of Sac7p Stu2p Interactant subunit of anaphase-promoting complex
YPL036w YDR420w YLL024c YNL318c YJL214w YJL219w YFL011w YDL194w YEL069c YMR011w YDR343c YDR342c	PMA2 HKR1 SSA2 HXT14 HXT8 HXT9 HXT10 SNF3 HXT13 HXT13 HXT2 HXT6 HXT7	H'-transporting P-type ATPase 2 Hansenula Mrakll k9 killer toxin-resistance protein heat-shock protein of HSP70 family, cytosolic hexose transport protein hexose transport protein hexose transport protein hexose transporter high-affinity plucose transporter high-affinity hexose transporter	YPL232W YBR067c YJR007W YIL147c YER125W YBR021W YHL016c YGL233W YJR040W YMR243c <i>organiz</i>	SSO1 TIP1 SUI2 SLN1 RSP5 FUR4 DUR3 SEC15 GEF1 ZRC1	syntaxin-related protein temp.shock induced protein of the Srp1ρ/Tip1p family translation initiation factor eIF2, α subunit two-component signal transducer ubiquitin-protein ligase uracil permease urea transport protein vesicular traffic control protein voltage-gated chloride channel protein zinc- and cadmium resistance protein ad biogenesis of cytoskeleton	YJR134c YPL105c YDR356w YNL126w YOL069w YGR059w YEL071w YOR134w YAL047c YKL022c	SPC98 NUF2 SPR3 BAG7 SPI6 CDC16	similarity to Nuf1p similarity to paramyosin, myosin similarity to Smy2p spindle pole body component spindle pole body component spindle pole body protein sporulation-specific septin strong similarity to Aip2p structural homologue of Sac7p Stu2p Interactant subunit of anaphase-promoting complex (cyclosome) subunit of anaphase-promoting complex (cyclosome)
YPL036w YDR420w YLL024c YNL318c YJL214w YJL219w YFL011w YDL194w YEL069c YMR011w YDR343c	PMA2 HKR1 SSA2 HXT14 HXT8 HXT9 HXT10 SNF3 HXT13 HXT2 HXT6	H'-transporting P-type ATPase 2 Hansenula Mrakll k9 killer toxin-resistance protein heat-shock protein of HSP70 family, cytosolic hexose transport protein hexose transport protein hexose transport protein hexose transporter high-affinity glucose transporter high-affinity hexose transporter high-affinity inorganic phosphate/H'	YPL232w YBR067c YJR007w YIL147c YER125w YHL016c YGL233w YJR040w YMR243c <b>organiz</b> YML085c	SSO1 TIP1 SUI2 SLN1 RSP5 FUR4 DUR3 SEC15 GEF1 ZRC1	syntaxin-related protein temp.shock induced protein of the Srp1p/Tip1p family translation initiation factor eIF2, α subunit two-component signal transducer ubiquitin-protein ligase uracil permease urea transport protein vesicular traffic control protein voltage-gated chloride channel protein zinc- and cadmium resistance protein ad biogenesis of cytoskeleton α-1 tubulin	YJR134c YPL105c YDR356w YNL126w YOL069w YGR059w YEL071w YOR134w YAL047c YKL022c	SPC98 NUF2 SPR3 BAG7 SPI6 CDC16	similarity to Nuf1p similarity to Paranyosin, myosin similarity to Smy2p spindle pole body component spindle pole body component spindle pole body protein sporulation-specific septin strong similarity to Aip2p structural homologue of Sac7p Stu2p Interactant subunit of anaphase-promoting complex (cyclosome) subunit of anaphase-promoting complex (cyclosome) subunit of anaphase-promoting complex (cyclosome)
YPL036w YDR420w YLL024c YNL318c YJL214w YJL219w YFL011w YDL194w YEL069c YMR011w YDR343c YDR342c YML123c	PMA2 HKR1 SSA2 HXT14 HXT8 HXT9 HXT10 SNF3 HXT13 HXT13 HXT2 HXT6 HXT7	H'-transporting P-type ATPase 2 Hansenula Mrakll k9 killer toxin-resistance protein heat-shock protein of HSP70 family, cytosolic hexose transport protein hexose transport protein hexose transporter high-affinity glucose transporter high-affinity hexose transporter high-affinity inorganic phosphate/H' symporter	YPL232W YBR067c YJR007W YIL147c YER125W YBR021W YHL016c YGL233W YJR040W YMR243c <i>organiz</i>	SSO1 TIP1 SUI2 SLN1 RSP5 FUR4 DUR3 SEC15 GEF1 ZRC1	syntaxin-related protein temp.shock induced protein of the Srp1ρ/Tip1p family translation initiation factor eIF2, α subunit two-component signal transducer ubiquitin-protein ligase uracil permease urea transport protein vesicular traffic control protein voltage-gated chloride channel protein zinc- and cadmium resistance protein ad biogenesis of cytoskeleton	YJR134c YPL105c YDR356w YNL126w YOL069w YGR059w YEL071w YOR134w YAL047c YKL022c	SPC98 NUF2 SPR3 BAG7 SPI6 CDC16	similarity to Nuf1p similarity to paranyosin, myosin similarity to Smy2p spindle pole body component spindle pole body component spindle pole body protein sporulation-specific septin strong similarity to Aip2p structural homologue of Sac7p Stu2p Interactant subunit of anaphase-promoting complex (cyclosome)
YPL036w YDR420w YLL024c YNL318c YJL214w YJL219w YFL011w YDL194w YEL069c YMR011w YDR343c YDR342c YML123c YNL142w	PMA2 HKR1 SSA2 HXT14 HXT8 HXT9 HXT10 SNF3 HXT13 HXT2 HXT7 PHO84	H'-transporting P-type ATPase 2 Hansenula Mrakll k9 killer toxin-resistance protein heat-shock protein of HSP70 family, cytosolic hexose transport protein hexose transport protein hexose transport protein hexose transporter high-affinity glucose transporter high-affinity hexose transporter high-affinity hexose transporter high-affinity hexose transporter high-affinity hexose transporter high-affinity inorganic phosphate/H' symporter high-affinity low-capacity ammonia permease	YPL232w YBR067c YJR007w YIL147c YER125w YBR021w YHL016c YGL233w YJR040w YMR243c <i>organiz</i> YML085c YML124c YFL039c YMR092c	SSO1 TIP1 SUI2 SLN1 RSP5 FUR4 DUR3 SEC15 GEF1 ZRC1 TUB1 TUB3 TUB1 TUB3 ACT1 AIP1	syntaxin-related protein temp.shock induced protein of the Srp1p/Tip1p family translation initiation factor eIF2, \alpha subunit two-component signal transducer ubiquitin-protein ligase uracil permease urea transport protein vostage-gated chloride channel protein voltage-gated chloride channel protein zinc- and cadmium resistance protein dibiogenesis of cytoskeleton \alpha-1 tubulin \alpha-3 tubulin actin cytoskeleton component	YJR134c YPL105c YDR356w YNL126w YOL069w YGR059w YEL071w YOR134w YAL047c YKL022c YHR166c YBL084c YDR484w YDR389w	SPC98 NUF2 SPR3 BAG7 SPI6 CDC16 CDC23 CDC27 SAC2 SAC7	similarity to Nuf1p similarity to Paranyosin, myosin similarity to Smy2p spindle pole body component spindle pole body component spindle pole body protein sporulation-specific septin strong similarity to Aip2p structural homologue of Sac7p Stu2p Interactant subunit of anaphase-promoting complex (cyclosome) subunit of anaphase-promoting complex (cyclosome) subunit of anaphase-promoting complex (cyclosome)
YPL036w YDR420w YLL024c YNL318c YJL214w YFL011w YDL194w YEL069c YMR011w YDR343c YDR342c YML123c YNL142w YGR055w	PMA2 HKR1 SSA2 HXT14 HXT8 HXT9 HXT10 SNF3 HXT13 HXT6 HXT7 PHO84 MEP2 MUP1	H'-transporting P-type ATPase 2 Hansenula Mrakll k9 killer toxin-resistance protein heat-shock protein of HSP70 family, cytosolic hexose transport protein hexose transport protein hexose transporter high-affinity glucose transporter high-affinity hexose transporter high-affinity hexose transporter high-affinity hexose transporter high-affinity hexose transporter high-affinity inorganic phosphate/H' symporter high-affinity low-capacity ammonia permease high-affinity methionine permease	YPL232w YBR067c YJR007w YIL147c YER125w YBR021w YHL016c YGL233w YJR040w YMR243c Organiz YML085c YML124c YFL039c YMR029c YMR029c YDR129c	SSO1 TIP1 SUI2 SLN1 RSP5 FUR4 DUR3 SEC15 GEF1 ZRC1 TUB1 TUB3 ACT1 AIP1 SAC6	syntaxin-related protein temp.shock induced protein of the Srp1ρ/Tip1p family translation initiation factor eIF2, α subunit two-component signal transducer ubiquitin-protein ligase uracil permease uracil permease uracil permease uracil traffic control protein vesicular traffic control protein voltage-gated chloride channel protein zinc- and cadmium resistance protein ad biogenesis of cytoskeleton α-1 tubulin α-3 tubulin actin actin cytoskeleton component actin filament bundling protein, fimbrin	YJR134c YPL105c YDR356w YNL126w YOL069w YGR059w YEL071w YOR134w YAL047c YKL022c YHR166c YBL084c YDR484w YDR389w YNL079c	SPC98 NUF2 SPR3 BAG7 SPI6 CDC16 CDC23 CDC27 SAC2 SAC7 TPM1	similarity to Nuf1p similarity to paramyosin, myosin similarity to Smy2p spindle pole body component spindle pole body component spindle pole body component spindle pole body protein sporulation-specific septin strong similarity to Aip2p structural homologue of Sac7p Stu2p Interactant subunit of anaphase-promoting complex (cyclosome) suppressor of actin mutation suppressor of actin mutation tropomyosin 1
YPL036w YDR420w YLL024c YNL318c YJL214w YJL219w YFL011w YDL194w YEL069c YMR011w YDR343c YDR342c YML123c YNL142w	PMA2 HKR1 SSA2 HXT14 HXT8 HXT9 HXT10 SNF3 HXT13 HXT2 HXT7 PHO84	H'-transporting P-type ATPase 2  Hansenula Mrakll k9 killer toxin-resistance protein heat-shock protein of HSP70 family, cytosolic hexose transport protein hexose transport protein hexose transport protein hexose transporter high-affinity plucose transporter high-affinity hexose transporter high-affinity inorganic phosphate/H' symporter high-affinity low-capacity ammonia permease high-affinity methionine permease high-affinity permease for basic amino	YPL232w YBR067c YJR007w YJL147c YER125w YBR021w YHL016c YGL233w YJR040w YMR243c Organiz YML108c YML109c YML109c YMR092c YDR129c YDL178w	SSO1 TIP1 SUI2 SLN1 SLN1 RSP5 FUR4 DUR3 SEC15 GEF1 ZRC1 TUB1 TUB1 ACT1 AIP1 AIP1 AAC6 AIP2	syntaxin-related protein temp.shock induced protein of the Srp1ρ/Tip1p family translation initiation factor eIF2, α subunit two-component signal transducer ubiquitin-protein ligase uracil permease urea transport protein vesicular traffic control protein voltage-gated chloride channel protein zinc- and cadmium resistance protein ad biogenesis of cytoskeleton α-1 tubulin α-3 tubulin actin cytoskeleton component actin filament bundling protein, fimbrin actin interacting protein 2	YJR134c YPL105c YDR356W YDR356W YOL069W YGR059W YGR059W YOR134W YAL047c YKL022c YHR166c YBL084c YDR484W YDR389W YNL079c YIL138c	SPC98 NUF2 SPR3 BAG7 SPI6 CDC16 CDC23 CDC27 SAC2 SAC2 SAC2 TPM1 TPM2	similarity to Nuf1p similarity to Puf1p similarity to Smy2p spindle pole body component spindle pole body component spindle pole body protein sporulation-specific septin strong similarity to Aip2p structural homologue of Sac7p Stu2p Interactant subunit of anaphase-promoting complex (cyclosome) suppressor of actin mutation suppressor of actin mutation tropomyosin 1 tropomyosin 1
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YPL036w YPL036w YDR420w YLL024c YNL318c YJL214w YFL011w YPL194w YFL011w YPL194w YPL0369c YMR011w YDR343c YDR342c YML123c YNL142w YGR055w YNL270c YJL129c YBR294w YOL020w YGR191w YBR140c YNL291c YHL019c YLR452c YCL051w YER118c YMR183c YLR157c YLR157c YLR158c YLR157c YLR158c YLR160c YMR319c YNL156w YHR034c YOL156w YHR034c YDR346c YNL266w YHR034c YNL268w YHR034c YNL368w	PMA2 HKR1 SSA2 HXT14 HXT8 HXT9 HXT10 SNF3 HXT13 HXT2 HXT7 PHO84 MEP2 MUP1 ALP1 TRK1 SUL1 SCM2 SST2 LRE1 SSU81 SSO2 ASP3A ASP3B ASP3C ASP3B ASP3C ASP3B ASP3C ASP3B LYP1 HXT1 HXT1 HXT1 HXT3 LYP1 HXT1 HXT1 HXT1 HXT1 HXT1 HXT1 HXT1 HXT	H'-transporting P-type ATPase 2  Hansenula Mrakll k9 killer toxin-resistance protein heat-shock protein of HSP70 family, cytosolic hexose transport protein hexose transport protein hexose transport protein hexose transporter high-affinity glucose transporter high-affinity hexose transporter high-affinity inorganic phosphate/H' symporter high-affinity wexpanic phosphate/H' symporter high-affinity permease for basic amino acids high-affinity permease for basic amino acids high-affinity sulphate transport protein high-affinity trytophan transport protein high-affinity trytophan transport protein high-affinity trytophan transport protein histidine permease inhibitory regulator protein of the RAS-cyclic AMP pathway involved in Ca* influx during mating involved in clathrin-dependent transport processes involved in desensitization to α-factor pheromone involved in laminarinase resistance involved in laminarinase resistance involved in vesicle transport from Golgi to plasma membrane L-asparaginase II low-affinity hexose transporter low-affinity hexose transporter lysine-specific high-affinity permease	YPL32w YBR067c YJR007w YJR007w YJR017w YBR021w YHL016c YGL233w YJR040w YMR243c Organiz YML085c YML124c YFL039c YML1085c YML124c YFL039c YML178w YJR065c YCR088w YDR129c YDL178w YJR1065c YCR088b YDR129c YDR119c YR1033w YNL138w YNL059c YR1033w YNL138w YNL059c YR1037w YNL059c YR1059c YR105	\$\$01 TIP1 \$UI2 \$UI2 \$LIN1 \$RSP5 FUR4 DUR3 \$EC15 GEF1 ZRC1 ation an TUB1 ACT1 AIP1 AIP1 ACT1 AIP1 ACT1 AIP1 ACT2 ARP10 ARP5 ARP6 ARP6 ARP6 ARP6 ARP9 \$SRV2 BEM1 BUD6 BNI1 CUD10 CDC20 CDC3 CDC3 CDC4 ACT5 CIN1 COC71 SLA1 SLA2 DNM1 SLA2 SLA2 SLA2 SLA2 SLA2 SLA2 SLA2 SLA2	syntaxin-related protein temp.shock induced protein of the Srp1ρ/Tip1p family translation initiation factor eIF2, α subunit two-component signal transducer ubiquitin-protein ligase uracil permease uracil velicacilar traffic control protein voltage-gated chloride channel protein zinc- and cadmium resistance protein da biogenesis of cytoskeleton α-1 tubulin α-3 tubulin actin actin extinesting protein 2 actin-related protein actin-binding protein actin-binding protein actin-related protein endiding protein cell division control protein cell division control protein cell division control protein cell division control protein centromere/microtubule binding protein confilin, actin binding and severing protein cytoskeleton assembly control protein	YJR134c YYPL105c YDR356W YNL126W YOL059W YGR059W YEL071W YOR134W YAL047c YKL022c YHR166c YBL084c YDR484W YDR389W YNL079c YIL138c YPL045W YLR337W Organiz reticulu YML075c YLR450W YJR131W YDR483W YER001W YGL038c YGL027c YGL167c YGR060W YMR015c YGR060W YMR015c YGR060W YMR115W	SPC98 NUF2 SPR3 NUF2 SPR3 BAG7 SP16 CDC16 CDC23 CDC27 SAC2 SAC7 TPM1 TPM2 VPS16 VRP1 ation ar Im and C HMG1 HMG2 MNS1 KRE2 MNN1 KRE2 MNN1 CCH1 CWH41 ALG1 ERG5 ERG25 ERG2 ERG2 ERG2 ERG2 ERG1 SG2 KEX1 PIS1	similarity to Nuf1p similarity to paramyosin, myosin similarity to Smy2p spindle pole body component spindle pole body component spindle pole body component spindle pole body component spindle pole body protein sporulation-specific septin strong similarity to Aip2p structural homologue of Sac7p Stu2p Interactant subunit of anaphase-promoting complex (cyclosome) suppressor of actin mutation su
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YPL036w YPL036w YDR420w YLL024c YNL318c YJL214w YFL011w YPL194w YFL011w YPL194w YPL069c YMR011w YDR343c YDR342c YML123c YNL142w YGR055w YNL270c YJL129c YBR294w YOL020w YGR191w YBR140c YNL291c YHL019c YLR452c YCL051w YER118c YMR183c YLR157c YLR157c YLR157c YLR157c YLR157c YLR158c YLR160c YMR319c YNL166w YHR094c YNL268w YDR345c	PMA2 HKR1 SSA2 HXT14 HXT8 HXT9 HXT10 SNF3 HXT2 HXT6 HXT7 PHO84 MEP2 MUP1 ALP1 TRK1 SUM2 HIP1 IRA1 MID1 APM2 SST2 LRE1 SSU81 SSO2 ASP3A ASP3B ASP3C ASP3B ASP3C ASP3B CASP3D FET1 HXT1 HXT1 HXT1 HXT1 HXT1 HXT1 HXT1 HX	H'-transporting P-type ATPase 2 Hansenula Mrakll k9 killer toxin-resistance protein heat-shock protein of HSP70 family, cytosolic hexose transport protein hexose transport protein hexose transport protein hexose transporter high-affinity glucose transporter high-affinity plucose transporter high-affinity hexose transporter high-affinity inorganic phosphate/H' symporter high-affinity permease protein high-affinity permease high-affinity permease for basic amino acids high-affinity published transport protein high-affinity typtophan transport protein high-affinity typtophan transport protein histidine permease inhibitory regulator protein of the RAS-cyclic AMP pathway involved in Ca* influx during mating involved in clathrin-dependent transport processes involved in laminarinase resistance involved in the HOG1 high-osmolarity signal transduction pathway involved in vesicle transport from Golgi to plasma membrane L-asparaginase II	YPL32w YBR067c YJR007w YJR007w YJR017w YBR021w YHL016c YGL233w YJR040w YMR243c  Organiz  YML086c YMR1026c YMR1026c YMR1026c YMR1026c YMR1026c YMR1029w YML059c YDR179w YJR065c YCR088w YML059c YDR179w YJR065c YCR088w YML059c YDR1169w YML059c YLR037w YDR106w YML059c YLR037w YDR106w YML059c YLR037w YDR106w YML029w YML059c YLR037w YDR106w YML029w YML059c YLR037w YMR200w YHR139c YR1037w YR1054c YR1057w YR1054c YR1057w YR1057	\$\$01 TIP1 \$UI2 \$UI2 \$SUN1 RSP5 FURA FURA SEC15 GEF1 ZRC1  ation an TUB1 ACT1 AIP1 ACT1 AIP1 ACT1 ARP10 ARP5 ARP10 ARP5 ARP10 ARP5 BUD6 BNI1 CUD10 CDC20 CDC3 CDC4 ACT5 CIN1 CDC10 CDC20 CDC3 CDC4 ACT5 CIN1 SLA1 SLA1 SLA1 SLA1 SLA1 SLA1 SLA1 DYN1 DYN1 DYN1 DYN1 DYN1 DYN1 DYN1 CAP1	syntaxin-related protein temp.shock induced protein of the Srp1p/Tip1p family translation initiation factor eIF2, α subunit two-component signal transducer ubiquitin-protein ligase uracil permease uracil protein descular traffic control protein zinc- and cadmium resistance protein zinc- and cadmium resistance protein actin flament bundling protein, fimbrin actin interacting protein 2 actin-related protein actin-binding protein actin-like protein actin-related protein cell division control protein centractin centractin centractin binding and severing protein cytoskeleton assembly control protein dynamin-related protein dynamin-related protein dynamin-related protein dynamin-related protein dynamin-related protein cytoskeleton assembly control protein dynamin-related protein for protein cytoskeleton assembly control protein dynamin-related protein in cytoskeleton assembly control protein dynamin-related protein cytoskeleton assembly control protein dynamin-related protein cytoskeleton assembly control protein dynamin-related protein in cytoskeleton assembly control protein dynamin-related protein in cytoskeleton assembly control protein dynamin-re	YJR134c   YJR1356W   YJR1356W   YJR126W   YOL069W   YGR059W   YGR050W   YG	SPC98 NUF2 SPR3 BAG7 SPR6 CDC16 CDC23 CDC27 SAC2 SAC7 TPM1 TPM2 VPS16 VRP1 ation arm and C HMG1 HMG2 MNS1 KRE2 MNN1 OCH1 CWH41 ALG1 ERG5 ERG25 ERG3 ERG25 ERG3 ERG25 ERG3 CHO1 CDS1 LHS1 PCT1 CDS1 LHS1 PCT1 APM4	similarity to Nuf1p similarity to paramyosin, myosin similarity to Smy2p spindle pole body component sportletin sportletin sportletin strong similarity to Aip2p structural homologue of Sac7p Stu2p Interactant subunit of anaphase-promoting complex (cyclosome) subpressor of actin mutation suppressor of actin
YPL036w YPL036w YDR420w YLL024e YNL318c YJL214w YFL011w YPL194w YFL069c YMR011w YDR343c YDR342c YML123c YNL142w YGR055w YNL270c YJL129c YBR294w YOL020w YGR191w YBR140c YNL291c YHL019c YLR452c YCL051w YER118c YMR183c YLR155c YLR157c YLR157	PMA2 HKR1 SSA2 HXT14 HXT8 HXT9 HXT10 SNF3 HXT13 HXT2 HXT6 HXT7 PH084 MEP2 MUP1 ALP1 TRK1 SUM2 HIP1 IRA1 MID1 APM2 SST2 LRE1 SSU81 SSO2 ASP3A ASP3B ASP3C ASP3B ASP3C ASP3D FET4 HXT1 HXT1 HXT1 HXT1 HXT1 HXT1 HXT1 HXT1	H'transporting P-type ATPase 2 Hansenula Mrakll k9 killer toxin-resistance protein heat-shock protein of HSP70 family, cytosolic hexose transport protein hexose transport protein hexose transport protein hexose transporter high-affinity glucose transporter high-affinity hexose transporter high-affinity hexose transporter high-affinity hexose transporter high-affinity hexose transporter high-affinity inorganic phosphate/H' symporter high-affinity low-capacity ammonia permease high-affinity permease for basic amino acids high-affinity potassium transport protein high-affinity putpophan transport protein high-affinity sulphate transport protein high-affinity pytophan transport protein high-affinity typtophan transport protein high-affinity pytophan transport protein high-affinity sulphate transport protein high-affinity sulphate transport protein high-affinity sulphate protein of the RAS- cyclic AMP pathway involved in Ca² influx during mating involved in desensitization to α-factor pheromone involved in the HOG1 high-osmolarity signal transduction pathway involved in vesicle transport from Golgi to plasma membrane L-asparaginase II R-asparaginase II R-aspara	YPL232w YBR067c YJR007w YJR007w YJR017w YBR021w YHL016c YGL233w YJR040w YMR243c  YML124c YFL039c YML124c YFL039c YML124c YFL039c YML129c YDL178w YJR065c YCR083w YDL029w YDR106w YDR109c YLR085c YOR141c YNL059c YER016w YBR1037w YNL059c YER016w YRL037w YNL059c YER016w YRL037w YNL059c YER016w YRL037w YNL059c YER016w YRL037w YNL059c YER016w YRL029w YRL037w YRL050c YER016w YRR016w YRR0	SSO1 TIP1 SUI2 SUN1 RSP5 FUR4 DUR3 SEC15 GEF1 ZRC1 TUB1 TUB3 ACT1 AIP1 SAC6 AIP2 ACT1 AIP1 ACT2 ARP10 ACT2 ARP1 ACT2 ARP1 ACT2 ARP1 ACT2 BEM1 BUD6 BIM1 TUB2 BEM1 BUD6 BIM1 TUB2 BEM1 CDC10 CDC3 CDC4 CDC20 CDC3 CDC4 CDC10 CDC20 CDC3 CDC4 DNM1 COF1 SLA1 DYN1 CM1 CM1 CM1 CM1 CM1 CM1 CM1 CM1 CM1 CM	syntaxin-related protein temp.shock induced protein of the Srp1ρ/Tip1p family translation initiation factor eIF2, α subunit two-component signal transducer ubiquitin-protein ligase uracil permease urea transport protein vesicular traffic control protein vesicular traffic control protein vesicular traffic control protein incomponent signal transducer ubiquitin-protein ligase uracil permease urea transport protein vesicular traffic control protein vesicular traffic control protein vesicular traffic control protein incomponent actin actine actine deadmium resistance protein actin filament bundling protein, firmbrin actin interacting protein 2 actin-related protein cell division control protein cell division control protein cell division control protein cell division control protein centractin centromere/microtubule binding protein cytoskeleton assembly control protein dynamin-related protein dynein leght chain 1, cytosolic dynein light chain 1, cytosolic	YJR134c   YJR1356W   YJR126W   YJR126W   YJR126W   YJR126W   YGR059W   YEL071W   YGR134W   YGR059W   YEL071W   YGR059W   YHL079C   YHR166C   YBL084W   YJR1337W   YJR137W   Organiz   reticulu   YML075c   YLR450W   YJR131W   YJR450W   YJR131W   YJR450W   YJR131W   YJR450W   YJR131W   YJR134W   Y	SPC98 NUF2 SPR3 BAG7 SPI6 CDC16 CDC23 CDC27 SAC2 SAC7 TPM1 TPM2 VPS16 VRP1 ation ar Im and G HMG1 HMG2 MNS1 KRE2 MNN1 CHH1 CWH41 ALG1 ERG5 ERG2 ERG2 ERG2 PMR1 CWH51 CWH61 CH61 CWH61 CWH6	similarity to Nuf1p similarity to Nuf1p similarity to Smy2p spindle pole body component spindle pole body component spindle pole body component spindle pole body protein sporulation-specific septin strong similarity to Aip2p structural homologue of Sac7p Stu2p Interactant subunit of anaphase-promoting complex (cyclosome) subpressor of actin mutation suppressor of

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YDL195w	SEC31	component of the COPII coat of ER-Golgi vesicles	YDR245w	MNN10	similarity to <i>S. pombe</i> galactosyltransferase	YGR274c	TAF145	TFIID subunit (TBP-associated factor), 145K
YGL200c	EMP24	component of the COPII-coated vesicles, 24K	YMR214w YHR123w		similarity to to <i>E. coli</i> dnaJ sn-1,2-diacylglycerol ethanolamine- and	YGR187c	HGH1	weak similarity to human Hmg1p and Hmg2p
YML012w	ERV25	component of the COPII-coated vesicles, 25K	YKL006c-a	SFT1	cholinephosphotransferase SNARE-like protein	YGR285c	ZUO1	zuotin (Z-DNA binding protein)
YHR007c	ERG11	cytochrome P450 lanosterol 14a-demethylase	YGR175c YGL055w		squalene monooxygenase stearoyl-CoA desaturase			organization and biogenesis
YNL130c YMR013c	CPT1 SEC59	diacylglycerol cholinephosphotransferase dolichol kinase	YLR080w YER087c-a	SEB1	strong similarity to Emp47p strong similarity to mammalian Sec61β	YHR037w YNL104c	LEU4	1-pyrroline-5-carboxylate dehydrogenase 2-isopropylmalalate synthase
YPL227c YPR183w	ALG5 DPM1	dolichol-P-glucose synthetase dolichyl-phosphate	YOR099w		subunit strong similarity to mannosyltransferases	YMR282c YIL125w	KGD1	2'-O-ribosyl phosphate transferase 2-oxoglutarate dehydrogenase complex
YJR143c	PMT4	β-D-mannosyltransferase dolichyl-phosphate-mannose-protein O-mannosyl transferase	YGL226c-a YDR297w		subunit of N-oligosaccharyltransferase, ζ subunit suppressor of <i>rvs161</i> and <i>rvs167</i>	YDR148c	KGD2	E1 component 2-oxoglutarate dehydrogenase complex E2 component
YDL212w YNL238w	SHR3 KEX2	endoplasmic reticulum membrane protein endoproteinase of late Golgi	YBL102w	SFT2	mutations suppressor of <i>sed5</i> ts mutants	YOL096c	COQ3	3,4-dihydroxy-5-hexaprenylbenzoate methyltransferase
YBL040c	ERD2	compartment ER lumen protein-retaining receptor	YLR026c YOR075w	SED5	syntaxin (T-SNARE) syntaxin (T-SNARE) of the ER	YMR287c	MSU1	3'-5' exonuclease for RNA 3' ss-tail, mitochondrial
YLR378c YPL094c	SEC61 SEC62	ER protein-translocation complex subunit ER protein-translocation complex subunit	YOR219c YMR022w		type IV dipeptidyl aminopeptidase ubiquitin-conjugating enzyme	YDR232w YML009c		5-aminolevulinate synthase 60S ribosomal protein, mitochondrial
YOR254c YBR171w	SEC63 SEC66	ER protein-translocation complex subunit ER protein-translocation complex subunit	YER100w YBR243c	UBC6 ALG7	ubiquitin-conjugating enzyme UDP-N-acetylglucosamine-1-phosphate	YMR108w YCL009c	ILV6	acetolactate synthase acetolactate synthase, regulatory subunit
YLR292c YDR086c	SEC72 SSS1	ER protein-translocation complex subunit ER protein-translocation complex subunit	YGR105w	VMA21	transferase vacuolar ATPase assembly integral	YAL054c YER069w	ACS1 ARG5,6	acetyl-CoA synthetase acetylglutamate kinase and
YDR331w YHR190w	GPI8 ERG9	essential for GPI-anchor attachment farnesyl-diphosphate farnesyltransferase	YBL017c	PEP1	membrane protein vacuolar protein sorting/targeting protein	YOL140w	ARG8	acetylglutamyl-phosphate reductase acetylornithine aminotransferase
YDR519w	FKB2	FK506/rapamycin-binding protein of the ER	YGL225w		vanadate-resistance protein		ACO1 LYS4	aconitate hydratase aconitate hydratase
YJR031c YEL022w	GEA1 GEA2	GDP/GTP exchange factor for ARF GDP/GTP exchange factor for ARF	organız structu		nd biogenesis of chromosome	YER170w YMR056c	AAC1	adenylate kinase, mitochondrial ADP/ATP carrier protein (MCF)
YNR026c YPR159w	SEC12 KRE6	GDP/GTP exchange factor for Sar1p glucan synthase subunit	YJL081c	ACT3	actin-related protein	YBL030c YBR085w		ADP/ATP carrier protein (MCF) ADP/ATP carrier protein (MCF)
	ALG8	glucan synthase subunit glucosyltransferase	YDL220c YBR195c	CDC13 MSI1	cell division control protein chromatin assembly complex, subunit	YER073w	ADH3	alcohol dehydrogenase III aldehyde dehydrogenase (NAD*)
YFL048c YDL192w	EMP47 ARF1	Golgi membrane protein GTP-binding protein of the ARF family	YML102w	CAC2	p50 chromatin assembly complex, subunit	YMR170c	ALD5	aldehyde dehydrogenase 2 (NAD <sup>+</sup> ), mitochondrial
YPL218w YFL038c	SAR1 YPT1	GTP-binding protein of the ARF family GTP-binding protein of the RAB family	YPR018w	RLF2	p60 chromatin assembly complex, subunit	YER086w	ILV1	anabolic serine and threonine dehydratase
YLR262c YPR165w	YPT6 RHO1	GTP-binding protein of the RAB family GTP-binding protein of the RHO subfamily	YGR218w	CRM1	p90 chromosome region maintenance protein	YJL209w	CBP1	apo-cytochrome b pre-mRNA processing protein
YNL090w	RHO2	of RAS-like proteins GTP-binding protein of the RHO subfamily	YNL216w	RAP1	DNA-binding protein with repressor and activator activity	YBR120c	CBP6	apo-cytochrome b pre-mRNA processing protein
YEL042w	GDA1	of RAS-like proteins guanosine diphosphatase	YER159c YMR072w	ABF2	functional homologue of human NC2α high-mobility group protein	YHL038c	CBP2	apo-cytochrome b pre-mRNA processing protein 2
YDR189w	SLY1	hydrophilic suppressor of <i>ypt1</i> and member of the Sec1p family	YDR225w		histone H1 protein histone H2A	YHR091c YCR024c	MSR1	arginyl-tRNA synthetase, mitochondrial asn-tRNA synthetase, mitochondrial
YCR075c YDL058w	ERS1 USO1	intracellular protein transport protein intracellular protein transport protein		HTB1	histone H2A.2 histone H2B	YKL106w YPL104w	AAT1 MSD1	aspartate transaminase, mitochondrial aspartate-tRNA ligase, mitochondrial
YLR220w YBR201w	DER1	involved in calcium regulation involved in degradation proteins in the ER	YBR010w	HTB2 HHT1	histone H2B.2 histone H3	YGR008c YDL130w-a		ATPase stabilizing factor ATPase stabilizing factor, 10K
YOR069w	VPS5	involved in Golgi retention and vacuolar sorting		HHT2 HHF1	histone H3 histone H4	YDR377w YMR301c		ATPase synthase subunit f ATP-binding cassette transporter protein,
YOR336w YHR072w YKR061w	ERG7	killer toxin-resistance protein lanosterol synthase mannosyltransferase	YNL030w YER161c YPL254w	SPT2 HFI1	histone H4 HMG-like chromatin protein interacts functionally with histone H2A	YBL022c YPL029w	PIM1 SUV3	mitochondrial ATP-dependent protease, mitochondrial ATP-dependent RNA helicase,
		mannosyltransferase mannosyltransferase	YNR010w YGR099w	CSE2 TEL2	interacts with centromeric element CDEII involved in controlling telomere length	YER061c	CEM1	mitochondrial β-keto-acyl-ACP synthase
YOR321w YBL082c		mannosyltransferase mannosyltransferase	YJR060w	CBF1	and position effect kinetochore protein	YHR208w	TWT1	branched chain amino-acid aminotransferase, mitochondrial
YJL139c YKR001c	YUR1 VPS1	mannosyltransferase member of the dynamin family of	YGR140w	CBF2	kinetochore protein complex CBF3, 110K subunit	YBR084w	MIS1	C1-tetrahydrofolate synthase, mitochondrial
YJR073c	OPI3	GTPases methylene-fatty-acyl-phospholipid	YMR094w		kinetochore protein complex CBF3, 58K subunit	YML042w YER026c	CAT2 CHO1	carnitine O-acetyltransferase CDP-diacylglycerol serine
YNL064c	YDJ1	synthase mitochondrial and ER import protein	YMR168c	CEP3	kinetochore protein complex CBF3, 71K subunit	YNR001c	CIT1	O-phosphatidyltransferase citrate (si)-synthase, mitochondrial
YPL085w YHR042w YFL025c	NCP1	multidomain vesicle coat protein NADPH-cytochrome P450 reductase	YDR328c		kinetochore protein complex CBF3, subunit D	YPR001w YBR291c	CIT3 CTP1	citrate (si)-synthase, mitochondrial citrate transport protein, mitochondrial
YJL034w	BST1 KAR2	negative regulator of COPII vesicle formation nuclear fusion protein	YIL072w YLR263w YLR457c	HOP1 RED1 NBP1	meiosis-specific protein meiosis-specific protein Nap1p-binding protein	YOR316c YOR017w	COT1 PET127	(MCF) cobalt accumulation protein component of mitochondrial translation
YJL002c YEL002c	OST1 WBP1	oligosaccharyltransferase α subunit oligosaccharyltransferase β subunit		NBP2	Nap1p-binding protein nonhistone chromosomal protein	YPR155c	NCA2	system control of mitochondrial synthesis of
YMR149w YOR103c		oligosaccharyltransferase δ subunit oligosaccharyltransferase ε subunit	YPR052c	NHP6A	nonhistorie chromosomal protein related to mammalian HMG1	YKL011c	CCE1	Atp6p and Atp8p cruciform-cutting endonuclease,
YOR085w YGL022w	OST3	oligosaccharyltransferase γ subunit oligosaccharyltransferase subunit	YDR174w YDL002c	HMO1 HMO2	nonhistone protein nonhistone protein	YML078w	CPR3	mitochondrial cyclophilin (peptidylprolyl isomerase),
YHR057c YCR069w	CYP2	peptidyl-prolyl <i>cis-trans</i> isomerase peptidyl-prolyl <i>cis-trans</i> isomerase	YKR048c YCL011c	NAP1 GBP2	nucleosome assembly protein I potential telomere-associated protein	YDR197w	CBS2	mitochondrial cytochrome b translational activator
YDR304c	CYP5	peptidyl-prolyl <i>cis-trans</i> isomerase D (cyclophilin D) of the ER	YGL238w YGL194c	CSE1 RTL1	probable kinetochore protein putative deacetylase	YIL043c	CBS2	protein cytochrome b5 reductase
YGR157w	CHO2	phosphatidylethanolamine N-methyltransferase	YBR275c YKL089w	RIF1 MIF2	Rap1p-interacting factor 1 required for normal chromosome	YKL150w YKL141w	MCR1 SDH3	cytochrome b5 reductase cytochrome b560 subunit of respiratory
YGR170w YDR518w	PSD2 EUG1	phosphatidylserine decarboxylase 2 protein disulphide isomerase	YJL074c	SMC3	segregation and spindle integrity required for structural maintenance of	YJR048w	CYC1	complex II cytochrome c isoform 1
YCL043c YHR079c	PDI1 IRE1	protein disulphide-isomerase protein kinase	YLR086w		chromosomes similarity to chromosome condensation	YEL039c YOR037w	CYC7 CYC2	cytochrome c isoform 2 cytochrome c mitochondrial import factor
YEL036c YCR067c	ANP1 SED4	protein of the endoplasmatic reticulum protein of the endoplasmic reticulum	YML069w	POB3	proteins similarity to HMG proteins	YER058w YPL132w	PET117 COX11	cytochrome c oxidase assembly factor cytochrome c oxidase assembly protein
YIL004c YDR040c	BET1 ENA1	protein transport protein P-type ATPase involved in Na <sup>+</sup> and Li <sup>+</sup>	YOR053w YNL206c		similarity to protamines similarity to structure-specific recognition	YML129c YDR079w	COX14 PET100	cytochrome c oxidase assembly protein cytochrome c oxidase assembly protein
YKL212w	SAC1	efflux recessive suppressor of secretory defect	YDL208w	NHP2	proteins strong similarity to high mobility group	YGL187c YNL052w	COX4 COX5A	cytochrome c oxidase subunit IV cytochrome c oxidase subunit V.A
YLR088w	GAA1	required for attachment of GPI anchor onto proteins	YEL026w	_	(HMG) family strong similarity to high mobility group-like	YIL111w YHR051w	COX5B	cytochrome c oxidase subunit Vb cytochrome c oxidase subunit VI
YPL050c YCL001w	MNN9 RER1	required for complex N-glycosylation required for correct localization of Sec12p	YOL012c	НТА3	protein Nhp2p strong similarity to histone H2A protein	YGL191w YLR038c	COX13 COX12	cytochrome c oxidase subunit VIa cytochrome c oxidase subunit VIB
YGL145w YDR414c	TIP20 ERD1	required for ER to Golgi transport required for retention of luminal ER	YKL049c YOR213c	CSE4	strong similarity to histone H3 subunit of the RSC complex	YMR256c YDL067c	COX7 COX9	cytochrome c oxidase subunit VII cytochrome c oxidase subunit VIIA
YMR004w		proteins required for vacuolar protein sorting	YCR052w YFR037c	RSC6 RSC8	subunit of the RSC complex subunit of the RSC complex	YLR395c YKR066c	COX8 CCP1	cytochrome c oxidase subunit VIII cytochrome c peroxidase
YDR498c YJR010c-a	SEC20	secretory pathway protein signal peptidase 10.8K subunit	YLR321c YIL126w	SFH1 STH1	subunit of the RSC complex subunit of the RSC complex	YOR065w YER141w	CYT1 COX15	cytochrome c1 cytochrome oxidase assembly factor
YML055w YDR292c		signal peptidase 18K subunit signal recognition particle receptor,	YDR285w YLR233c	ZIP1 EST1	synaptonemal complex protein telomere elongation protein	YER154w YOR386w	OXA1 PHR1	cytochrome oxidase biogenesis protein deoxyribodipyrimidine photo-lyase
YIR022w	SEC11	α subunit signal sequence processing protein	YBL088c YPL128c	TEL1 TBF1	telomere length control protein telomere TTAGGG repeat-binding factor 1	YLR348c YFL018c	LPD1	dicarboxylate carrier protein dihydrolipoamide dehydrogenase
YAL058w	CNE1	similarity to calnexin				YNL071w		dihydrolipoamide S-acetyltransferase

YJR016c	ILV3	dihydroxy-acid dehydratase	YNL131w	TOM22	mitochondrial outer membrane import	VRI 038w/	MRPI 16	ribosomal protein, mitochondrial
YDL174c	DLD1	D-lactate ferricytochrome c			receptor subunit	YMR193w	MRPL24	ribosomal protein, mitochondrial
YML061c	PIF1	oxidoreductase (D-LCR) DNA helicase involved in mitochondrial	YGR082w	TOM20	mitochondrial outer membrane import receptor subunit, 20K	YMR024w YMR286w		ribosomal protein, mitochondrial ribosomal protein, mitochondrial
YHR120w	MOUI	DNA repair and telomere length	YMR060c	TOM37	mitochondrial outer membrane import	YLR439w		ribosomal protein, mitochondrial
THRIZOW		DNA mismatch repair protein, mitochondrial	YMR203w	TOM40	receptor subunit, 37K mitochondrial outer membrane import	YGR220c	MRPL9	ribosomal protein, mitochondrial ribosomal protein, mitochondrial
YOR330c	MIP1	DNA-directed DNA polymerase γ, catalytic subunit, mitochondrial	YOR045w	TOM6	receptor subunit, 40K mitochondrial outer membrane import	YDR337w YNL137c	MRPS28 NAM9	ribosomal protein, mitochondrial ribosomal protein, mitochondrial
YFL036w	RPO41	DNA-directed RNA polymerase,			receptor subunit, 6K	YOR158w	PET123	ribosomal protein, mitochondrial
YBR252w	DUT1	mitochondrial dUTP pyrophosphatase, mitochondrial	YNL070w	TOM7	mitochondrial outer membrane import receptor subunit, 7K	YCR046c YFR049w		ribosomal protein, mitochondrial ribosomal protein, mitochondrial
YOR211c	MGM1	dynamin-like protein	YNL055c	POR1	mitochondrial outer membrane porin			RNA helicase of the DEAD box family,
	ETF-β	electron-transferring flavoprotein, β subunit	YNL121c	TOM70	mitochondrial outer membrane specialized import receptor	YMR228w	MTF1	mitochondrial RNA polymerase specific factor,
YLR393w YNL315c	ATP10 ATP11	F1F0 ATPase complex assembly protein F1F0-ATPase complex assembly protein	YGL143c YLR163c	MRF1 MAS1	mitochondrial peptide chain release factor mitochondrial processing peptidase	YOR334w	MRS2	mitochondrial RNA splicing protein and member of the
YJL180c	ATP12	F1F0-ATPase complex assembly protein	YHR024c	MAS2	mitochondrial processing peptidase,			mitochondrial carrier family (MCF)
YKL016c YBL099w	ATP7 ATP1	F1F0-ATPase complex, F0 D subunit F1F0-ATPase complex, F1 α subunit	YMR150c	IMP1	catalytic 53K (α) subunit mitochondrial protease	YJL133w	MRS3	RNA splicing protein and member of the mitochondrial carrier family (MCF)
YJR121w YDL004w	ATP2	F1F0-ATPase complex, F1 β subunit F1F0-ATPase complex, F1 δ subunit	YDR375c	BCS1	mitochondrial protein of the CDC48/PAS1/SEC18 (AAA) family of	YKR052c	MRS4	RNA splicing protein and member of the mitochondrial carrier family (MCF)
YPL078c	ATP4	F1F0-ATPase complex, F1 δ subunit			ATPases	YOR201c	PET56	rRNA (guanosine-2'-O-)-methyltransferase
YPL271w YBR039w		F1F0-ATPase complex, F1 ε subunit F1F0-ATPase complex, F1 γ subunit	YDR120c	TRM1	N2,N2-dimethylguanine tRNA methyltransferase	YBR263w	SHM1	serine hydroxymethyltransferase, mitochondrial
YDR298c YLR295c		F1F0-ATPase complex, OSCP subunit F1F0-ATPase complex, subunit h	YML120c YOR355w	NDI1 GDS1	NADH-ubiquinone-6 oxidoreductase nam9-1 suppressor	YPR037c YDR376w	ARH1	similarity to Erv1p and rat ALR protein similarity to human adrenodoxin
YIL134w	FLX1	FAD carrier protein, mitochondrial (MCF)	YJL208c	NUC1	nuclease, mitochondrial		ZULL	reductase
YPL172c YOR176w		farnesyl transferase ferrochelatase	YAR035w	YAT1	outer carnitine acetyltransferase, mitochondrial	YBL013w		similarity to methionyl-tRNA formyltransferase
YPL262w YOL033w	FUM1 MSE1	fumarate hydratase	YNR041c	COQ2	para-hydroxybenzoate-	YJR113c		similarity to mitochondrial ribosomal
YOL059W	GPD3	glutamyl-tRNA synthetase, mitochondrial glycerol-3-phosphate dehydrogenase	YPR047w	MSF1	polyprenyltransferase phenylalanine-tRNA ligase α subunit,	YKL120w	PMT	protein S7 similarity to mitochondrial uncoupling
YIL155c	GUT2	(NAD*), mitochondrial glycerol-3-phosphate dehydrogenase,	YJR077c	MIR1	mitochondrial phosphate transport protein,	YMR244w		protein (MCF) similarity to NCA3 and SUN4 protein
		mitochondrial			mitochondrial (MCF)	YOR150w	140010	similarity to ribosomal protein L13
YMR189w YDR019c	GSD2 GCV1	glycine decarboxylase subunit glycine decarboxylase T subunit	YNL169c YLR203c	PSD1 MSS51	phosphatidylserine decarboxylase 1 possibly involved in translational		MSS18 PET54	splicing protein splicing protein and translational activator,
YFL016c YOR232w	MDJ1 MGE1	heat-shock protein - chaperone heat-shock protein - chaperone	YGL068w		activation of COX1 and COB mRNA probable ribosomal protein L12	YCR028c-a	RIM1	mitochondrial ssDNA-binding protein, mitochondrial
YLR259c		heat-shock protein - chaperone,	YLR168c	(MSF1)	probably involved in intramitochondrial	YKL192c		strong similarity to acyl-carrier proteins
YJR045c	SSC1	mitochondrial heat-shock protein 70-related protein,	YLR142w	PUT1	protein sorting proline oxidase	YBR024w YHR117w	SCO2 TOM71	strong similarity to Sco1p strong similarity to Tom70p/Mas70p
YDR258c	HSP78	mitochondrial heat-shock protein of clpb family of ATP-	YER017c	AFG3	protease of the SEC18/CDC48/PAS1 family of ATPases (AAA)	YKL148c YLL041c	SDH1 SDH2	succinate dehydrogenase flavoprotein succinate dehydrogenase iron-sulphur
		dependent proteases, mitochondrial	YPR024w	YME1	protease of the SEC18/CDC48/PAS1			protein subunit
YBR003w YMR072w		hexaprenyl pyrophosphate synthetase high mobility group protein	YMR089c	YTA12	family of ATPases (AAA) protease of the SEC18/CDC48/PAS1	YDR178w	SDH4	succinate dehydrogenase membrane anchor subunit for Sdh2p
YAL039c	CYC3	holocytochrome c synthase (cytochrome c haem lyase)	YDL044c	MTF2	family of ATPases (AAA) protein involved in mRNA splicing and	YHR008c YHR050w	SOD2 SMF2	superoxide dismutase (Mn), mitochondrial suppressor of mitochondrial matrix
YKL087c		holocytochrome c1 synthase		OM45	protein synthesis, mitochondrial		MST1	mutant
YMR038c YDL181w	INH1	homocitrate dehydrogenase inhibitor of mitochondrial ATPase	YIL136w		protein of the outer mitochondrial membrane			threonine-tRNA ligase, mitochondrial translation elongation factor G,
YMR267w YLL009c		inorganic pyrophosphatase, mitochondrial interacts genetically with SCO1 and SCO2	YAL011w YJL023c	FUN36 PET130	protein of unknown function protein synthesis protein, mitochondrial	YOR187w	TUF1	mitochondrial translation elongation factor TU,
YGR028w		in cytochrome oxidase assembly intra-mitochondrial sorting protein	YER014w	HEM14	protoporphyrinogen oxidase, mitochondrial	YJL102w		mitochondrial translation elongation factor,
YJR034w		involved in assembly of cytochrome	YER178w	PDA1	pyruvate dehydrogenase (lipoamide)			mitochondrial
YMR302c	PRP12	oxidase involved in early maturation of pre-rRNA	YBR221c	PDB1	α subunit pyruvate dehydrogenase (lipoamide)	YDL069c	IFM1 CBS1	translation initiation factor 2, mitochondrial translational activator of cob mRNA
YOL009c YAL010c		involved in mitochondrial inheritance involved in mitochondrial morphology and	YGR193c	PDX1	β subunit pyruvate dehydrogenase complex protein	YER153c	PET122	translational activator of cytochrome c oxidase subunit III
		inheritance involved in mitochondrial RNA splicing of			X		PET494 MOD5	translational activator, mitochondrial
YIR021w	MRS1	COB mRNA	YJR095w YBR091c	ACR1 MRS5	regulator of acetyl-CoA synthetase activity regulator of mitochondrial intron splicing	YER168c	CCA1	tRNA isopentenyltransferase tRNA nucleotidyltransferase
YBR037c	SCO1	involved in stabilization of Cox1p and Cox2p	YPL215w	CBP3	required for assembly of cytochrome bc1 complex	YDR268w	MSW1	tryptophanyl-tRNA synthetase, mitochondrial
YNL066w YCL017c	SUN4 NFS1	involved in the aging process involved in tRNA processing and	YEL059c-a	SOM1	required for mitochondrial Imp1 peptidase function	YPL097w YFR033c	MSY1 QCR6	tyrosyl-tRNA synthetase
		mitochondrial metabolsim	YLL006w	MMM1	required for mitochondrial shape and			ubiquinol-cytochrome c reductase 17K protein
YNL037c	IDH1	isocitrate dehydrogenase (NAD*) subunit 1, mitochondrial	YKL093w	MBR1	structure required for optimal growth on glycerol	YPR191w	QCR2	ubiquinol-cytochrome c reductase 40K subunit II
YOR136w	IDH2	isocitrate dehydrogenase (NAD*) subunit 2, mitochondrial	YLR067c	PET309	required for stability and translation of COX1 mRNA	YBL045c	COR1	ubiquinol-cytochrome c reductase 44K core protein
YDL066w	IDP1	isocitrate dehydrogenase (NADP*), mitochondrial	YMR257c YBL080c	PET111 PET112	required for translation of COX2 mRNA required to maintain RHO <sup>+</sup> mitochondrial	YHR001w-a	QCR10	ubiquinol-cytochrome c reductase 8.5K subunit
YPL040c	ISM1	isoleucine-tRNA ligase, mitochondrial			DNA	YGR174c	CBP4	ubiquinol-cytochrome c reductase
YLR355c YML054c	ILV5 CYB2	ketol-acid reducto-isomerase lactate dehydrogenase cytochrome b2	YBR185c YML091c	MBA1 RPM2	respiratory chain assembly protein ribonuclease P, mitochondrial	YGL119w	ABC1	assembly factor ubiquinol-cytochrome c reductase
YLR382c YOR196c	NAM2	leucine-tRNA ligase, mitochondrial lipoic acid synthase	YKL170w YJL063c	MRPL38 MRPL8	ribosomal protein L14, mitochondrial	YEL024w	RIP1	complex assembly protein ubiquinol-cytochrome c reductase iron-
YNL073w	MSK1	lysyl-tRNA synthetase, mitochondrial	YPR166c	MRP2	ribosomal protein S14			sulphur protein
YKL085w YOR130c		malate dehydrogenase, mitochondrial member of the mitochondrial carrier	YPL013c YBR251w	MRPS5	ribosomal protein S16, mitochondrial ribosomal protein S5, mitochondrial	YDR529c	QCR7	ubiquinol-cytochrome c reductase subunit 7
YDL198c	ҮНМ1	family (MCF) member of the mitochondrial carrier	YBR146w YKR006c	MRPS9 MRPL13	ribosomal protein S9, mitochondrial ribosomal protein YmL13, mitochondrial	YGR183c	QCR9	ubiquinol-cytochrome c reductase subunit 9
		family (MCF)	YNL005c	MRPL2	ribosomal protein YmL2, mitochondrial	YJL166w	QCR8	ubiquinol-cytochrome c reductase subunit
YGR171c YGR029w	MSM1 ERV1	methionyl-tRNA synthetase mitochondrial biogenesis and regulation	YKR085c YBR282w	MRPL20 MRPL27	ribosomal protein YmL20, mitochondrial ribosomal protein YmL27, mitochondrial	YML021c	UNG1	VIII uracil-DNA glycosylase
YBR192w	RIM2	of cell cycle mitochondrial carrier protein (MCF)	YDR462w YNL252c		ribosomal protein YmL28, mitochondrial ribosomal protein YmL30, mitochondrial	YGR094w YIL114c	VAS1 POR2	valyl-tRNA synthetase voltage-dependent anion channel
YPR058w YBR104w	YMC1 YMC2	mitochondrial carrier protein (MCF)	YKL138c YCR003w	MRPL31 MRPL32	ribosomal protein YmL31, mitochondrial		YTP1	(YVDAC2)
YOR020c	HSP10	mitochondrial carrier protein (MCF) mitochondrial chaperonin	YBR122c	MRPL36	ribosomal protein YmL32, mitochondrial ribosomal protein YmL36, mitochondrial	YNL237w	TIFI	weak similarity to mitochondrial electron transport proteins
YJR144w	MGM101	mitochondrial genome maintenance protein	YBR268w YPL173w	MRPL37	ribosomal protein YmL37, mitochondrial ribosomal protein YmL40, mitochondrial	peroxis	omal or	ganization and biogenesis
YMR023c	MSS1	mitochondrial GTPase involved in expression of COX1	YGR076c	MRPL25	ribosomal protein YmR26 (YML25), mitochondrial	YIL160c	POT1	acetyl-CoA C-acyltransferase, peroxisomal
YNR017w	MAS6	mitochondrial inner membrane import translocase subunit	YMR225c YML025c	MRPL44	ribosomal protein YmR44, mitochondrial ribosomal protein, mitochondrial	YAL054c	ACS1 POX1	acetyl-CoA synthetase acyl-CoA oxidase
YJL143w	TIM17	mitochondrial inner membrane import	YDR347w		ribosomal protein, mitochondrial	YBR222c	PCS60	AMP-binding protein, peroxisomal
YIL022w	TIM44	translocase subunit mitochondrial inner membrane import	YGR084c YKL003c	MRP13 MRP17	ribosomal protein, mitochondrial ribosomal protein, mitochondrial		CTA1	carnitine O-acetyltransferase catalase A, peroxisomal
YMR035w	IMP2	translocase subunit mitochondrial inner membrane protease	YDR405w YHL004w	MRP20 MRP4	ribosomal protein, mitochondrial ribosomal protein, mitochondrial	YCR005c YKR009c	CIT2 FOX2	citrate (si)-synthase, peroxisomal hydratase-dehydrogenase-epimerase,
		subunit	YKL167c	MRP49 MRP8	ribosomal protein, mitochondrial		ICL1	peroxisomal
YKL134c	(MIP1)	mitochondrial intermediate peptidase	YKL142w YLR312w-a		ribosomal protein, mitochondrial ribosomal protein, mitochondrial	YER065c YKL188c	PAT1	isocitrate lyase long-chain-fatty-acid transporter

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YPL147W YER015W YDL078c YNL117W YIR031c YDR329c YDR265W YJL210W YNL329c YDR142c YOL147c YLR191W	PXA1 FAA2 MDH3 MLS1 DAL7 PAS3 PAS4 PAS5 PAS8 PAS7 PMP27 PAS20	long-chain-fatty-acid transporter long-chain-fatty-acid-CoA ligase malate dehydrogenase, peroxisomal malate synthase 1 malate synthase 2 peroxisomal assembly protein peroxisomal import protein peroxisomal import protein peroxisomal membrane protein peroxisomal protein involved in protein import
	PAS10	putative peroxisomal targeting signal receptor
YLR109w		similarity to <i>C. boidinii</i> peroxisomal membrane protein 20K A
YGR077c		similarity to peroxisomal matrix protein Per1p
YLR251w		similarity to peroxisomal rat membrane protein PMP22
YNL202w YGR133w YBR204c	SPS19 PAS2	sporulation-specific protein ubiquitin-conjugating enzyme weak similarity to peroxisomal serine- active lipase

#### endosomal organization and biogenesis

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YKL135c	APL2	β-adaptin
YNL192w	CHS1	chitin synthase I
YBR023c	CHS3	chitin synthase III
YJR058c	APS2	clathrin-associated protein 17, small
		subunit
YJR005w	APL1	clathrin-associated protein complex,
		β subunit
YBR288c	APM3	clathrin-associated protein complex,
		medium subunit
YLR170c	APS1	clathrin-associated protein complex, sma
		subunit AP19
YDL145c	RET1	coatomer complex α subunit
YDR238c	SEC26	coatomer complex $\beta$ subunit of secretory
		pathway vesicles
YGL137w	SEC27	coatomer complex β subunit
YFR051c	RET2	coatomer complex δ subunit
YNL287w	SEC21	coatomer complex $\gamma$ subunit
YPL010w	RET3	coatomer complex ζ subunit
YPR181c	SEC23	component of COPII coat of ER-golgi
VDD170*	0507	vesicles component of non-clathrin vesicle coat
YDR170c YLR083c	SEC7 EMP70	endosomal protein
YPR017c	DSS4	GDP/GTP exchange factor for Sec4p
YOR089c	VPS21	GTP-binding protein
YDL137w	ARF2	GTP-binding protein of the ARF family
YML001w	YPT7	GTP-binding protein of the RAB family
YFL005w	SEC4	GTP-binding protein of the RAS
11 200011	OLO	superfamily
YI R268w	SEC22	high copy suppressor of ypt1 null
		mutation
YPL085w	SEC16	multidomain vesicle protein
YLR208w	SEC13	protein transport protein
YKL196c		similarity to Sec22p
YLR080w		strong similarity to Emp47p
YDR107c		strong similarity to Emp70p
YAL030w	SNC1	strong similarity to synaptic vesicle-
		associated membrane protein
YOR327c	SNC2	strong similarity to synaptobrevin
YBL050w	SEC17	transport vesicle fusion protein
YNR006w	VPS27	vacuolar protein sorting-associated
VDD000-	05010	protein
YBR080c	SEC18	vesicular-fusion protein, functional
YI R078c	BOS1	homologue of NSF weak similarity to synaptobrevin
I LNU/80	DUOI	(V-SNARE)
		(VOIVAIL)

## vacuolar and lysosomal organization and biogenesis

YGL156w YBR286w YKL103c YPL154c YDL128w	AMS1 APE3 LAP4 PEP4 VCX1	α-mannosidase aminopeptidase Y, vacuolar aminopeptidase yscl, vacuolar aspartyl protease Ca*-transport (H*/Ca** exchange) protein, vacuolar
YGL006w YMR297w YHR028c YDR135c	PMC1 PRC1 DAP2 YCF1	Ca*-transporting P-type ATPase carboxypeptidase y, serine-type protease dipeptidyl aminopeptidase B glutathione S-conjugate transporter, vacuolar
YJL172w YKL119c YHR039c-a	CPS1 VPH2 VMA10	Gly-X carboxypeptidase YSCS H*-ATPase assembly protein, vacuolar H*-ATPase V0 domain 13K subunit,
YEL027w	CUP5	vacuolar H*-ATPase V0 domain 17K subunit, vacuolar
YPL234c	TFP3	H <sup>+</sup> -ATPase V0 domain 17K subunit,
YLR447c	VMA6	H <sup>+</sup> -ATPase V0 domain 36K subunit,
YOR270c	VPH1	H*-ATPase V0 domain 95K subunit,
YGR020c	VMA7	H*-ATPase V1 domain 14K subunit,
YOR332w	VMA4	H <sup>+</sup> -ATPase V1 domain 27K subunit,
YEL051w	VMA8	H <sup>+</sup> -ATPase V1 domain 32K subunit,
YKL080w	VMA5	H <sup>+</sup> -ATPase V1 domain 42K subunit, vacuolar

YPR036w	VMA13	H <sup>+</sup> -ATPase V1 domain 54K subunit,
YBR127c	VMA2	H <sup>+</sup> -ATPase V1 domain 60K subunit,
YDL185w	TFP1	vacuolar H <sup>+</sup> -ATPase V1 domain 69K subunit, vacuolar
YFR019w YEL060c	FAB1 PRB1	probable PI P 5-kinase protease B, vacuolar
YDR481c	PHO8	repressible vacuolar alkaline phosphatas
YIL099w	SGA1	sporulation specific glucan  1.4—glucosidase
YOR036w	PEP12	syntaxin (T-SNARE)
YOR106w	VAM3	syntaxin related protein
YMR231w	PEP5	vacuolar biogenesis protein
YLR148w	PEP3	vacuolar membrane protein
YGL212w	VAM7	vacuolar morphogenesis protein
YJL053w	PEP8	vacuolar protein-sorting/targeting protein
YJL154c YDR323c	VPS35 PFP7	vacuolar protein-sorting protein vacuolar segregation protein
YPI 045w	VPS16	vacuolar segregation protein
YDR495c	VPS3	vacuolar sorting protein
YLR396c	VPS33	vacuolar sorting protein
YPR173c	VPS4	vacuolar sorting protein

## other cellular organization and biogenesis activities

YKL157W YIL015W YJL174W YJR0092C YLR286C YLR300W YIR019C YPL187W YGL089C YDR461W YNL145W YKL163W YBR093C YKL164C YML008C YAR071W YHR215W YHL160W YHR215W YBR046C YMR215W	APE2 BAR1 KRE9 PHO3 CTS1 EXG1 STA1 MFa1 MFa2 MFA2 PHO5 PIR1 ERG6 PHO11 PHO12 YGP1 SSP120 ZTA1	aminopeptidase yscII barrier pepsin cell wall synthesis protein constitutive acid phosphatase endochitinase exo-1,3—glucanase (I/II), major isoform extracellular α-1,4-glucan glucosidase mating pheromone α-1 factor mating pheromone α-2 factor mating pheromone α-factor 1 mating pheromone α-factor 1 mating pheromone α-factor 2 member of the Pirtp/Pir2p/Pir3p family repressible acid phosphatase required for tolerance to heat-shock S-adenosyl-methionine δ-24-sterol-c-methyltransferase secreted acid phosphatase secreted acid phosphatase secreted acid phosphatase secreted glycoprotein secretory protein similarity to ζ-crystallin similarity to ζ-crystallin similarity to fundance in the secretory protein similarity to human band 3 anion
YIL162w	SUC2	transport protein sucrose hydrolyzing enzyme

#### **Signal transduction**

#### pheromone response generation

pnerom	one res	sponse generation
YDR264c	AKR1	ankyrin repeat-containing protein
YPL161c	BEM4	bud emergence protein
YCL027w	FUS1	cell fusion protein
YNL053w	MSG5	dual-specifity protein phosphatase
YJL157c	FAR1	factor arrest protein
YAL041w	CDC24	GDP/GTP exchange factor for Cdc42p
YHR005c	GPA1	GTP-binding protein α subunit of the pheromone pathway
YOR212w	STF4	GTP-binding protein β subunit of the
101121200	OIL4	pheromone pathway
YIR086w	STF18	GTP-binding protein $\gamma$ subunit of the
131100011	01210	pheromone pathway
YLR229c	CDC42	GTP-binding protein of RAS superfamily
YNL173c	MDG1	GTP-binding protein of the pheromone
		pathway
YER020w	GPA2	guanine nucleotide-binding regulatory
\ // D 450	0070	protein
YLR452c	SST2	involved in desensitization to α-factor
YMR052w	FAR3	pheromone involved in pheromone-mediated cell
TIVINUSZW	FANS	cvcle arrest
YDR461w	MFA1	mating pheromone a-factor 1
YII 047c	SYG1	member of the major facilitator
		superfamily
YBL016w	FUS3	mitogen-activated protein kinase (MAP
		kinase)
YFL026w	STE2	pheromone α-factor receptor
YKL178c	STE3	pheromone α-factor receptor
YCL032w	STE50	pheromone response pathway protein
YDR103w	STE5	pheromone signal transduction pathway
YGR040w	KSS1	protein ser/thr protein kinase of the MAP kinase
101104000	KOOT	family
YI R362w	STF11	ser/thr protein kinase of the MEKK family
YHL007c	STE20	ser/thr protein kinase of the pheromone
		pathway
YDL159w	STE7	ser/thr/tyr protein kinase of MAP kinase
		kinase family
YHR146w		similarity to pheromone-response
\/\ ID004	07510	G-protein YNL173c
YHR084w	STE12	transcriptional activator

genesis
STE12

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YBR200w YPL161c YBR109c YAL041w YGR070w	BEM1 BEM4 CMD1 CDC24 ROM1	bud emergence mediator bud emergence protein calmodulin GDP/GTP exchange factor for Cdc42p GDP/GTP exchange protein for Rho1p

YLR371w YPL115c	ROM2 BEM3	GDP/GTP exchange protein for Rho1p GTPase-activating protein for Cdc42p and						
YLR229c YPR165w	CDC42 RHO1	Rho1p GTP-binding protein of RAS superfamily GTP-binding protein of the RHO subfamily						
YNL090w	RHO2	of RAS-like proteins GTP-binding protein of the RHO subfamily of RAS-like proteins						
YPL106c YOR149c YPL140c	SSE1 SMP3 MKK2	heat-shock protein of HSP70 family protein kinase C pathway protein protein kinase of the MAP kinase kinase (MEK) family						
YDL135c	RDI1	RHO GDP dissociation inhibitor with activity towards Rho1p						
YOR231w	MKK1	ser/thr protein kinase						
YBL105c	PKC1	ser/thr protein kinase						
YHR030c	SLT2	ser/thr protein kinase of MAP kinase family						
YJL095w	BCK1	ser/thr protein kinase of the MEKK family						
YER167w	BCK2	ser/thr protein kinase of the protein kinase C pathway						
YOL113w YGL106w YKL161c	SKM1	Ste20p/PÁK-like protein kinase strong similarity to calmodulins strong similarity to ser/thr-specific protein kinase Stt2o						
YPL089c	RLM1	transcription factor of the MADS box family						
YGL095c	VPS45	vacuolar protein sorting-associated protein						
osmosensing								

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YDL022w	GPD1	glycerol-3-phosphate dehydrogenase (NAD*), cytoplasmic
YFL014w YER118c	HSP12 SSU81	heat-shock protein involved in the <i>HOG1</i> high-osmolarity
YCR073c	SSK22	signal transduction pathway MAP kinase kinase kinase
YNR031c	SSK2	MAP kinase kinase kinase of the high- osmolarity signal transduction pathway
YDL006w YLR113w	PTC1 HOG1	protein ser/thr phosphatase 2c ser/thr protein kinase of MAP kinase
YHR030c	SLT2	(MAPK) family ser/thr protein kinase of MAP kinase family
YKL161c		strong similarity to ser/thr-specific protein kinase Slt2p
YIL147c YLR006c YJL128c	SLN1 SSK1 PBS2	two-component signal transducer two-component signal transducer tyrosine protein kinase of the MAP kinase
YDR069c	DOA4	kinase family ubiquitin-specific protease

#### nutritional response

YJL005w	CYR1	adenylate cyclase
YLR178c	TFS1	cdc25-dependent nutrient- and ammonia- response cell-cycle regulator
YBR195c	MSI1	chromatin assembly complex, subunit p50
YI I 016w	SDC25	GDP/GTP exchange factor
YLR310c	CDC25	GDP/GTP exchange factor for Ras1p and Ras2p
YOR101w	RAS1	GTP-binding protein
YNL098c	RAS2	GTP-binding protein
YER020w	GPA2	guanine nucleotide-binding regulatory protein
YPL106c	SSE1	heat-shock protein of HSP70 family
YBR140c	IRA1	inhibitory regulator protein of the RAS- cyclic AMP pathway
YIL119c	RPI1	negative regulator of RAS-cAMP pathway
YIR026c	YVH1	protein tyrosine phosphatase
YOR208w	PTP2	protein-tyrosine-phosphatase
YOL110w	SHR5	RAS suppressor
YPL084w	BRO1	required for normal response to nutrient limitation
YLR362w	STE11	ser/thr protein kinase of the MEKK family
YDL159w	STE7	ser/thr/tyr protein kinase of MAP kinase kinase family
YHR084w	STE12	transcriptional activator

other signal-transduction activities									
YPL268w	PLC1	1-phosphatidylinositol-4,5-bisphosphate phosphodiesterase							
YNL138w	SRV2	adenylate cyclase-associated protein, 70K							
YFR014c	CMK1	Ca <sup>2+</sup> /calmodulin-dependent ser/thr protein kinase, type I							
YOL016c	CMK2	Ca <sup>2+</sup> /calmodulin-dependent ser/thr protein kinase, type II							
YPL203w	TPK2	cAMP-dependent protein kinase 2, catalytic subunit							
YKL166c	TPK3	cAMP-dependent protein kinase 3, catalytic subunit							
YJL164c	SRA3	cAMP-dependent protein kinase, catalytic subunit 1							
YMR028w	TAP42	component of the Tor signalling pathway							
YML064c	TEM1	GTP-binding protein of the RAS superfamily							
YJL146w	IDS2	IME2-dependent signalling protein							
YJR066w	TOR1	phosphatidylinositol 3-kinase							
YKL203c	TOR2	phosphatidylinositol 3-kinase							
YLR240w	VPS34	phosphatidylinositol 3-kinase							
YNL267w	PIK1	phosphatidylinositol 4-kinase							
YNL106c	PIE3	phosphatidylinositol phosphate phosphatase							
YLR305c	STT4	phosphatidylinositol-4-kinase							
YDI 101c	DUN1	protein kinase							



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YHR079c YMR016c	IRE1 SOK2	protein kinase regulatory protein in the PKA signal transduction pathway	YGL178w YGR159c	MPT5 NSR1	multicopy suppressor of pop2 nuclear localization sequence binding protein	YDR059c YER125w YKL210w	UBC5 RSP5 UBA1	ubiquitin-conjugating enzyme ubiquitin-protein ligase ubiquitin-protein ligase
YGR216c	GPI1	required for N-acetylglucosaminyl phosphatidylinositol synthesis	YGL115w YJR051w	SNF4 OSM1	nuclear regulatory protein osmotic growth protein			ect repair, base excision repair
YPL153c YHR046c	SPK1	ser/thr/tyr protein kinase similarity to bovine myo-inositol-1(or 4)-	YMR175w YBR070c		osmotic stress protein osmotolerance protein	and nuc	ieotiae	excision repair)
		monophosphatase	YHR057c	CYP2	peptidyl-prolyl cis-trans isomerase	YER142c		3-methyladenine DNA glycosylase
YBR260c		similarity to <i>C. elegans</i> GTPase-activating protein	YOR014w	RTS1	potential regulatory subunit of protein phosphatase 2A	YML060w YKL114c	APN1	8-oxoguanine DNA glycosylase AP endonuclease
YGR136w		similarity to chicken growth factor	YMR174c	PAI3 IRE1	protease A (ysca) inhibitor IA3	YJL092w	HPR5 HRR25	ATP-dependent DNA helicase
YDR379w		receptor-binding protein GRB2 homologue similarity to Dbm1p	YHR079c YPL140c	MKK2	protein kinase protein kinase of the MAP kinase kinase	YPL204w YPL022w	RAD1	casein kinase I, ser/thr/tyr protein kinase component of the nucleotide excision
YDR208w YCR027c	MSS4	similarity to human PI P 5-kinase similarity to human Ras-related GTP-	YOL064c	MET22	(MEK) family protein ser/thr phosphatase	YDL108w	KIN28	repairosome cyclin-dependent ser/thr protein kinase
		binding protein	YDL006w	PTC1	protein ser/thr phosphatase 2c	YOR386w	PHR1	deoxyribodipyrimidine photo-lyase
YDR287w YLR150w	MPT4	similarity to inositol monophosphatase specific affinity for guanine-rich	YDR436w	PPZ2	protein ser/thr phosphatase of the PP-1 family	YOR368w YER176w	RAD17	DNA damage checkpoint control protein DNA dependent ATPase/DNA helicase B
		quadruplex nucleic acids	YOR208w	PTP2	protein-tyrosine-phosphatase	YLR032w	RAD5	DNA helicase
YPR054w YNL132w	SMK1	sporulation-specific MAP kinase strong similarity to A. ambisexualis	YJR090c	GRR1	required for glucose repression and for glucose and cation transport	YIL143c YML061c	SSL2 PIF1	DNA helicase DNA helicase involved in mitochondrial
YHR206w	QVN17	antheridiol steroid receptor transcription factor with similarity to Hsf1p	YPL084w	BRO1	required for normal response to nutrient limitation	YER171w	RAD3	DNA repair and telomere length DNA helicase/ATPase
TTITIZOOW	OKIVI	transcription ractor with similarity to hisrip	YKL164c	PIR1	required for tolerance to heat-shock	YDL164c	CDC9	DNA ligase
0.11			YPR005c YNL160w	HAL1 YGP1	salt-induced protein secreted glycoprotein	YEL019c YAL015c	MMS21 NTG1	DNA repair protein DNA repair protein
Cellr	escu	е	YGL190c	CDC55	ser/thr phosphatase 2A regulatory subunit B	YMR137c YML095c	PSO2 RAD10	DNA repair protein DNA repair protein
stress	respons	se generation	YML016c	PPZ1	ser/thr phosphatase required for normal	YCR066w	RAD18	DNA repair protein
YFR052w	NINI1	26S proteasome regulatory subunit	YJL165c	HAL5	osmoregulation ser/thr protein kinase	YER095w YDR076w	RAD51 RAD55	DNA repair protein DNA repair protein
YIL075c	SEN3	26S proteasome regulatory subunit	YOR231w	MKK1	ser/thr protein kinase	YDR004w	RAD57	DNA repair protein
YDR074w	TPS2	α,α-trehalose-phosphate synthase, 105K subunit	YBL105c YLR113w	PKC1 HOG1	ser/thr protein kinase ser/thr protein kinase of MAP kinase	YOR346w YDR369c	REV1 XRS2	DNA repair protein DNA repair protein
YBR126c	TPS1	α,α-trehalose-phosphate synthase, 56K		SLT2	(MAPK) family	YGL163c	RAD54	DNA-dependent ATPase of the Snf2p
YPR026w		subunit acid trehalase, vacuolar	YHR030c	ULIZ	ser/thr protein kinase of MAP kinase family	YDL102w	CDC2	family DNA-directed DNA polymerase δ,
YIL033c	SRA1	cAMP dependent protein kinase, regulatory subunit	YDL025c		ser/thr protein kinase of the DEAD/DEAH box family	YFR023w	PES4	catalytic 125K subunit DNA-directed DNA polymerase ε
YDR477w	SNF1	carbon catabolite derepressing ser/thr	YJL095w	BCK1	ser/thr protein kinase of the MEKK family			suppressor
YHR135c	YCK1	protein kinase casein kinase I isoform	YER167w	BCK2	ser/thr protein kinase of the protein kinase C pathway	YNL262w	POL2	DNA-directed DNA polymerase ε, catalytic subunit A
YNL154c YGR088w	YCK2	casein kinase I isoform catalase T, cytosolic	YDR227w YKL088w	SIR4	silencing regulatory protein similarity to <i>C. tropicalis</i> hal3 protein, to C-	YPL167c YKR056w	REV3 RNC1	DNA-directed DNA polymerase ζ endo-exonuclease
YDR251w		coiled-coil protein multicopy suppressor	TIKLOOOW		term. of Sis2p and to hypothetical protein	YOL043c	NTG2	endonuclease III-like glycosylase 2
YOR010c	TIR2	of loss of PP2A cold shock induced protein	YBR044c		YOR054c similarity to chaperonin HSP60 proteins	YER162c YLR288c	RAD4 MEC3	excision repair protein G2-specific checkpoint protein
YER011w	TIR1	cold-shock induced protein of the Tir1p,	YJR147w		similarity to heat-shock transcription	YFL014w	HSP12 MMS19	heat-shock protein
YDR155c	CPH1	Tip1p family cyclophilin (peptidylprolyl isomerase)	YGR249w	MGA1	factors similarity to heat-shock transcription	YIL128w		involved in repair and RNA polymerase transcription
YEL039c YER062c	CYC7 HOR2	cytochrome c isoform 2 DL-glycerol phosphatase	YBR054w	YRO2	factors similarity to HSP30 heat-shock protein	YMR035w	IMP2	mitochondrial inner membrane protease subunit
YDR263c	DIN7	DNA damage inducible protein DNA damage-responsive protein			Yro1p	YKR095w	MLP1 RAD14	myosin-like protein related to Uso1p
YGL021w YAL015c	NTG1	DNA repair protein	YAR020c		similarity to members of the Srp1p/Tip1p family	YMR201c YBR114w	RAD16	nucleotide excision repair protein nucleotide excision repair protein
YDR519w	FKB2	FK506/rapamycin-binding protein of the ER	YCR008w	SAT4	similarity to Npr1p and Hal5p protein kinases	YEL037c YJR052w	RAD23 RAD7	nucleotide excision repair protein nucleotide excision repair protein
YGR234w YIR037w	YHB1 HYR1	flavohemoglobin glutathione peroxidase	YOR009w YCR060w		similarity to SRP1 and TIR2 proteins similarity to stress inducible protein Sti1p	YDL200c	MGT1	O6-methylguanine DNA repair methyltransferase
YLL043w	FPS1	glycerol channel protein	YMR037c		stress responsive regulatory protein	YDL101c	DUN1	protein kinase
YNL098c YHR064c	RAS2	GTP-binding protein heat-shock protein	YOR027w YBL009w	STI1	stress-induced protein strong similarity to DNA damage	YML032c YIL139c	RAD52 REV7	recombination and DNA repair protein required for DNA damage induced
YMR173w YOL052c-a		heat-shock protein			responsive Alk1p			mutagenesis
YMR186w	HSC82	heat-shock protein heat-shock protein	YLR369w		strong similarity to heat-shock protein 70- related proteins	YBR073w YIL066c	RDH54 RNR3	required for meiosis ribonucleotide reductase, repair inducible
YLL026w YFL014w		heat-shock protein heat-shock protein	YHL046c		strong similarity to members of the Srp1p/Tip1p family	YPL153c	SPK1	large subunit ser/thr/tyr protein kinase
YBR072w	HSP26	heat-shock protein	YIL011w		strong similarity to members of the	YDR061w	0, 11,	similarity to E. coli deoxyribodipyrimidine
YCR021c YPL240c	HSP30 HSP82	heat-shock protein heat-shock protein	YOL161c		Srp1p/Tip1p family strong similarity to members of the	YAL019w	FUN30	photolyase similarity to helicases of the Snf2/Rad54
YFL016c YLR259c	MDJ1 HSP60	heat-shock protein - chaperone heat-shock protein - chaperone,	YJL223c	PAU1	Srp1p/Tip1p family strong similarity to members of the	YLR035c		family similarity to human mutL protein
		mitochondrial			Srp1p/Tip1p family			homologue
YJR045c	SSC1	heat-shock protein 70-related protein, mitochondrial	YEL049w	PAU2	strong similarity to members of the Srp1p/Tip1p family	YPR056w		similarity to human transcription factor BTF2/TFIIH subunit p34
YDR258c	HSP78	heat-shock protein of clpb family of ATP- dependent proteases, mitochondrial	YCR104w	PAU3	strong similarity to members of the Srp1p/Tip1p family	YFR038w		strong similarity to mouse lymphocyte specific helicase
YEL030w	QQA+	heat-shock protein of HSP70 family heat-shock protein of HSP70 family	YFL020c	PAU5	strong similarity to members of the	YOR206W	RAD2	strong similarity to Rad4p
YAL005c YER103w	SSA1 SSA4	heat-shock protein of HSP70 family	YLR461w	PAU4	Srp1p/Tip1p family strong similarity to members of the	YGR258c		structure-specific nuclease of the nucleotide excision repairosome
YPL106c YLL024c	SSE1 SSA2	heat-shock protein of HSP70 family heat-shock protein of HSP70 family,	YNR076w	PAU6	Tir1p/Tip1p family strong similarity to members of the	YDL088c	ASM4	suppressor of temperature-sensitive mutations in Pol3p
		cytosolic		50	Tir1p/Tip1p family	YDR311w	TFB1	TFIIH subunit (transcription initiation
YBL075c	SSA3	heat-shock protein of HSP70 family, cytosolic	YDR033w		strong similarity to putative heat-shock protein Yro2p	YPR025c	CCL1	factor), 75K TFIIH subunit (transcription initiation
YBR169c YGL073w	SSE2 HSF1	heat-shock protein of the HSP70 family heat-shock transcription factor	YKL161c		strong similarity to ser/thr-specific protein kinase Slt2p	YLR005w	SSL1	factor), cyclin C component TFIIH subunit (transcription initiation
YMR251w-	aHOR7	hyperosmolarity-responsive protein	YOR054c		strong similarity to SIS2 protein and C.			factor), factor B
YMR273c		involved in negative regulation of cell polarity	YBR067c	TIP1	tropicalis hal3 protein temp.shock induced protein of the	YPL122c YDR460w	TFB2 TFB3	TFIIH subunit (transcription/repair factor) TFIIH subunit (transcription/repair factor)
YER118c	SSU81	involved in the <i>HOG1</i> high-osmolarity signal transduction pathway	YGR144w	THI4	Srp1p/Tip1p family thiamine-repressed protein	YGL058w	RAD6	ubiquitin-conjugating enzyme
YDR293c	SSD1	involved in the tolerance to high	YBL093c	ROX3	transcription factor	detoxif	icaton	
YKL143w	LTV1	concentration of Ca <sup>2+</sup> low-temperature viability protein	YGL181w	GTS1	transcription factor of the Gcs1p/Glo3p/Sps18p family	YOL052c	SPE2	adenosylmethionine decarboxylase
YGR100w YCR073c	MIC1 SSK22	Mac1p interacting protein MAP kinase kinase kinase	YMR043w	MCM1	transcription factor of the MADS box family	YFL050c YML116w	ALR2 ATR1	aluminum resistance protein aminotriazole and 4-nitroguinoline
YNR031c	SSK2	MAP kinase kinase kinase of the high-	YHR206w		transcription factor with similarity to Hsf1p			resistance protein
YJL158c		osmolarity signal transduction pathway member of the Pir1p/Hsp150p/Pir3p	YKL062w YML007w		transcriptional activator transcriptional activator involved in	YNL259c	ATX1	antioxidant protein and metal homeostasis factor
YJL159w		family member of the Pir1p/Hsp150p/Pir3p	YIL147c	SLN1	oxidative stress response two-component signal transducer	YLR398c YKL004w	SKI2 AUR1	antiviral protein and putative helicase aureobasidin-resistance protein
		family	YLR006c	SSK1	two-component signal transducer	YDR256c	CTA1	catalase A, peroxisomal
YJL160c		member of the Pir1p/Hsp150p/Pir3p family	YJL128c	PBS2	tyrosine protein kinase of the MAP kinase kinase family	YGR088w YJR104c	CTT1 SOD1	catalase T, cytosolic copper-zinc superoxide dismutase
YKL163w YMR021c	PIR3 MAC1	member of the Pir1p/Pir2p/Pir3p family metal binding activator	YLL039c YMR022w	UBI4 QRI8	ubiquitin ubiquitin-conjugating enzyme	YKR066c YPR198w	CCP1 SGE1	cytochrome c peroxidase drug resistance protein
YNL064c	YDJ1	mitochondrial and ER import protein	YBR082c	UBC4	ubiquitin-conjugating enzyme	YJL101c	GSH1	glutamate-cysteine ligase

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YDR513w TTR1	glutaredoxin	YNL066w		involved in the ageing process	YJR067c	YAE1	protein of unknown function
YPL091w GLR1 YDR135c YCF1	glutathione reductase (NADPH) glutathione S-conjugate transporter,	YKR042w YHL003c	UTH1 LAG1	involved in the ageing process longevity-assurance protein	YGR172c YNL044w	YIP1 YIP3	protein of unknown function protein of unknown function
I DIVISSC TOLL	vacuolar	YER167w	BCK2	ser/thr protein kinase of the protein	YBR111c	YSA1	protein of unknown function
YGR197c SNG1	involved in nitroguanidine resistance	\/D.D007	0/04	kinase C pathway	YGR123c	PPT1	protein ser/thr phosphatase
YDL168w SFA1 YCR023c	long-chain alcohol dehydrogenase member of major facilitator superfamily	YDR227w YKL008c	SIK4	silencing regulatory protein strong similarity to Lag1p	YDL230w YER075c	PTP1 PTP3	protein tyrosine phosphatase protein tyrosine phosphatase
	multidrug-resistance protein family 2	YIL123w		strong similarity to Sun4p,Nca3p	YPR073c	LTP1	protein-tyrosine-phosphatase
YNR055c HOL1	member of major facilitator superfamily multidrug-resistance protein subfamily 1	doarad	ation of	exogenous polynucleotides	YNL128w YCL039w		putative phosphatase regulatory protein of the β-transducin
YHR053c CUP1A	metallothionein	uegrau	ationoi	exogenous polynucieotides	I CLUSSW		family
YHR055c CUP1B	metallothionein	YGL213c	SKI8	antiviral protein of the β-transducin (WD-	YJR055w	HIT1	required for growth at high temperature
YOR079c ATX2	multicopy suppressor of SOD-linked defects			40) repeat family	YNL085w	MKT1	required for propagation of M2 dsRNA satellite of L-A virus
YDR011w SNQ2	multidrug resistance protein	other c	ell-resc	ue activities	YLL046c	RNP1	ribonucleoprotein
YHR042w NCP1 YOR018w ROD1	NADPH-cytochrome P450 reductase O-dinitrobenzene,calcium and zinc	YPR189w	SKI3	antiviral protein	YOR046c YDR466w	DBP5	RNA helicase ser/thr protein kinase
	resistance protein	YJR069c	HAM1	controls 6-N-hydroxylaminopurine	YDR490c		ser/thr protein kinase
YKL064w MNR2	overexpression overcomes manganese	VODO40+	DTA	sensitivity and mutagenesis	YGL179c		ser/thr protein kinase
YOR266w PNT1	toxicity pentamidine resistance factor	YGR213c YKL110c	RTA1 KTI12	involved in 7-aminocholesterol resistance involved in resistance to K. lactis killer	YGL180w YKL168c		ser/thr protein kinase ser/thr protein kinase
YDR538w PAD1	phenylacrylic acid decarboxylase			toxin	YKL171w		ser/thr protein kinase
YOR153w PDR5 YBL005w PDR3	pleiotropic drug resistance protein pleiotropic drug resistance regulatory	YER076c YER187w		similarity to killer toxin Khr1p similarity to killer toxin KHS	YLR063w YMR291w		ser/thr protein kinase ser/thr protein kinase
TBEOOSW TBNS	protein	I LIVIO/W		Similarity to killer toxiii Kirio	YNL161w		ser/thr protein kinase
YGL016w PDR6	pleiotropic drug resistance regulatory				YOL045w YOL100w		ser/thr protein kinase
YIL120w	protein similarity to antibiotic resistance proteins	Uncla	assific	e <b>d proteins</b>	YAR018c	KIN3	ser/thr protein kinase ser/thr protein kinase
YIL121w	similarity to antibiotic resistance proteins				YOR233w	KIN4	ser/thr protein kinase
YLR299w	similarity to <i>B. subtilis</i> γ-glutamyltransferase	YEL052w YDR184c	AFG1 BAT1	ATPase family gene binds Aip3p	YCR091w YLL019c	KIN82 KNS1	ser/thr protein kinase ser/thr protein kinase
YHL040c	similarity to C. carbonum toxin pump	YCR072c		β-transducin family (WD-40 repeat) protein	YHR082c	KSP1	ser/thr protein kinase
YHL047c	similarity to C. carbonum toxin pump	YLR459w	CDC91	cell division control protein	YDL079c	MRK1	ser/thr protein kinase
YBR180w YDL100c	similarity to drug resistance proteins similarity to <i>E. coli</i> arsenical pump-driving	YJL079c	PRY1	contains homology to the plant PR-1 class of pathogen related proteins	YOR267c		ser/thr protein kinase with similarity to Npr1p
	ATPase	YKR013w	PRY2	contains homology to the plant PR-1	YMR216c		ser/thr protein kinase with similarity to S.
YLL015w YBR293w	similarity to metal resistance proteins similarity to multidrug resistance proteins	YJL078c	PRY3	class of pathogen related proteins contains homology to the plant PR-1	YKL116c		pombe dsk1 ser/thr protein kinase with similarity to S.
YGR138c	similarity to multidrug resistance proteins			class of pathogen related proteins			pombe nim1 protein
YHR048w YKR103w	similarity to multidrug resistance proteins	YOR302W	CPA1-I DAT1	CPA1 leader peptide	YBL056w YDR507c	PTC3 GIN4	ser/thr protein phosphatase PP2C ser/thr-protein kinase
YKR104w	similarity to multidrug resistance proteins similarity to multidrug resistance proteins	YML113w YKL020c	SPT23	datin, oligo(dA)/oligo(dT)-binding protein dosage-dependent suppressor of Ty-	YKL126w	YPK1	ser/thr-specific protein kinase
YLL028w	similarity to multidrug resistance proteins			induced promotor mutations	YOR007c		similarities to protein phosphatases
YPR156c YOR273c	similarity to multidrug resistance proteins similarity to resistance proteins	YJL168c YOR123c	EZL1 LEO1	enhancer of zeste-like extremely hydrophilic protein	YOR119c YLR405w	RIO1	similarity to a <i>C. elegans</i> ZK632.3 protein similarity to <i>A. brasilense</i> nifR3 protein
YOR251c	similarity to resistance proteins	YLL065w	GIN11	growth inhibitory protein	YML079w		similarity to A. brasilense nift3 protein
VOD047	sulphurtransferases	YDL213c		has an RNA recognition domain in the N-	YML080w		similarity to A. brasilense nifR3 protein
YOR247w	similarity to vanadate-sensitive suppressor Svs1p	YDR505c	PSP1	terminal region high copy suppressor of ts of mutations	YDR205w		similarity to A. eutrophus cation efflux system membrane protein czcD, rat zinc
YJR025c	strong similarity to 3-hydroxyanthranilate	YNL087w		in DNA polymerase α	VDI 000+		transport protein ZnT-1 and Cot1p
YOL130w	3,4-dioxygenase strong similarity to Alr2p	YLR161w		homology to YOR086c identical to hypothetical proteins YLR156w	YDL228c		similarity to A. klebsiana glutamate dehydrogenase
YMR279c	strong similarity to aminotriazole	\/I D450		and YLR161w	YLL005c		similarity to A. thaliana hyp1 protein
YOR378w	resistance protein strong similarity to aminotriazole	YLR156w		identical to hypothetical proteins YLR159w and YLR161w	YMR266w YOL084w		similarity to A. thaliana hyp1 protein similarity to A. thaliana hyp1 protein
	resistance protein	YLR159w		identical to hypothetical proteins YLR161w	YNL317w		similarity to A. thaliana PRL1 protein
YBR008c	strong similarity to benomyl/methotrexate resistance protein	YHR212c		and YLR156w identical with hypothetical protein	YOL105c		similarity to a-agglutinin core protein AGA1 and mucin proteins
YCL069w	strong similarity to drug resistance protein			YAR060c	YPL252c		similarity to adrenodoxin and ferrodoxin
YKL026c	SGE1 strong similarity to glutathione peroxidase	YHR214w		identical with hypothetical protein YAR066w	YMR110c YIL112w		similarity to aldehyde dehydrogenase similarity to ankyrin and coiled-coil
YBR244w	strong similarity to glutathione	YAR066w		identical with hypothetical protein YIL169c			proteins
YKL033w-a	peroxidases strong similarity to holacid-	YCR020c-a	MAK31	involved in stability of L-A dsRNA- containing particles	YLR064w		similarity to Anopheles NADH-ubiquinone oxidoreductase, subunit 4
	halidohydrolase	YPL049c	DIG1	MAP kinase-associated protein, down-	YMR153w		similarity to Asm4p
YFR022w YLR046c	strong similarity to Rod1p strong similarity to Rta1p and Rtm1p	YKL034w		regulator of invasive growth member of Kazal serine protease	YDR349c YDR072c		similarity to aspartyl proteases similarity to Aur1p
I LINOHOC	protein	I NLUS4W		inhibitors family	YMR305c		similarity to Au τρ similarity to B. japonicum putative β-(-6)
YER185w	strong similarity to Rtm1p strong similarity to Sge1p and	YLR397c	AFG2	member of the Sec18p, Pas1p, Cdc48p,	VDD004		glucan transferase similarity to <i>B. subtilis</i> helicases
YKR105c	hypothetical protein YCL069w	YCR007c		TBP-1 family of ATPases member of the YBR302c family	YDR291w YPR201w		similarity to <i>B. subtilis</i> hypothetical protein
YJR015w	strong similarity to Sng1p	YGL036w		Mtf1 two hybrid clone 2	YPR002w		similarity to B. subtilis mmgE protein
YNR070w YBL064c	strong similarity to Snq2p strong similarity to thiol-specific	YMR200w YAL059w	ROT1 SIM1	mutant suppresses tor2 mutation mutants are hypersensitive to calcofluor	YPL258c		similarity to <i>B. subtilis</i> transcriptional activator tenA, and strong similarity to
	antioxidant enzyme			white			hypothetical proteins YOL055c and
YDR453c	strong similarity to thiol-specific antioxidant protein	YCR019w	MAK32	necessary for structural stability of L-A dsRNA-containing particles	YPR121w		YPR121w similarity to <i>B. subtilis</i> transcriptional
YGL254w FZF1	sulphite resistance protein	YNL061w	NOP2	nucleolar protein	111112100		activator tenA, strong similarity to
YPL092w SSU1 YHR008c SOD2	sulphite sensitivity protein	YFR011c	PWP1	ochre suppressor tyr-tRNA			hypothetical proteins YPL258c and
YHRUU8C SUD2 YOR031w CRS5	superoxide dismutase (Mn), mitochondrial suppressor of <i>cup1</i> deletion.	YLR196w YDL235c	YPD1	periodic tryptophan protein phosphorelav intermediate between SIn1p	YIL159w		YOL055c similarity to BNI1 protein
	metallothionein-like protein			and Ssk1p	YDL119c		similarity to bovine Graves disease carrier
YML028w TSA1 YLR043c TRX1	thiol-specific antioxidant thioredoxin I	YOR014w	RTS1	potential regulatory subunit of protein phosphatase 2A	YNR068c		protein similarity to Bul1p
YGR209c TRX2	thioredoxin II	YOR181w		proline-rich protein	YNL218w		similarity to C. burnetii trxB, spollIE and
YGL013c PDR1	transcription factor	YER129w	PAK1	protein kinase protein of unknown function	YCR102c		serS genes
YMR043w MCM1	transcription factor of the MADS box family	YOR223w YHR093w		protein of unknown function	YNL134c		similarity to <i>C. carbonum</i> toxD gene similarity to <i>C. carbonum</i> toxD gene
YDR423c CAD1	transcriptional activator	YDL167c		protein of unknown function	YJR013w		similarity to <i>C. elegans</i> B0491.1 protein
YPL163c SVS1 YLL060c	vanadate sensitive suppressor weak similarity to glutathione transferase	YHR191c YAL008w	CTF8 FUN14	protein of unknown function protein of unknown function	YPR040w YGR257c		similarity to <i>C. elegans</i> C02C2.6 protein similarity to <i>C. elegans</i> C16C10.1
YMR243c ZRC1	zinc- and cadmium resistance protein	YAR002w	FUN17	protein of unknown function	YGR054w		similarity to C. elegans E04D5.1 protein
detoxification invol	ving cytochrome P450	YAR014c	FUN2 FUN21	protein of unknown function	YMR012w		similarity to <i>C. elegans</i> hypothetical
YMR015c ERG5	C-22 sterol desaturase	YAL031c YAL014c	FUN21 FUN34	protein of unknown function protein of unknown function	YLR022c		139.9K protein F55H2.6 similarity to <i>C. elegans</i> hypothetical
YDR402c DIT2	cytochrome P450 56	YAR008w	FUN4	protein of unknown function			protein
YHR007c ERG11	cytochrome P450 lanosterol 14a- demethylase	YAL033w YDL234c	FUN53 GYP7	protein of unknown function protein of unknown function	YNL127w		similarity to <i>C. elegans</i> hypothetical protein
YLL057c	similarity to E. coli dioxygenase	YPL054w	LEE1	protein of unknown function	YKL095w	YJU2	similarity to <i>C. elegans</i> hypothetical
YDR403w DIT1	spore wall maturation protein	YDR335w YIR006c	MSN5 PAN1	protein of unknown function protein of unknown function	YML014w		protein similarity to <i>C. elegans</i> hypothetical
cell death and a	ageing	YDL105w	QRI2	protein of unknown function			protein C14B1.5
YOR101w RAS1	GTP-binding protein	YLR204w YLL003w	QRI5 SFI1	protein of unknown function protein of unknown function	YKL099c		similarity to <i>C. elegans</i> hypothetical protein C16C10.2
YNL098c RAS2	GTP-binding protein	YDR350c	TCM10	protein of unknown function	YEL004w		similarity to <i>C. elegans</i> hypothetical
YOL025w LAG2	involved in determining longevity	YDL169c	UGX2	protein of unknown function	VI II 222		protein C53B4.6
YJL116c NCA3	involved in regulation of synthesis of Atp6p and Atp8p	YJR050w YEL035c	UTR3 UTR5	protein of unknown function protein of unknown function	YHL030w		similarity to <i>C. elegans</i> hypothetical protein D2045.2
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YOL093w	similarity to C. elegans hyp	pothetical   YLR050c		similarity to human MAC30 C-terminus	YGL228w	similarity to hypothetical protein YFR039c
	protein F25H8.1	YCR071c		similarity to human NOF1 protein	YBR281c	similarity to hypothetical protein YFR044c
YDL008w	similarity to C. elegans hyp	pothetical YOR001w		similarity to human nucleolar 100K	YDL001w	similarity to hypothetical protein YFR048w,
	protein F35G12.9			polymyositis-scleroderma protein		YDR282c and S. pombe hypothetical
YKL151c	similarity to C. elegans hyp	pothetical YEL016c		similarity to human nucleotide		protein SPAC12G12.14
VDD400	protein R107.2			pyrophosphatase	YPL216W	similarity to hypothetical protein YGL133w
YDR196c	similarity to <i>C. elegans</i> hyp	pothetical YIL153w		similarity to human phosphotyrosyl	YPL219w	similarity to hypothetical protein YGL134w
YJL029c	protein T05G5.5 similarity to <i>C. elegans</i> hyp	pothetical YDR280w		phosphatase activator similarity to human PM-ScI-75 autoantigen	YDR444w	similarity to hypothetical protein YGL144c and YDL1009c
17110290	protein T05G5.8	YPR108w		similarity to human protein GPS1	YLR047c	similarity to hypothetical protein YGL160w
YNL223w	similarity to <i>C. elegans</i> hyp			similarity to human protein KIAA0171 and	YER132c	similarity to hypothetical protein YGL197w
ITTELLOW	protein ZK792.1	7212000		hypothetical protein YDL161w	YFR039c	similarity to hypothetical protein YGL228w
YOL003c	similarity to C. elegans hyp	pothetical YNL265c		similarity to human protein KIAA0174	YHR036w	similarity to hypothetical protein YGL247w
	protein, YDR126w, YNL326			similarity to human ragA protein	YGR031w	similarity to hypothetical protein YGR015c
YDR049w	similarity to C. elegans K06	6H7.3 protein YDR096w	GIS1	similarity to human retinoblastoma	YGR015c	similarity to hypothetical protein YGR031w
YGR278w	similarity to C. elegans LE			binding protein 2	YBR105c	similarity to hypothetical protein YGR066c
YHR004c	similarity to C. elegans SPA			similarity to human Sm protein F	YLR373c	similarity to hypothetical protein YGR071c
V/1 41 050	protein	YGR112w		similarity to human SURF-1 protein	YPR158w	similarity to hypothetical protein YGR142w
YML059c	similarity to C. elegans ZK			similarity to human tyrosine kinase A6	YHR149c YHR158c	similarity to hypothetical protein YGR221c
YNL168c	similarity to <i>C. elegans</i> ZK6 and <i>E. coli</i> hpcEp	688.3 protein YDL060w		similarity to hypothetical <i>C. elegans</i> protein	YMR295c	similarity to hypothetical protein YGR238c similarity to hypothetical protein YGR273c
YPR188c	similarity to calmodulin and	id calmodulin- YDR183w		similarity to hypothetical <i>C. elegans</i>	YMR310c	similarity to hypothetical protein YGR283c
11111000	related proteins	a carriodanii		protein	YDR338c	similarity to hypothetical protein YHR032w
YPR128c	similarity to carrier protein	FLX1 YDR427w		similarity to hypothetical C. elegans	YGL247w	similarity to hypothetical protein YHR036w
YPL202c	similarity to cell size regula	ation protein		protein	YDR309c	similarity to hypothetical protein YHR061c
	Rcs1p	YDR473c		similarity to hypothetical C. elegans	YNL075w	similarity to hypothetical protein YHR088w
YPR154w	similarity to chicken growth			protein	YDR348c	similarity to hypothetical protein YHR097c
	receptor-binding protein GI			similarity to hypothetical C. elegans	YNL144c	similarity to hypothetical protein YHR131c
YNL091w	similarity to chicken h-cald and hypothetical protein YI			protein	YNL156c	similarity to hypothetical protein YHR133c
VDI 1760	similarity to chinese hamst			similarity to hypothetical C. elegans	YGR221c YOR147w	similarity to hypothetical protein YHR149c
YPL176c	receptor protein	YGR194c		protein similarity to hypothetical <i>C. elegans</i>	YER175c	similarity to hypothetical protein YHR194w similarity to hypothetical protein YHR209w
YDR259c	similarity to Cin5p	1311340		protein	YJR108w	similarity to hypothetical protein YIL015c-a
YGL241w	similarity to Cse1p	YGR245c		similarity to hypothetical C. elegans	YER064c	similarity to hypothetical protein YIL056w
YNL305c	similarity to C-term. of A. n	nidulans		protein	YLR036c	similarity to hypothetical protein YIL089w
	regulatory protein (qutR)	YHL010c		similarity to hypothetical C. elegans	YFL034c-b	similarity to hypothetical protein YIL106w
YPR127w	similarity to C-term. of N. ta			protein	YNL058c	similarity to hypothetical protein YIL117c
VDI	induced protein	YJR070c		similarity to hypothetical C. elegans	YNL074c YMK1	similarity to hypothetical protein YIL135c
YDL112w	similarity to C-terminus of I			protein	YKR100c	similarity to hypothetical protein YIL158w
YMR304w	protein similarity to <i>D. melanogast</i>	YML094w	1	similarity to hypothetical <i>C. elegans</i> protein	YKR015c YBR273c	similarity to hypothetical protein YJL043w similarity to hypothetical protein YJL048c
11011130400	gene	YMR002v	,	similarity to hypothetical <i>C. elegans</i>	YLL031c	similarity to hypothetical protein YJL062w
YGR003w	similarity to D. melanogast		•	protein	YKR010c	similarity to hypothetical protein YJL076w
YLL013c	similarity to D. melanogast			similarity to hypothetical C. elegans	YKR019c	similarity to hypothetical protein YJL083w
	protein	·		protein and YLR243w	YKR029c	similarity to hypothetical protein YJL105p
YNL023c	similarity to D. melanogast	ter shuttle craft YOL060c		similarity to hypothetical C. elegans	YDR131c	similarity to hypothetical protein YJL149w
	protein			protein M02F4.4	YDL123w	similarity to hypothetical protein YJL151c
YKL201c	similarity to D. melanogast	ter sperm-tail- YDL097c		similarity to hypothetical C. elegans	YBR162c	similarity to hypothetical protein YJL171c
VOI 001	specific protein	VED004-		proteins	YJR030c	similarity to hypothetical protein YJL181w
YCL001w-a	similarity to Dom34p	YER004w		similarity to hypothetical E. coli and C.	YJL181w YPR114w	similarity to hypothetical protein YJR030c
YIL103w YGL018c	similarity to Dph2 protein similarity to E. coli dnaJ ho	omologue YDL238c		elegans proteins similarity to hypothetical E. coli protein	YKL002w	similarity to hypothetical protein YJR116w similarity to hypothetical protein YKL041w
YHL014c YL				similarity to hypothetical L. con protein	YMR031c	similarity to hypothetical protein YKL050c
YLR011w	similarity to E. coli hypothe			protein		and human restin
	protein	YDR496c		similarity to hypothetical human protein	YMR086w	similarity to hypothetical protein YKL105c
YGL037c	similarity to E. coli hypothe	etical 23K YDR524c		similarity to hypothetical human protein	YMR171c	similarity to hypothetical protein YKL124w
	protein	YHR098c		similarity to hypothetical human protein	YMR115w	similarity to hypothetical protein YKL133c
YOR131c	similarity to E. coli hypothe			similarity to hypothetical human protein	YNL101w	similarity to hypothetical protein YKL146w
V/DD 400	protein	YOR215c		similarity to hypothetical M. xanthus	YJL076w	similarity to hypothetical protein YKR010c
YDR400w	similarity to E. coli hypothe			protein	YJL043w	similarity to hypothetical protein YKR015c similarity to hypothetical protein YKR019c
YDR539w	protein in nfo-frua intergen similarity to E. coli hypothe			similarity to hypothetical mouse protein similarity to hypothetical <i>N. crassa</i> 32K	YJL083w YJL105w	similarity to hypothetical protein YKR019C similarity to hypothetical protein YKR029c
10110000	protein in rfah-rfe intergeni			protein	YIL158W	similarity to hypothetical protein YKR100c
YDR332w						
		etical protein YOR324c				
YGR021w	similarity to <i>E. coli</i> hypothe similarity to <i>E. coli</i> hypothe			similarity to hypothetical protein YAL028w	YLR019w	similarity to hypothetical protein YLL010c similarity to hypothetical protein YLL010c similarity to hypothetical protein YLR008c
	similarity to E. coli hypothe	etical protein YOR371c				similarity to hypothetical protein YLL010c
YGR021w YJL046w YIL003w	similarity to <i>E. coli</i> hypothe similarity to <i>E. coli</i> hypothe similarity to <i>E. coli</i> lipoate-p similarity to <i>E. coli</i> MRP pr	etical protein YOR371c protein ligase A YJR115w rotein YER093c-		similarity to hypothetical protein YAL028w similarity to hypothetical protein YAL056w similarity to hypothetical protein YBL043w similarity to hypothetical protein YBL059w	YLR019w YNL328c	similarity to hypothetical protein YLL010c similarity to hypothetical protein YLR008c
YGR021W YJL046W YIL003W YOR165W	similarity to <i>E. coli</i> hypothe similarity to <i>E. coli</i> hypothe similarity to <i>E. coli</i> lipoate- similarity to <i>E. coli</i> MRP pri similarity to <i>E. histolytica</i> s	etical protein YOR371c protein ligase A YJR115w rotein YER093c- surface lectin YPR030w		similarity to hypothetical protein YAL028w similarity to hypothetical protein YAL056w similarity to hypothetical protein YBL043w similarity to hypothetical protein YBL059w similarity to hypothetical protein YBL101c	YLR019w YNL328c YPL063w	similarity to hypothetical protein YLL010c similarity to hypothetical protein YLR008c similarity to hypothetical protein YLR019w and <i>S. pombe</i> hypothetical protein SPAC2F7.02c
YGR021w YJL046w YIL003w	similarity to <i>E. coli</i> hypothe similarity to <i>E. coli</i> hypothe similarity to <i>E. coli</i> lipoate- similarity to <i>E. coli</i> MRP pr similarity to <i>E. histolytica</i> s similarity to <i>E. histolytica</i> n	etical protein YOR371c protein ligase A YJR115w rotein YER093c- surface lectin yPR030w nitrogen fixation YMR101c		similarity to hypothetical protein YAL028w similarity to hypothetical protein YAL056w similarity to hypothetical protein YBL043w similarity to hypothetical protein YBL059w similarity to hypothetical protein YBL101c similarity to hypothetical protein YBR002c	YLR019w YNL328c YPL063w YIL089w	similarity to hypothetical protein YLL010c similarity to hypothetical protein YLR008c similarity to hypothetical protein YLR019w and <i>S. pombe</i> hypothetical protein SPAC2F702c similarity to hypothetical protein YLR036c
YGR021w YJL046w YIL003w YOR165w YNR015w SN	similarity to <i>E. coli</i> hypothe similarity to <i>E. coli</i> inpothe similarity to <i>E. coli</i> lipoate- similarity to <i>E. coli</i> MRP pn similarity to <i>E. histolytica</i> s similarity to <i>E. histolytica</i> n regulatory protein-3 homol	etical protein protein ligase A rotein surface lectin hitrogen fixation logue  YOR371c YJR115w YER093c- YPR030w YMR101c YGR066c		similarity to hypothetical protein YAL028w similarity to hypothetical protein YAL056w similarity to hypothetical protein YBL043w similarity to hypothetical protein YBL043w similarity to hypothetical protein YBL059w similarity to hypothetical protein YBL010tc similarity to hypothetical protein YBR002c similarity to hypothetical protein YBR105c	YLR019W YNL328c YPL063W YIL089W YLL023c	similarity to hypothetical protein YLL010c similarity to hypothetical protein YLR008c similarity to hypothetical protein YLR019w and <i>S. pombe</i> hypothetical protein SPAC2F702c similarity to hypothetical protein YLR036c similarity to hypothetical protein YLR036w
YGR021W YJL046W YIL003W YOR165W YNR015W SN YER113c	similarity to <i>E. coli</i> hypothe similarity to <i>E. coli</i> hypothe similarity to <i>E. coli</i> lipoate- similarity to <i>E. coli</i> MRP pr similarity to <i>E. histolytica</i> s similarity to <i>E. histolytica</i> n regulatory protein-3 homol similarity to Emp70p	etical protein protein ligase A protein ligase A rotein surface lectin very protein surface lectin very protein very prote		similarity to hypothetical protein YAL028w similarity to hypothetical protein YAL066w similarity to hypothetical protein YBL043w similarity to hypothetical protein YBL043w similarity to hypothetical protein YBL059w similarity to hypothetical protein YBR002c similarity to hypothetical protein YBR002c similarity to hypothetical protein YBR105c similarity to hypothetical protein YBR162c	YLR019W YNL328c YPL063W YIL089W YLL023c YFL043c	similarity to hypothetical protein YLL010c similarity to hypothetical protein YLR008c similarity to hypothetical protein YLR019w and S. pombe hypothetical protein SPAC2F702c similarity to hypothetical protein YLR036c similarity to hypothetical protein YLR036c similarity to hypothetical protein YLR046w similarity to hypothetical protein YLR072w
YGR021W YJL046W YIL003W YOR165W YNR015W <i>SN</i> YER113C YDR036C	similarity to E. coli hypothe similarity to E. coli inpoate- similarity to E. coli ilipoate- similarity to E. coli MRP pri similarity to E. histolytica similarity to E. histolytica similarity to Enpropriational programme	etical protein protein ligase A rotein surface lectin hitrogen fixation logue  dratase  YOR371c YJR115w YER030c YJR030c YMR101c YGR066c YJL171c YER145c		similarity to hypothetical protein YAL028w similarity to hypothetical protein YAL056w similarity to hypothetical protein YBL043w similarity to hypothetical protein YBL043w similarity to hypothetical protein YBL101c similarity to hypothetical protein YBR002c similarity to hypothetical protein YBR105c protein YBR105c similarity to hypothetical protein YBR207w	YLR019W YNL328c YPL063W YIL089W YLL023c YFL043c YNR067c	similarity to hypothetical protein YLL010c similarity to hypothetical protein YLR008c similarity to hypothetical protein YLR019w and <i>S. pombe</i> hypothetical protein SPAC2F702c similarity to hypothetical protein YLR036c similarity to hypothetical protein YLR064w similarity to hypothetical protein YLR072w similarity to hypothetical protein YLR072w similarity to hypothetical protein YLR044c
YGR021W YJL046W YIL003W YOR165W YNR015W SN YER113c	similarity to E. coli hypothe similarity to E. coli hypothe similarity to E. coli lipoatel, similarity to E. coli MRP prosimilarity to E. histolytica similarity to E. histolytica similarity to E. histolytica negulatory protein-3 homolo similarity to Emp70p similarity to enoyl-CoA hyd similarity to finger protein  Similarity to Imper protein \text{ Similarity	etical protein protein ligase A protein ligase A rotein surface lectin hitrogen fixation logue dratase YKL222c, YR375 YOR3715 YCR308c YJL171c YER145c YKL222c, YLR387c		similarity to hypothetical protein YAL028w similarity to hypothetical protein YAL056w similarity to hypothetical protein YBL043w similarity to hypothetical protein YBL043w similarity to hypothetical protein YBL059w similarity to hypothetical protein YBR002c similarity to hypothetical protein YBR105c similarity to hypothetical protein YBR165c similarity to hypothetical protein YBR165c similarity to hypothetical protein YBR267w similarity to hypothetical protein YBR267w	YLR019w YNL328c YPL063w YIL089w YLL023c YFL043c YNR067c YDR501w	similarity to hypothetical protein YLL010c similarity to hypothetical protein YLR008c similarity to hypothetical protein YLR019w and <i>S. pombe</i> hypothetical protein SPAC2F7.02c similarity to hypothetical protein YLR036c similarity to hypothetical protein YLR064w similarity to hypothetical protein YLR072w similarity to hypothetical protein YLR074c similarity to hypothetical protein YLR144c similarity to hypothetical protein YLR183c
YGR021w YJL046w YJL003w YOR165w YNR015w SM YER113c YDR036c YOR172w	similarity to E. coli hypothe similarity to E. coli hypothe similarity to E. coli ilipoate-similarity to E. coli ilipoate-similarity to E. coli MRP prosimilarity to E. histolytica similarity to E. histolytica similarity to Emp70p similarity to Emp70p similarity to Emp70p similarity to finger protein YOR162c and YLR266c, we transcription factors	etical protein protein ligase A protein ligase A yIR115w yER093c yPR030w yPR030w yPR030w yR116w yGR066c yJL17ic dratase yKL222c, eak similarity to yIL048c YFR044c		similarity to hypothetical protein YAL.028w similarity to hypothetical protein YAL.056w similarity to hypothetical protein YBL.043w similarity to hypothetical protein YBL.043w similarity to hypothetical protein YBL.059w similarity to hypothetical protein YBR.05c similarity to hypothetical protein YBR.267w similarity to hypothetical protein YBR.267w similarity to hypothetical protein YBR.273c similarity to hypothetical protein YBR.273c similarity to hypothetical protein YBR.281c	YLR019W YNL328c YPL063W YIL089W YLL023c YFL043c YNR067c YDR501W YNL278W YDR200c	similarity to hypothetical protein YLL010c similarity to hypothetical protein YLR008c similarity to hypothetical protein YLR008c similarity to hypothetical protein YLR019w and <i>S. pombe</i> hypothetical protein SPAC2F702c similarity to hypothetical protein YLR066c similarity to hypothetical protein YLR066w similarity to hypothetical protein YLR072w similarity to hypothetical protein YLR184c similarity to hypothetical protein YLR183w similarity to hypothetical protein YLR187w similarity to hypothetical protein YLR238w
YGR021W YJL046W YIL003W YOR165W YNR015W <i>SN</i> YER113C YDR036C	similarity to E. coli hypothe similarity to E. coli ippoate- similarity to E. coli ilipoate- similarity to E. coli MRP pro- similarity to E. histolytica se similarity to E. histolytica negulatory protein-3 homolo similarity to Emp70p similarity to emp70p similarity to finger protein YOR162c and YLR266c, we transcription factors similarity to finger proteins	etical protein protein ligase A protein protein ligase A protein surface lectin pitrogen fixation logue dratase YKL222c, eak similarity to SYKL222c, YKL222c, YKL222c, YKL222c, YKL221c, YKL222c, YKL222c, YKL222c, YKL222c,		similarity to hypothetical protein YAL028w similarity to hypothetical protein YAL056w similarity to hypothetical protein YBL043w similarity to hypothetical protein YBL043w similarity to hypothetical protein YBL059w similarity to hypothetical protein YBL050c similarity to hypothetical protein YBR105c similarity to hypothetical protein YBR165c similarity to hypothetical protein YBR165c similarity to hypothetical protein YBR207w similarity to hypothetical protein YBR267w similarity to hypothetical protein YBR281c similarity to hypothetical protein YBR281c similarity to hypothetical protein YBR281c	YLR019w YNL328c YPL063w YIL089w YLL023c YFL043c YNR067c YDR501w YNL278w YDR200c YOR262w	similarity to hypothetical protein YLL010c similarity to hypothetical protein YLR008c similarity to hypothetical protein YLR008c similarity to hypothetical protein YLR019w and <i>S. pombe</i> hypothetical protein SPAC2F7.02c similarity to hypothetical protein YLR036c similarity to hypothetical protein YLR064w similarity to hypothetical protein YLR072w similarity to hypothetical protein YLR144c similarity to hypothetical protein YLR183c similarity to hypothetical protein YLR187w similarity to hypothetical protein YLR238w similarity to hypothetical protein YLR243w
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YGR021W YJL046W YJL003W YOR165W YNR015W SN YER136 YDR036c YOR172W YOR162c	similarity to E. coli hypothe similarity to E. coli hypothe similarity to E. coli lipoate-psimilarity to E. coli MRP prosimilarity to E. soli MRP prosimilarity to E. histolytica similarity to E. histolytica similarity to Emp70p similarity to Emp70p similarity to Emp70p similarity to finger protein YOR162c and YLR266c, we transcription factors similarity to finger proteins YOR162c and YLR266c, we transcription factors	etical protein protein ligase A protein protein ligase A protein surface lectin pitrogen fixation logue  dratase YKL222c, eak similarity to SYKL222c, eak similarity to SYKL222c, eak similarity to SYKL222c, eak similarity to		similarity to hypothetical protein YAL028w similarity to hypothetical protein YAL056w similarity to hypothetical protein YBL043w similarity to hypothetical protein YBL043w similarity to hypothetical protein YBL059w similarity to hypothetical protein YBR105c similarity to hypothetical protein YBR105c similarity to hypothetical protein YBR162c similarity to hypothetical protein YBR267w similarity to hypothetical protein YBR267w similarity to hypothetical protein YBR273c similarity to hypothetical protein YBR273c similarity to hypothetical protein YCR058c similarity to hypothetical protein YCR058c similarity to hypothetical protein YCR058c similarity to hypothetical protein YCR059c	YLR019W YNL328c YPL063W YIL089W YLL023c YFL043c YNR067c YDR501W YNL278W YDR200c YOR262W YDR126W	similarity to hypothetical protein YLL010c similarity to hypothetical protein YLR008c similarity to hypothetical protein YLR008c similarity to hypothetical protein YLR019w and S. pombe hypothetical protein SPAC2F702c similarity to hypothetical protein YLR036c similarity to hypothetical protein YLR064w similarity to hypothetical protein YLR072w similarity to hypothetical protein YLR183c similarity to hypothetical protein YLR183w similarity to hypothetical protein YLR238w similarity to hypothetical protein YLR243w similarity to hypothetical protein YLR248w and YOL003c
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YKR078w		similarity to hypothetical protein YOR069w	YNL006w		similarity to Met30p	YGL164c		similarity to S. pombe hypothetical protein
YHR194w YAL028w		similarity to hypothetical protein YOR147w similarity to hypothetical protein YOR324c	YNL293w		similarity to Mic1p and human	YPL236c		SPAC31A2.10
YLR361c		similarity to hypothetical protein			transforming protein tre-2, and strong similarity to hypothetical protein YOL112w	TFLZ30C		similarity to <i>S. pombe</i> hypothetical protein SPAC3H1.13
		YOR3329c	YNR047w		similarity to microtubule-associated	YAL032c	FUN20	similarity to S. pombe hypothetical protein
YAL034c YAL056w	FUN19	similarity to hypothetical protein YOR338w	YPL137c		ser/thr protein kinases	YEL007w		SPAC8A4.06
YFR021w		similarity to hypothetical protein YOR371c similarity to hypothetical protein YPL100w	TPL1370		similarity to microtubule-interacting protein Mhp1p and to hypothetical protein	YLR247c		similarity to <i>S. pombe</i> pac2 protein similarity to <i>S. pombe</i> rad8 protein
YML117w		similarity to hypothetical protein YPL184c			YOR227w	YJL062w		similarity to S. pombe SPAC13G6.3 protein
YGL133w YGL134w		similarity to hypothetical protein YPL216w similarity to hypothetical protein YPL219w	YIL151c		similarity to mitochondrial aldehyde dehydrogenase Ald1p	YHR009c YBL051c		similarity to <i>S. pombe</i> YAM3 protein similarity to <i>S. pombe</i> Z66568_C protein
YMR180c		similarity to hypothetical protein YPL228w	YGR058w		similarity to mouse calcium-binding	YOR240w		similarity to <i>S. pombe</i> ZK1058.5 protein
YMR181c		similarity to hypothetical protein YPL229w			protein	YPL150w		similarity to ser/thr kinases
YJR116w YLR454w		similarity to hypothetical protein YPR114w similarity to hypothetical protein YPR117w	YBL047c YLR200w	YKE2	similarity to mouse eps15R protein similarity to mouse KE2 protein	YGR052w YAL017w	FUN31	similarity to ser/thr protein kinases similarity to ser/thr protein kinases
YOL027c		similarity to hypothetical protein YPR125w	YIL023c	TALL	similarity to mouse MHC H-2K/t-w5-linked	YOR090c	7 01401	similarity to ser/thr protein phosphatases
YGR142w		similarity to hypothetical protein YPR158w	VODOOO		ORF	YBR059c		similarity to ser/thr-specific protein kinase
YOL048c		similarity to hypothetical proteins YAL018c and YOL047c	YCR033w		similarity to mouse nuclear receptor co- repressor N-Cor	YBR274w		Pak1p similarity to ser/thr-specific protein
YOL047c		similarity to hypothetical proteins YAL018c	YER030w		similarity to mouse nucleolin			kinases
YMR210w		and YOL048c similarity to hypothetical proteins YBR177c	YDR060w		similarity to mouse putative CCAAT binding factor 1	YLR118c YMR077c		similarity to several esterases similarity to SNF7 protein
11011121000		and YPL095c	YBR187w		similarity to mouse putative	YLR313c		similarity to SPA2 protein
YML052w		similarity to hypothetical proteins			transmembrane protein FT27	YIR033w		similarity to Spt23p
YLR246w		YDL222c and YNL194c similarity to hypothetical proteins	YGR284c YGR127w		similarity to mouse Surf-4 protein similarity to mouse T10 protein	YBL109w		similarity to subtelomeric encoded proteins
I LIIL TOW		YDR126w, YNL326c and YOL003c	YMR192w		similarity to mouse Tbc1 protein	YEL074w		similarity to subtelomeric encoded
YER072w		similarity to hypothetical proteins	YPL249c		similarity to mouse Tbc1 protein	\/O1 000		proteins
YLR072w		YFL004w and YPL019c similarity to hypothetical proteins	YHR181w YDR109c		similarity to mouse TEG-261 protein similarity to MPA43p	YGL263w		similarity to subtelomeric encoded proteins
		YFL042c, YFL043c, YDR326c and	YDL038c		similarity to mucin proteins	YHL042w		similarity to subtelomeric encoded
YGL028c		YHR080c similarity to hypothetical proteins	YER085c YJL112w		similarity to myosins similarity to <i>N. crassa</i> sulphur controller-2	YHL043w		proteins similarity to subtelomeric encoded
TGLUZOC		YGR279c and YMR305c	YDR395w		similarity to NMD and CSE1 proteins	T II LU43W		proteins
YFL042c		similarity to hypothetical proteins	YPR072w		similarity to N-terminal part of Cdc39p	YHL044w		similarity to subtelomeric encoded
YNL097c		YHR080c, YDR326c and YLR072w similarity to hypothetical proteins	YBL024w YDR071c		similarity to nucleolar Nop2p similarity to <i>O. aries</i> arylalkylamine	YIL177c		proteins similarity to subtelomeric encoded
		YHR090c and YHR090c			N-acetyltransferase			proteins
YJR061w		similarity to hypothetical proteins YKL200c	YOL164w		similarity to P. aeruginosa alkyl	YKL219w		similarity to subtelomeric encoded
YMR313c		and YKL201c similarity to hypothetical proteins YKR089c and YOR081c	YMR099c		sulphatase similarity to <i>P. ciliare</i> possible apospory- associated protein	YMR326c		proteins similarity to subtelomeric encoded proteins
YOL019w		similarity to hypothetical proteins YMR063w and YFR012w	YNR029c YDR472w		similarity to <i>P. denitrificans</i> cobW protein similarity to <i>P. falciparum</i> 41-2 protein	YLR177w YNL191w		similarity to suppressor protein Gin5p similarity to Synechocystis hypothetical
YPR027c		similarity to hypothetical proteins YNL019c			antigen	\		protein
YNL056w		and YNL033w similarity to hypothetical proteins	YNL136w		similarity to <i>P. falciparum</i> mature-parasite- infected erythrocyte surface antigen	YGR036c YDR485c		similarity to <i>T. denticola</i> phosphatase similarity to trichohyalin
\ A !! 000		YNL032w and YNL099c	\/// 0.40		MESA	YOR195w	2005	similarity to USO1 protein
YNL099c		similarity to hypothetical proteins YNL032w, YNL056w and YDR067c	YIL010w		similarity to <i>P. falciparum</i> merozoite cap protein-1	YPL188w	POS5	similarity to Utr1p and hypothetical protein YEL041w
YNL032w		similarity to hypothetical proteins	YLR107w		similarity to <i>P. troglodytes</i> prot GOR	YLR213c		similarity to UTR2 protein
YOL101c		YNL099c, YNL056w and YDR067c similarity to hypothetical proteins	YOL065c		similarity to Pie3p and hypothetical proteins YIL002c	YGR189c YGL220w		similarity to Utr2p similarity to <i>V. alginolyticus</i> bolA protein
		YOL002c and YDR492w	YNL047c		similarity to probable transcription factor	YGR203w		similarity to X. laevis protein-tyrosin-
YNL326c		similarity to hypothetical proteins YOL003c, YLR246w and <i>C. elegans</i>			Ask10p and hypothetical protein YPR115w, and strong similarity to hypothetical			phosphatase cdc homologue 2 and to hypothetical protein YPR200c
		hypothetical protein ZK757.1			protein YIL105c	YDR284c		similarity to YDR503c
YML072c		similarity to hypothetical proteins YOR3141c and YNL087w and weak	YBR125c YNR038w		similarity to protein phosphatase 2C similarity to Prp5p	YEL003w YIL135c		similarity to Yke2p similarity to Ymk1p
		similarity to synaptogamines	YER150w		similarity to P1959 similarity to putative cell surface	YOL082w		similarity to YOL083w
YLR152c		similarity to hypothetical proteins			glycoprotein Sed1p	YDR534c		similarity to YOR383c,Sta1p and pig
YNL165w		YOR3165w and YNL095c similarity to hypothetical proteins	YGL099w		similarity to putative human GTP-binding protein HSR1	YBL101c		mucin similarity to YPR030w
TIVETOSVV		YOR385w and YMR316w	YPR062w		similarity to <i>R. corallinus</i> N-ethylammeline	YCR062w		similarity to Ytp1p protein
YMR316w		similarity to hypothetical proteins	V/II 055		chlorohydrolase trzA	YFR024c-a		strong similarity hypothetical protein
YDR083w		YOR385w and YNL165w similarity to hypothetical <i>S. pombe</i> protein	YJL055w		similarity to <i>R. fascians</i> hypothetical protein 6	YPL151c		YHR016c strong similarity to A. thaliana PRL1 and
YDR346c		similarity to hypothetical S. pombe protein	YOR191w		similarity to RAD5 protein			PRL2 proteins
YGR272c YLR241w		similarity to hypothetical <i>S. pombe</i> protein similarity to hypothetical <i>S. pombe</i> protein	YGL059w		similarity to rat branched-chain α-ketoacid dehydrogenase kinase	YOR034c YOR374w		strong similarity to Akr1p strong similarity to aldehyde
YML005w		similarity to hypothetical <i>S. pombe</i> protein	YBR053c		similarity to rat regucalcin	101137400		dehydrogenase
YOL098c		similarity to hypothetical S. pombe protein	YDL015c		similarity to rat synaptic glycoprotein SC2	YIL113w		strong similarity to C. albicans dual-
YOR091w		similarity to hypothetical <i>S. pombe</i> protein D83992 G	YDR457w YBR028c		similarity to rat URE-B1 similarity to ribosomal protein kinases	YLR460c		specificity phosphatase MSG5 strong similarity to <i>C. carbonum</i> toxD
YOL071w		similarity to hypothetical S. pombe protein	YLR276c		similarity to RNA helicases			protein
YFR048w		SPAC12B10.06c similarity to hypothetical <i>S. pombe</i> protein	YPR112c YPR016c		similarity to RNA-binding proteins similarity to S. acidocaldarius ao2sac	YKL013c		strong similarity to <i>C. elegans</i> hypothetical protein
111104000		SPAC12G12.14 and to YDL001w and	11 110100		protein	YNL288w		strong similarity to <i>C. elegans</i>
VODOSS		YDR282c	YOL154w		similarity to S. fumigata Asp FII			hypothetical protein
YOR322c		similarity to hypothetical <i>S. pombe</i> protein SPAC1F12.05	YHR029c YFL033c		similarity to <i>S. lincolnensis</i> ImbX protein similarity to <i>S. pombe</i> cek1	YOL077c		strong similarity to <i>C. elegans</i> K12H4.3 protein
YOR250c		similarity to hypothetical S. pombe protein			serine/threonine protein kinase	YGL080w		strong similarity to <i>C. elegans</i> R07E5.13
YER143w		SPAC22H10.05c	YIL144w YKR051w		similarity to <i>S. pombe</i> hypothetical protein similarity to <i>S. pombe</i> hypothetical protein	YPR194c		protein strong similarity to C-term. of <i>S. pombe</i>
1 EN 143W		similarity to hypothetical <i>S. pombe</i> protein SPAC56F8.08	YCK051W YOL087c		similarity to S. pombe hypothetical protein	1 F N 1940		isp4 protein
YDR504c		similarity to hypothetical T. brucei protein	YBR004c		similarity to S. pombe hypothetical protein	YAR023c		strong similarity to Fun55p, Fun59p,
YDR223w YAL035w	FUN12	similarity to lfh1p similarity to lfm1p	YKR079c		SPAC18B11.05 similarity to <i>S. pombe</i> hypothetical protein			YGL051w, YCR007c, YGL053w, YAR031w and YAR028w
YOR109w	, 0,,,,	similarity to inositol polyphosphate 5-			SPAC1D4.10	YAR028w		strong similarity to Fun55p, YGL053w,
YEL013w		phosphatases similarity to intracellular attachement	YNL308c		similarity to <i>S. pombe</i> hypothetical protein SPAC22G7.05	YGL051w		YCR007c, YAR031w, Fun59p and YGL051w strong similarity to Fun59p
		proteins	YAL042w	FUN9	similarity to <i>S. pombe</i> hypothetical protein	YGL236c		strong similarity to gidA E. coli protein
YPR042c		similarity to Jsn1p			SPAC24B11.08c	YAL036c	FUN11	strong similarity to GTP-binding proteins
YMR226c YGR232w		similarity to ketoreductases similarity to <i>L. mactans</i> α-latroinsectotoxin	YNL310c		similarity to <i>S. pombe</i> hypothetical protein SPAC24H6.02c	YMR290c		strong similarity to helicases of the DEAD/DEAH box family
YER010c		similarity to L. pneumophila dlpA protein	YGR125w		similarity to S. pombe hypothetical protein	YDR276c		strong similarity to Hordeum blt101 protein
YGR210c		similarity to <i>M. capricolum</i> hypothetical protein SGC3	YMR075w		SPAC24H6.11c similarity to <i>S. pombe</i> hypothetical protein	YDL103c YDR373w	QRI1	strong similarity to human AgX-1 antigen strong similarity to human BDR-1 protein
YMR095c		similarity to <i>M. leprae</i> hisH protein	WC/Univir		SPAC2F7.07c	I DINO/OW		and other calcium binding proteins
YBR079c		similarity to M. musculus p162 protein	YDR175c		similarity to S. pombe hypothetical protein	YNR053c		strong similarity to human breast tumor
YNL335w		similarity to <i>M. verrucaria</i> cyanamide hydratase, identical to hypothetical protein	YFL047w		SPAC2F7.15 similarity to <i>S. pombe</i> hypothetical protein	YDL120w		associated autoantigen strong similarity to human frataxin
V/1 1 0 C :		YFL061w			SPAC2F7.18c			(Friedreichs ataxia)
YLL034c YMR166c		similarity to mammalian valosin similarity to members of the mitochondrial	YLR023c		similarity to <i>S. pombe</i> hypothetical protein SPAC30D11.11	YGR173w		strong similarity to human GTP-binding protein
		carrier protein family	YDR180w		similarity to S. pombe hypothetical protein	YKL056c		strong similarity to human IgE-dependent
YIR041w		similarity to members of the Srp1p/Tip1p family			SPAC31A2.05c			histamine-releasing factor
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L VDI 150		atura a similarita da la caraca alcanalest una d	L VDI 100-		L VC DOO4	
YPL152w		strong similarity to human phosphotyrosyl phosphatase activator	YDL109c	strong similarity to hypothetical protein YGL144c	YGR004w	strong similarity to hypothetical protein YLR324w
YPR028w YCL059c		strong similarity to human protein TB2 strong similarity to human Rev interacting	YER037w	strong similarity to hypothetical protein YGL224c	YGR010w	strong similarity to hypothetical protein YLR328w
YLR146c		protein Rip-1 strong similarity to human spermidine	YOR387c	strong similarity to hypothetical protein YGL258w	YGR038w ORA	11 strong similarity to hypothetical protein YLR350w
YNL200c		synthase strong similarity to human TGR-CL10C	YLR324w	strong similarity to hypothetical protein YGR004w	YGR056w	strong similarity to hypothetical protein YLR357w
YBL036c		strong similarity to hypothetical  C. elegans protein	YLR328w	strong similarity to hypothetical protein YGR010w	YKL187c	strong similarity to hypothetical protein YLR413w
YBL078c		strong similarity to hypothetical	YLR350w	strong similarity to hypothetical protein YGR038w	YPR172w	strong similarity to hypothetical protein YLR456w
YMR292w		C. elegans protein strong similarity to hypothetical	YLR357w	strong similarity to hypothetical protein	YDR438w	strong similarity to hypothetical protein
YDR430c		C. elegans protein strong similarity to hypothetical	YPL004c	YGR056w strong similarity to hypothetical protein	YBR002c	YML018c strong similarity to hypothetical protein
YOR365c		C. perfringens protein strong similarity to hypothetical protein	YPR157w	YGR086c strong similarity to hypothetical protein	YKL121w	YMR101c strong similarity to hypothetical protein
YHR214w-a		YAL053w strong similarity to hypothetical protein	YHR162w	YGR141w strong similarity to hypothetical protein	YPL224c	YMR102c strong similarity to hypothetical protein
YPR032w		YAR068w strong similarity to hypothetical protein	YBR300c	YGR243w strong similarity to hypothetical protein	YOR295w	YMR177w strong similarity to hypothetical protein
YDR003w		YBL106c strong similarity to hypothetical protein	YHR054c	YGR293c strong similarity to hypothetical protein	YKL046c	YMR233w strong similarity to hypothetical protein
YDR210w		YBR005w strong similarity to hypothetical protein	YDR358w	YHR056c strong similarity to hypothetical protein	YPL264c	YMR238w strong similarity to hypothetical protein
YDL012c		YBR016w strong similarity to hypothetical protein	YNL116w	YHR108w strong similarity to hypothetical protein	YGR279c	YMR253c strong similarity to hypothetical protein
YDR018c		YBR016w and YDR210w strong similarity to hypothetical protein	YGR238c	YHR115c strong similarity to hypothetical protein	YOR385w	YMR305c strong similarity to hypothetical protein
YOL092w		YBR042c strong similarity to hypothetical protein	YGR243w	YHR158c strong similarity to hypothetical protein	YNL034w	YMR316w strong similarity to hypothetical protein
		YBR147w	YHR199c	YHR162w		YNL018c
YPL095c		strong similarity to hypothetical protein YBR177c		strong similarity to hypothetical protein YHR198c	YNL033w	strong similarity to hypothetical protein YNL019c
YPL087w		strong similarity to hypothetical protein YBR183w	YHR198c	strong similarity to hypothetical protein YHR199c	YNL019c	strong similarity to hypothetical protein YNL033w
YGL056c		strong similarity to hypothetical protein YBR214w	YAR060c	strong similarity to hypothetical protein YHR212c	YNL018c	strong similarity to hypothetical protein YNL034w
YGL060w		strong similarity to hypothetical protein YBR216c	YAR068w	strong similarity to hypothetical protein YHR214w-a	YIL109c	strong similarity to hypothetical protein YNL049c
YGL107c		strong similarity to hypothetical protein YBR238c	YPR071w	strong similarity to hypothetical protein YIL029c	YOR086c	strong similarity to hypothetical protein YNL087w and weak similarity to
YGL101w		strong similarity to hypothetical protein YBR242w	YER067w	strong similarity to hypothetical protein YIL057c	YOR092w	synaptogamines strong similarity to hypothetical protein
YJL058c		strong similarity to hypothetical protein YBR270c	YDL175c	strong similarity to hypothetical protein YIL079c	YOR110w	YNL095c strong similarity to hypothetical protein
YGR293c		strong similarity to hypothetical protein YBR300c	YIL014c-a	strong similarity to hypothetical protein YIL102c	YHR115c	YNL108c strong similarity to hypothetical protein
YDR514c		strong similarity to hypothetical protein YCL036w	YNL049c	strong similarity to hypothetical protein YIL109c	YDL222c	YNL116w strong similarity to hypothetical protein
YGL144c		strong similarity to hypothetical protein YDL109c	YOL162w	strong similarity to hypothetical protein YIL166c	YLR144c	YNL194c and similarity to YML052w strong similarity to hypothetical protein
YIL079c		strong similarity to hypothetical protein YDL175c	YJL038c	strong similarity to hypothetical protein YJL037w	YDR492w	YNR067c strong similarity to hypothetical protein
YNL194c		strong similarity to hypothetical protein YDL222c and similarity to hypothetical	YJL037w	strong similarity to hypothetical protein YJL038c	YPR125w	YOL002c strong similarity to hypothetical protein
YBR005w		protein YML052w strong similarity to hypothetical protein	YBR270c	strong similarity to hypothetical protein YJL058c	YBR147w	YOL027c strong similarity to hypothetical protein
YBR042c		YDR003w strong similarity to hypothetical protein	YKR018c	strong similarity to hypothetical protein YJL082w	YDR391c	YOL092w
YLR108c		YDR018c	YKR021w	strong similarity to hypothetical protein		strong similarity to hypothetical protein YOR013w
		strong similarity to hypothetical protein YDR132c	YKR053c	YJL084c strong similarity to hypothetical protein	YAL007c	strong similarity to hypothetical protein YOR016c, similarity to hamster COP-
YPL235w		strong similarity to hypothetical protein YDR190c	YML047c	YJL134w strong similarity to hypothetical protein	YKR089c	coated vesicle membrane protein strong similarity to hypothetical protein
YNL281w		strong similarity to hypothetical protein YDR214w	YKL200c	YJR054w strong similarity to hypothetical protein	YNL095c	YOR081c strong similarity to hypothetical protein
YLR225c		strong similarity to hypothetical protein YDR222w	YDR399w	YJR061w strong similarity to hypothetical protein	YNL108c	YOR092w strong similarity to hypothetical protein
YHR032w EF	RC1	strong similarity to hypothetical protein YDR338c	YMR238w	YJR133w strong similarity to hypothetical protein	YLR260w	YOR110w strong similarity to hypothetical protein
YHR097c		strong similarity to hypothetical protein YDR348c	YMR040w	YKL046c strong similarity to hypothetical protein	YLR270w	YOR171c strong similarity to hypothetical protein
YHR108w		strong similarity to hypothetical protein YDR358w	YMR102c	YKL065c strong similarity to hypothetical protein	YLR284c	YOR173w strong similarity to hypothetical protein
YOR013w		strong similarity to hypothetical protein YDR391c	YLR413w	YKL121w strong similarity to hypothetical protein	YLR243w	YOR180c strong similarity to hypothetical protein
YJR133w		strong similarity to hypothetical protein YDR399w	YJL082w	YKL187c strong similarity to hypothetical protein	YMR233w	YOR262w strong similarity to hypothetical protein
YOL002c		strong similarity to hypothetical protein YDR492w	YJL084c	YKR018c strong similarity to hypothetical protein	YGL258w	YOR295w strong similarity to hypothetical protein
YOR383c		strong similarity to hypothetical protein YDR534c and similarity to L. mexicana	YJL134w	YKR021w strong similarity to hypothetical protein	YPL279c	YOR387c strong similarity to hypothetical protein
YPR193c		secreted acid phosphatase 2 strong similarity to hypothetical protein	YOR081c	YKR053c strong similarity to hypothetical protein	YGR086c	YOR390w strong similarity to hypothetical protein
YGL224c		YEL066w strong similarity to hypothetical protein	YIR013c	YKR089c strong similarity to hypothetical protein	YFL004w	YPL004c strong similarity to hypothetical protein
YIL057c		YER037w strong similarity to hypothetical protein	YLL010c	YLR013w strong similarity to hypothetical protein	YBR183w	YPL019c strong similarity to hypothetical protein
		YER067w		YLR019w		YPL087w
YPL019c		strong similarity to hypothetical protein YFL004w	YDR123c	strong similarity to hypothetical protein YLR099c	YBR177c	strong similarity to hypothetical protein YPL095c
YMR096w		strong similarity to hypothetical protein YFL059w, YNL333w, and Para rubber tree	YDR132c	strong similarity to hypothetical protein YLR108c	YOR227w	strong similarity to hypothetical protein YPL137c and to microtubule-interacting
YHR016c YS	5C84	ethylene-responsive protein 1 strong similarity to hypothetical protein	YDR185c	strong similarity to hypothetical protein YLR168c	YGL084c	protein MHP1 strong similarity to hypothetical protein
YBR214w		YFR024c-a strong similarity to hypothetical protein	YDL161w	strong similarity to hypothetical protein YLR206w and to human KIAA0171 protein	YGL082w	YPL189w strong similarity to hypothetical protein
YBR216c		YGL056c strong similarity to hypothetical protein	YDR222w	strong similarity to hypothetical protein YLR225c	YGL139w	YPL191c strong similarity to hypothetical protein
YPL191c		YGL060w strong similarity to hypothetical protein	YDR213w	strong similarity to hypothetical protein YLR228c	YMR177w	YPL221w strong similarity to hypothetical protein
YPL189w		YGL082w strong similarity to hypothetical protein	YOR171c	strong similarity to hypothetical protein YLR260w	YDR190c	YPL224c strong similarity to hypothetical protein
YBR242w		YGL084c strong similarity to hypothetical protein	YOR173w	strong similarity to hypothetical protein YLR270w	YMR253c	YPL235w strong similarity to hypothetical protein
		YGL101w	YOR180c	strong similarity to hypothetical protein YLR284c		YPL264c
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YOR390w	strong similarity to hypothetical protein YPL279c	YHL017w		strong similarity to putative transmembrane protein PTM1	YLR466w		strong similarity to subtelomeric encoded proteins
YIL029c	strong similarity to hypothetical protein	YHR017w	YSC83	strong similarity to S. douglasii YSD83	YLR467w		strong similarity to subtelomeric encoded
YDL242w	YPR071w	YDL219w		strong similarity to <i>S. equisimilis</i>	YML132w		proteins
T DL242W	strong similarity to hypothetical protein YPR079w	YPL118w		hypothetical protein strong similarity to <i>S. kluyveri</i> hypothetical	TIVILISZW		strong similarity to subtelomeric encoded proteins
YGR141w	strong similarity to hypothetical protein YPR157w	YNR046w		protein strong similarity to <i>S. pombe</i> hypothetical	YNL336w		strong similarity to subtelomeric encoded
YLR456w	strong similarity to hypothetical protein			protein SPAC31A2.02	YNL337w		proteins strong similarity to subtelomeric encoded
YEL066w	YPR172w strong similarity to hypothetical protein	YNL072w		strong similarity to <i>S. pombe</i> hypothetical protein SPAC4G9.02	YNL338w		proteins strong similarity to subtelomeric encoded
I LLOOOW	YPR193c	YDR032c		strong similarity to <i>S. pombe</i> obr1	TIVESSOV		proteins
YGL053w	strong similarity to hypothetical proteins YAR031, YGL051w, YAR028w,Fun55p and	YOL010w		strong similarity to <i>S. pombe</i> SPAC12G12.06c protein	YNL339c		strong similarity to subtelomeric encoded
	YCR007c	YOR163w		strong similarity to <i>S. pombe</i> SPAC13G6.14	YNR077c		proteins strong similarity to subtelomeric encoded
YMR324c	strong similarity to hypothetical proteins YBL108w, YCR103c and YKL223w	YOR256c		protein	YOL158c		proteins
YNR048w	strong similarity to hypothetical proteins	10112300		strong similarity to secretory protein SSP134	TOLISEC		strong similarity to subtelomeric encoded proteins
YNL323w	YCR094w and YNL323w strong similarity to hypothetical proteins	YCL024w		strong similarity to ser/thr protein kinase GNP1	YPL282c		strong similarity to subtelomeric encoded proteins
TIVESESVV	YCR094w and YNR048w	YOR310c		strong similarity to SIK1 protein	YPL283c		strong similarity to subtelomeric encoded
YBR016w	strong similarity to hypothetical proteins YDL012c and YDR210w	YDR247w 07535		strong similarity to Sks1p strong similarity to subtelomeric encoded	YPR202w		proteins strong similarity to subtelomeric encoded
YNL334c	strong similarity to hypothetical proteins			proteins			proteins
YPL221w	YFL060c and YMR095c strong similarity to hypothetical proteins	YAL068c		strong similarity to subtelomeric encoded proteins	YPR203w		strong similarity to subtelomeric encoded proteins
	YGL139w and YAL053w	YBL108w		strong similarity to subtelomeric encoded	YPR204w		strong similarity to subtelomeric encoded
YDR326c	strong similarity to hypothetical proteins YHR080c, YFL042c and YLR072w	YBL111c		proteins strong similarity to subtelomeric encoded	YNR075w	EDL1	proteins strong similarity to subtelomeric encoded
YMR251w	strong similarity to hypothetical proteins			proteins		LDLI	proteins
YGR154c	YKR076w and YGR154c strong similarity to hypothetical proteins	YBL112c		strong similarity to subtelomeric encoded proteins	YER042w		strong similarity to transcription factors and peptide methionine sulphoxide
	YKR076w and YMR251w	YBL113c		strong similarity to subtelomeric encoded			reductases
YKR076w	strong similarity to hypothetical proteins YMR251w and YGR154c	YBR302c		proteins strong similarity to subtelomeric encoded	YJL186w YEL041w		strong similarity to Ttp1p strong similarity to Utr1p
YFL060c	strong similarity to hypothetical proteins			proteins	YCR063w		strong similarity to Xenopus G10 and
YCR094w	YNL334c and YMR095c strong similarity to hypothetical proteins	YCL073c		strong similarity to subtelomeric encoded proteins	YAR027w	FUN55	human edg-2 protein strong similarity to YAR028w, YCR007c,
	YNR048w and YNL323w	YCR103c		strong similarity to subtelomeric encoded	17 11 10 27 11	, 0,,00	YGL053w, YAR031w, FUN59p and
YOR230w	strong similarity to hypothetical proteins YOR229w and YPL139c	YDL248w		proteins strong similarity to subtelomeric encoded	YAR029w	FUN57	YGL051w strong similarity to YAR031w, YGL053w,
YPL139c	strong similarity to hypothetical proteins			proteins			Fun55p, Fun59p and YGL051w
YOR229w	YOR230w and YOR229w strong similarity to hypothetical proteins	YDR542w		strong similarity to subtelomeric encoded proteins	YAR033w	FUN59	strong similarity to YGL051w, YGL053w, YAR031w, Fun55p, YAR028w and
	YOR230w and YPL139c	YDR543c		strong similarity to subtelomeric encoded			YCR007c
YAL053w	strong similarity to hypothetical proteins YOR365c,YGL139w,YPL221w	YDR544c		proteins strong similarity to subtelomeric encoded	YAR031w		strong similarity to YGL053w, Fun59p, YGL051w, Fun55p, YAR028w and
YPL280w	strong similarity to hypothetical proteins			proteins	VIII 400 -		YCR007c
YMR321c	YOR391c, YMR322c and YDR533c strong similarity to hypothetical proteins	YDR545w		strong similarity to subtelomeric encoded proteins	YIL102c YBR025c		strong similarity to YIL014c-a strong similarity to YIf1p
YLL062c	YPL273w and YLL062c strong similarity to hypothetical proteins	YEL075c		strong similarity to subtelomeric encoded	YKL065c YOL112w		strong similarity to YMR040w strong similarity to YNL293w, similarity to
T LLUOZC	YPL273w, weak similarity to <i>M. leprae</i>	YEL076c-b		proteins strong similarity to subtelomeric encoded	TOLTIZW		Mic1p and human transforming protein
YOR391c	metH2 protein strong similarity to hypothetical proteins	YER188c-a		proteins strong similarity to subtelomeric encoded	YBL106c		tre-2 strong similarity to YPR032w
		I LITTIOGG G			YLR045c	STU2	
	YPL280w, YMR322c and YDR533c			proteins			suppressor of a cs tubulin mutation
YDR533c	strong similarity to hypothetical proteins	YER189w		strong similarity to subtelomeric encoded	YER120w	SCS2	suppressor of an inositol auxotrophic and
YDR533c YMR322c	strong similarity to hypothetical proteins YPL280w, YOR391c and YMR322c strong similarity to hypothetical proteins	YER189w YER190w		strong similarity to subtelomeric encoded proteins strong similarity to subtelomeric encoded	YER120w YCR044c	SCS2	suppressor of an inositol auxotrophic and a choline sensitive mutant suppressor of cdc1-1 ts growth defect
	strong similarity to hypothetical proteins YPL280w, YOR391c and YMR322c			strong similarity to subtelomeric encoded proteins	YER120w		suppressor of an inositol auxotrophic and a choline sensitive mutant
YMR322c YHR069c	strong similarity to hypothetical proteins YPL280w, YOR391c and YMR322c strong similarity to hypothetical proteins YPL280w, YOR391c and YDR533c strong similarity to hypothetical <i>S. pombe</i> and human proteins	YER190w YFL062w		strong similarity to subtelomeric encoded proteins	YER120w YCR044c YGL083w YDR510w	SCS2 SCY1 SMT3	suppressor of an inositol auxotrophic and a choline sensitive mutant suppressor of cdc1-1 ts growth defect suppressor of GTPase mutant suppressor of mil2 temperature-sensitive mutation
YMR322c	strong similarity to hypothetical proteins YPL280w, YOR391c and YMR322c strong similarity to hypothetical proteins YPL280w, YOR391c and YDR533c strong similarity to hypothetical <i>S. pombe</i>	YER190w		strong similarity to subtelomeric encoded proteins strong similarity to subtelomeric encoded proteins strong similarity to subtelomeric encoded proteins	YER120w YCR044c YGL083w YDR510w YKL124w YLR197w	SCS2 SCY1 SMT3 SSH4 SIK1	suppressor of an inositol auxotrophic and a choline sensitive mutant suppressor of cdc1-1 ts growth defect suppressor of GTPase mutant suppressor of mil2 temperature-sensitive
YMR322c YHR069c	strong similarity to hypothetical proteins YPL280w, YOR391c and YMR322c strong similarity to hypothetical proteins YPL280w, YOR391c and YDR533c strong similarity to hypothetical <i>S. pombe</i> and human proteins strong similarity to hypothetical <i>S. pombe</i> protein strong similarity to hypothetical <i>S. pombe</i> protein similarity to hypothetical <i>S. pombe</i>	YER190w YFL062w		strong similarity to subtelomeric encoded proteins strong similarity to subtelomeric encoded	YER120W YCR044c YGL083W YDR510W YKL124W YLR197W YOL102c	SCS2 SCY1 SMT3 SSH4	suppressor of an inositol auxotrophic and a choline sensitive mutant suppressor of cdc1-1 ts growth defect suppressor of GTPase mutant suppressor of mif2 temperature-sensitive mutation suppressor of shr3 suppressor of toxicity of Gal4-IKB tRNA 2'-phosphotransferase
YMR322c YHR069c YMR288w	strong similarity to hypothetical proteins YPL280w, YOR391c and YMR322c strong similarity to hypothetical proteins YPL280w, YOR391c and YDR533c strong similarity to hypothetical <i>S. pombe</i> and human proteins strong similarity to hypothetical <i>S. pombe</i> protein	YER190W YFL062W YFL063W		strong similarity to subtelomeric encoded proteins	YER120W YCR044c YGL083W YDR510W YKL124W YLR197W YOL102c YIL080W YBR015c	SCS2 SCY1 SMT3 SSH4 SIK1	suppressor of an inositol auxotrophic and a choline sensitive mutant suppressor of cdc1-1 ts growth defect suppressor of GTPase mutant suppressor of mif2 temperature-sensitive mutation suppressor of shr3 suppressor of toxicity of Gal4-IKB tRNA 2'-phosphotransferase Ty3-2 orf C fragment type II membrane protein
YMR322c YHR069c YMR288w YER049w YNL240c	strong similarity to hypothetical proteins YPL280w, YOR391c and YMR322c strong similarity to hypothetical proteins YPL280w, YOR391c and YDR533c strong similarity to hypothetical <i>S. pombe</i> and human proteins strong similarity to hypothetical <i>S. pombe</i> protein strong similarity to hypothetical <i>S. pombe</i> protein YER049W strong similarity to <i>K. marxianus</i> LET1 protein	YER190W YFL062W YFL063W YFL064c YFL065c		strong similarity to subtelomeric encoded proteins	YER120W YCR044c YGL083W YDR510W YKL124W YLR197W YOL102c YIL080W	SCS2 SCY1 SMT3 SSH4 SIK1 TPT1	suppressor of an inositol auxotrophic and a choline sensitive mutant suppressor of cdc1-1 ts growth defect suppressor of GTPase mutant suppressor of mil2 temperature-sensitive mutation suppressor of shr3 suppressor of toxicity of Gal4-IKB tRNA 2'-phosphotransferase Ty3-2 orf C fragment type II membrane protein weak similarity to A. niger carbon
YMR322c YHR069c YMR288w YER049w YNL240c YBR301w	strong similarity to hypothetical proteins YPL280w, YOR391c and YMR322c strong similarity to hypothetical proteins YPL280w, YOR391c and YDR533c strong similarity to hypothetical <i>S. pombe</i> and human proteins strong similarity to hypothetical <i>S. pombe</i> protein strong similarity to hypothetical <i>S. pombe</i> protein YER049W strong similarity to <i>K. marxianus</i> LET1 protein strong similarity to members of the Srp1p/Tip1p family	YER190W YFL062W YFL063W YFL064c YFL065c YFL066c		strong similarity to subtelomeric encoded proteins	YER120W YCR044c YGL083W YDR510W YKL124W YLR197W YOL102c YIL080W YBR015c	SCS2 SCY1 SMT3 SSH4 SIK1 TPT1	suppressor of an inositol auxotrophic and a choline sensitive mutant suppressor of cdc1-1 ts growth defect suppressor of GTPase mutant suppressor of mif2 temperature-sensitive mutation suppressor of shr3 suppressor of toxicity of Gal4-IKB tRNA 2'-phosphotransferase Ty3-2 orf C fragment type II membrane protein weak similarity to A. niger carbon catabolite repressor protein weak similarity to A. parasiticus nor-1
YMR322c YHR069c YMR288w YER049w YNL240c	strong similarity to hypothetical proteins YPL280w, YOR391c and YMR322c strong similarity to hypothetical proteins YPL280w, YOR391c and YDR533c strong similarity to hypothetical <i>S. pombe</i> and human proteins strong similarity to hypothetical <i>S. pombe</i> protein strong similarity to hypothetical <i>S. pombe</i> protein YER049W strong similarity to <i>K. marxianus</i> LET1 protein Strong similarity to members of the Srp1p/Tip1p family strong similarity to members of the	YER190W YFL062W YFL063W YFL064c YFL065c		strong similarity to subtelomeric encoded proteins strong similarity to subtelomeric encoded	YER120W YCR044c YGL083W YDR510W YKL124W YLR197W YOL102c YIL080W YBR015c YBR066c YKL071W	SCS2 SCY1 SMT3 SSH4 SIK1 TPT1	suppressor of an inositol auxotrophic and a choline sensitive mutant suppressor of cdc1-1 ts growth defect suppressor of GTPase mutant suppressor of mif2 temperature-sensitive mutation suppressor of shr3 suppressor of toxicity of Gal4-IKB tRNA 2'-phosphotransferase Ty3-2 orf C fragment type II membrane protein weak similarity to A. niger carbon catabolite repressor protein weak similarity to A. parasiticus nor-1 protein
YMR322c YHR069c YMR288w YER049w YNL240c YBR301w	strong similarity to hypothetical proteins YPL280w, YOR391c and YMR322c strong similarity to hypothetical proteins YPL280w, YOR391c and YDR633c strong similarity to hypothetical <i>S. pombe</i> and human proteins strong similarity to hypothetical <i>S. pombe</i> protein strong similarity to hypothetical <i>S. pombe</i> protein YER049W strong similarity to <i>K. marxianus</i> LET1 protein strong similarity to members of the Srp1p/Tip1p family strong similarity to members of the Srp1p/Tip1p family strong similarity to members of the Srp1p/Tip1p family strong similarity to members of the	YER190W YFL062W YFL063W YFL064c YFL065c YFL066c		strong similarity to subtelomeric encoded proteins strong similarity to subtelomeric encoded strong similarity to subtelomeric encoded	YER120W YCR044c YGL083W YDR510W YKL124W YLR197W YOL102c YIL080W YBR015c YBR066c	SCS2 SCY1 SMT3 SSH4 SIK1 TPT1	suppressor of an inositol auxotrophic and a choline sensitive mutant suppressor of cdc1-1 ts growth defect suppressor of GTPase mutant suppressor of mif2 temperature-sensitive mutation suppressor of shr3 suppressor of toxicity of Gal4-IKB tRNA 2'-phosphotransferase Ty3-2 of C fragment type II membrane protein weak similarity to A. niger carbon catabolite repressor protein weak similarity to A. parasiticus nor-1 protein weak similarity to A. thaliana nitrilase 3 weak similarity to A. thaliana protein
YMR322c YHR069c YMR288w YER049w YNL240c YBR301w YGL261c	strong similarity to hypothetical proteins YPL280w, YOR391c and YMR322c strong similarity to hypothetical proteins YPL280w, YOR391c and YDR533c strong similarity to hypothetical <i>S. pombe</i> and human proteins strong similarity to hypothetical <i>S. pombe</i> protein strong similarity to hypothetical <i>S. pombe</i> protein YER049W strong similarity to <i>K. marxianus</i> LET1 protein strong similarity to members of the Srp1p/Tip1p family strong similarity to members of the	YER190W YFL062W YFL063W YFL064C YFL065C YFL066C YGL260W		strong similarity to subtelomeric encoded proteins	YER120W YCR044c YGL083W YDR510W YKL124W YLR197W YOL102c YIL080W YBR015c YBR066c YKL071W YJL126W	SCS2 SCY1 SMT3 SSH4 SIK1 TPT1	suppressor of an inositol auxotrophic and a choline sensitive mutant suppressor of cdc1-1 ts growth defect suppressor of GTPase mutant suppressor of GTPase mutant suppressor of mif2 temperature-sensitive mutation suppressor of toxicity of Gal4-IKB tRNA 2'-phosphotransferase Ty3-2 orf C fragment type II membrane protein weak similarity to A. niger carbon catabolite repressor protein weak similarity to A. parasiticus nor-1 protein weak similarity to A. thaliana nitrilase 3
YMR322c YHR069c YMR288w YER049w YNL240c YBR301w YGL261c YGR294w YIL176c	strong similarity to hypothetical proteins YPL280w, YOR391c and YMR322c strong similarity to hypothetical proteins YPL280w, YOR391c and YDR633c strong similarity to hypothetical <i>S. pombe</i> and human proteins strong similarity to hypothetical <i>S. pombe</i> protein strong similarity to hypothetical <i>S. pombe</i> protein YER049W strong similarity to <i>K. marxianus</i> LET1 protein strong similarity to members of the Srp1p/Tip1p family	YER190W YFL062W YFL063W YFL064c YFL065c YFL066c YGL260W YGR295c YGR296W		strong similarity to subtelomeric encoded proteins	YER120W YCR044c YGL083W YDR510W YKL124W YLR197W YOL102c YIL080W YBR015c YBR066c YKL071W YJL126W YCR079W YHR143W	SCS2 SCY1 SMT3 SSH4 SIK1 TPT1	suppressor of an inositol auxotrophic and a choline sensitive mutant suppressor of cdc1-1 ts growth defect suppressor of CdTPase mutant suppressor of mif2 temperature-sensitive mutation suppressor of shr3 suppressor of toxicity of Gal4-IKB tRNA 2'-phosphotransferase Ty3-2 orf C fragment type II membrane protein weak similarity to A. niger carbon catabolite repressor protein weak similarity to A. parasiticus nor-1 protein weak similarity to A. thaliana nitrilase 3 weak similarity to A. thaliana protein phosphatase 2C weak similarity to a-agglutinin core protein AGA1
YMR322c YHR069c YMR288W YER049W YNL240c YBR301W YGL261c YGR294W YIL176c YKL224c	strong similarity to hypothetical proteins YPL280w, YOR391c and YMR322c strong similarity to hypothetical proteins YPL280w, YOR391c and YDR533c strong similarity to hypothetical <i>S. pombe</i> and human proteins strong similarity to hypothetical <i>S. pombe</i> protein strong similarity to hypothetical <i>S. pombe</i> protein YER049W strong similarity to <i>K. marxianus</i> LET1 protein strong similarity to members of the Srp1p/Tip1p family	YER190W YFL062W YFL063W YFL064C YFL065C YFL066C YGL260W YGR295C YGR296W YHL045W		strong similarity to subtelomeric encoded proteins	YER120W YCR044c YGL083w YDR510W YKL124W YLR197W YOL102c YIL080w YBR015c YBR066c YKL071W YJL126W YCR079W YHR143W YOR353c YER158c	SCS2 SCY1 SMT3 SSH4 SIK1 TPT1	suppressor of an inositol auxotrophic and a choline sensitive mutant suppressor of cdc1-1 ts growth defect suppressor of Cdc1-1 ts growth defect suppressor of GTPase mutant suppressor of mif2 temperature-sensitive mutation suppressor of toxicity of Gal4-IKB tRNA 2'-phosphotransferase Ty3-2 of C fragment type II membrane protein weak similarity to A. niger carbon catabolite repressor protein weak similarity to A. parasiticus nor-1 protein weak similarity to A. thaliana nitrilase 3 weak similarity to A. thaliana protein phosphatase 2C weak similarity to a-agglutinin core protein AGA1 weak similarity to adenylate cyclases
YMR322c YHR069c YMR288w YER049w YNL240c YBR301w YGL261c YGR294w YIL176c	strong similarity to hypothetical proteins YPL280w, YOR391c and YMR322c strong similarity to hypothetical proteins YPL280w, YOR391c and YDR533c strong similarity to hypothetical <i>S. pombe</i> and human proteins strong similarity to hypothetical <i>S. pombe</i> protein strong similarity to hypothetical <i>S. pombe</i> protein YER049W strong similarity to <i>K. marxianus</i> LET1 protein strong similarity to members of the Srp1p/Tip1p family strong similarity to members of the	YER190W YFL062W YFL063W YFL064c YFL065c YFL066c YGL260W YGR295c YGR296W		strong similarity to subtelomeric encoded proteins	YER120W YCR044c YGL083W YDR510W YKL124W YLR197W YOL102c YIL080W YBR015c YBR066c YKL071W YJL126W YCR079W YHR143W YOR353c YER158c YBR074W	SCS2 SCY1 SMT3 SSH4 SIK1 TPT1	suppressor of an inositol auxotrophic and a choline sensitive mutant suppressor of cdc1-1 ts growth defect suppressor of cdc1-1 ts growth defect suppressor of mil2 temperature-sensitive mutation suppressor of mil2 temperature-sensitive mutation suppressor of shr3 suppressor of toxicity of Gal4-IKB tRNA 2'-phosphotransferase Ty3-2 orf C fragment type II membrane protein weak similarity to A. niger carbon catabolite repressor protein weak similarity to A. parasiticus nor-1 protein weak similarity to A. thaliana nitrilase 3 weak similarity to A. thaliana protein phosphatase 2C weak similarity to a-agglutinin core protein AGA1 weak similarity to adenylate cyclases weak similarity to adenylate cyclases weak similarity to aminopeptidase Y
YMR322c YHR069c YMR288W YER049W YNL240c YBR301W YGL261c YGR294W YIL176c YKL224c	strong similarity to hypothetical proteins YPL280w, YOR391c and YMR322c strong similarity to hypothetical proteins YPL280w, YOR391c and YDR533c strong similarity to hypothetical <i>S. pombe</i> and human proteins strong similarity to hypothetical <i>S. pombe</i> protein strong similarity to hypothetical <i>S. pombe</i> protein YER049W strong similarity to <i>K. marxianus</i> LET1 protein strong similarity to members of the Srp1p/Tip1p family	YER190W YFL062W YFL063W YFL064C YFL065C YFL066C YGL260W YGR295C YGR296W YHL045W		strong similarity to subtelomeric encoded proteins	YER120W YCR044c YGL083w YDR510W YKL124W YLR197W YOL102c YIL080w YBR015c YBR066c YKL071W YJL126W YCR079W YHR143W YOR353c YER158c	SCS2 SCY1 SMT3 SSH4 SIK1 TPT1	suppressor of an inositol auxotrophic and a choline sensitive mutant suppressor of cdc1-1 ts growth defect suppressor of Cdc1-1 ts growth defect suppressor of GTPase mutant suppressor of mif2 temperature-sensitive mutation suppressor of toxicity of Gal4-IKB tRNA 2'-phosphotransferase Ty3-2 of C fragment type II membrane protein weak similarity to A. niger carbon catabolite repressor protein weak similarity to A. parasiticus nor-1 protein weak similarity to A. thaliana nitrilase 3 weak similarity to A. thaliana protein phosphatase 2C weak similarity to a-agglutinin core protein AGA1 weak similarity to adenylate cyclases
YMR322c YHR069c YMR288w YER049w YNL240c YBR301w YGL261c YGR294w YIL176c YKL224c YLL025w YLL064c	strong similarity to hypothetical proteins YPL280w, YOR391c and YMR322c strong similarity to hypothetical proteins YPL280w, YOR391c and YDR533c strong similarity to hypothetical <i>S. pombe</i> and human proteins strong similarity to hypothetical <i>S. pombe</i> protein strong similarity to hypothetical <i>S. pombe</i> protein YER049W strong similarity to <i>K. marxianus</i> LET1 protein strong similarity to members of the Srp1p/Tip1p family	YER190W YFL062W YFL063W YFL064c YFL065c YFL066c YGL260W YGR295c YGR296W YHL045W YHL048W YHR217c		strong similarity to subtelomeric encoded proteins	YER120W YCR044c YGL083w YDR510W YKL124W YLR197W YOL102c YIL080t YBR066c YKL071W YJL126W YCR079W YHR143W YOR353c YER158c YBR074W YCR051W	SCS2 SCY1 SMT3 SSH4 SIK1 TPT1	suppressor of an inositol auxotrophic and a choline sensitive mutant suppressor of cdc1-1 ts growth defect suppressor of cdc1-1 ts growth defect suppressor of mil2 temperature-sensitive mutation suppressor of mil2 temperature-sensitive mutation suppressor of shr3 suppressor of toxicity of Gal4-IKB tRNA 2'-phosphotransferase Ty3-2 orf C fragment type II membrane protein weak similarity to A. niger carbon catabolite repressor protein weak similarity to A. parasiticus nor-1 protein weak similarity to A. thaliana nitrilase 3 weak similarity to A. thaliana protein phosphatase 2C weak similarity to a-agglutinin core protein AGA1 weak similarity to adenylate cyclases weak similarity to adenylate cyclases weak similarity to aminopeptidase Y weak similarity to aminopeptidase Y weak similarity to Anopheles mitochondrial NADH dehydrogenase
YMR322c YHR069c YMR288W YER049W YNL240c YBR301W YGL261c YGR294W YIL176c YKL224c YLL025W YLL064c YLR037c	strong similarity to hypothetical proteins YPL280w, YOR391c and YMR322c strong similarity to hypothetical proteins YPL280w, YOR391c and YDR633c strong similarity to hypothetical <i>S. pombe</i> and human proteins strong similarity to hypothetical <i>S. pombe</i> protein strong similarity to hypothetical <i>S. pombe</i> protein YER049W strong similarity to <i>K. marxianus</i> LET1 protein strong similarity to members of the Srp1p/Tip1p family	YER190W YFL062W YFL063W YFL064c YFL065c YFL066c YGL260W YGR296c YGR296W YHL045W YHL048W YHR217c YHR218W-a		strong similarity to subtelomeric encoded proteins	YER120W YCR044c YGL083W YDR510W YKL124W YLR197W YOL102c YIL080W YBR015c YBR066c YKL071W YJL126W YCR079W YHR143W YOR353c YER158c YBR074W YCR051W YNR039c YMR152W	SCS2 SCY1 SMT3 SSH4 SIK1 TPT1	suppressor of an inositol auxotrophic and a choline sensitive mutant suppressor of cdc1-1 ts growth defect suppressor of cdc1-1 ts growth defect suppressor of GTPase mutant suppressor of mil2 temperature-sensitive mutation suppressor of toxicity of Gal4-IKB tRNA 2'-phosphotransferase Ty3-2 of C fragment type II membrane protein weak similarity to A. niger carbon catabolite repressor protein weak similarity to A. parasiticus nor-1 protein weak similarity to A. thaliana nitrilase 3 weak similarity to A. thaliana protein phosphatase 2C weak similarity to a-agglutinin core protein AGA1 weak similarity to adenylate cyclases weak similarity to atfr1p weak similarity to aminopeptidase Y weak similarity to aminopeptidase Y weak similarity to ankyrins weak similarity to ADH dehydrogenase subunit 2 weak similarity to AST1 and AST2 protein
YMR322c YHR069c YMR288w YER049w YNL240c YBR301w YGL261c YGR294w YIL176c YKL224c YLL025w YLL064c	strong similarity to hypothetical proteins YPL280w, YOR391c and YMR322c strong similarity to hypothetical proteins YPL280w, YOR391c and YDR533c strong similarity to hypothetical <i>S. pombe</i> and human proteins strong similarity to hypothetical <i>S. pombe</i> protein strong similarity to hypothetical <i>S. pombe</i> protein YER049W strong similarity to <i>K. marxianus</i> LET1 protein strong similarity to members of the Srp1p/Tip1p family strong similarity to members of the	YER190W YFL062W YFL063W YFL064c YFL065c YFL066c YGL260W YGR295c YGR296W YHL045W YHL048W YHR217c		strong similarity to subtelomeric encoded proteins strong similarity to subtelomeric encoded strong similarity to subtelomeric encoded strong similarity to subtelomeric encoded	YER120W YCR044c YGL083W YDR510W YKL124W YLR197W YOL102c YIL080W YBR016c YKL071W YJL126W YCR079W YHR143W YOR353c YER158c YER158c YBR074W YCR051W YNR039c	SCS2 SCY1 SMT3 SSH4 SIK1 TPT1	suppressor of an inositol auxotrophic and a choline sensitive mutant suppressor of cdc1-1 ts growth defect suppressor of cdc1-1 ts growth defect suppressor of GTPase mutant suppressor of mil2 temperature-sensitive mutation suppressor of shr3 suppressor of toxicity of Gal4-IKB tRNA 2'-phosphotransferase Ty3-2 orf C fragment type II membrane protein weak similarity to A. niger carbon catabolite repressor protein weak similarity to A. parasiticus nor-1 protein weak similarity to A. thaliana nitrilase 3 weak similarity to A. thaliana protein phosphatase 2C weak similarity to a-agglutinin core protein AGA1 weak similarity to adenylate cyclases weak similarity to aninopeptidase Y weak similarity to aninopeptidase Y weak similarity to aninopeptidase Y mitochondrial NADH dehydrogenase subunit 2 weak similarity to AST1 and AST2 protein weak similarity to ATPase Drs2p
YMR322c YHR069c YMR288W YER049W YNL240c YBR301W YGL261c YGR294W YIL176c YKL224c YLL025W YLL064c YLR037c	strong similarity to hypothetical proteins YPL280w, YOR391c and YMR322c strong similarity to hypothetical proteins YPL280w, YOR391c and YDR633c strong similarity to hypothetical <i>S. pombe</i> and human proteins strong similarity to hypothetical <i>S. pombe</i> protein strong similarity to hypothetical <i>S. pombe</i> protein YER049W strong similarity to <i>K. marxianus</i> LET1 protein strong similarity to members of the Srp1p/Tip1p family strong similarity to members of the	YER190W YFL062W YFL063W YFL064c YFL065c YFL066c YGL260W YGR296c YGR296W YHL045W YHL048W YHR217c YHR218W-a		strong similarity to subtelomeric encoded proteins strong similarity to subtelomeric encoded	YER120W YCR044c YGL083W YDR510W YKL124W YLR197W YOL102c YIL080W YBR015c YBR066c  YKL071W YJL126W YCR079W YHR143W YOR353c YER158c YBR074W YCR051W YNR039c  YMR152W YJL109c YIR002c	SCS2 SCY1 SMT3 SSH4 SIK1 TPT1	suppressor of an inositol auxotrophic and a choline sensitive mutant suppressor of cdc1-1 ts growth defect suppressor of cdc1-1 ts growth defect suppressor of GTPase mutant suppressor of mil2 temperature-sensitive mutation suppressor of toxicity of Gal4-IKB tRNA 2'-phosphotransferase Ty3-2 of C fragment type II membrane protein weak similarity to A. niger carbon catabolite repressor protein weak similarity to A. parasiticus nor-1 protein weak similarity to A. thaliana nitrilase 3 weak similarity to A. thaliana protein phosphatase 2C weak similarity to a-agglutinin core protein AGA1 weak similarity to adenylate cyclases weak similarity to adenylate cyclases weak similarity to aminopeptidase Y weak similarity to ankyrins weak similarity to ankyrins weak similarity to Art 1p weak similarity to Art 2p weak similarity to ATPase Drs2p weak similarity to ATPase Drs2p weak similarity to ATP-dependent RNA helicases
YMR322c YHR069c YMR288W YER049W YNL240c YBR301W YGL261c YGR294W YIL176c YKL224c YLL025W YLL064c YLR037c YMR325W	strong similarity to hypothetical proteins YPL280w, YOR391c and YMR322c strong similarity to hypothetical proteins YPL280w, YOR391c and YDR533c strong similarity to hypothetical S. pombe and human proteins strong similarity to hypothetical S. pombe protein strong similarity to hypothetical S. pombe protein YER049W strong similarity to K. marxianus LET1 protein strong similarity to members of the Srp1p/Tip1p family	YER190W YFL062W YFL063W YFL064c YFL065c YFL066c YGL260W YGR295c YGR296W YHL045W YHL045W YHR217c YHR218W-a YIR040c YJL225c		strong similarity to subtelomeric encoded proteins	YER120W YCR044c YGL083w YDR610W YKL124W YLR197W YOL102c YIL080C YKL071W YJL126W YCR079W YHR143W YOR353c YER158c YBR074W YCR051W YNR039c YMR152W YJL109c YIR002c YMR211W	SCS2 SCY1 SMT3 SSH4 SIK1 TPT1	suppressor of an inositol auxotrophic and a choline sensitive mutant suppressor of cdc1-1 ts growth defect suppressor of cdc1-1 ts growth defect suppressor of GTPase mutant suppressor of GTPase mutant suppressor of shr3 suppressor of toxicity of Gal4-IKB tRNA 2'-phosphotransferase Ty3-2 orf C fragment type II membrane protein weak similarity to A. niger carbon catabolite repressor protein weak similarity to A. niger carbon catabolite repressor protein weak similarity to A. thaliana nitrilase 3 weak similarity to A. thaliana protein phosphatase 2C weak similarity to a-agglutinin core protein AGA1 weak similarity to adenylate cyclases weak similarity to aff1p weak similarity to aminopeptidase Y weak similarity to ankyrins weak similarity to Anopheles mitochondrial NADH dehydrogenase subunit 2 weak similarity to AST1 and AST2 protein weak similarity to ATPase Drs2p weak similarity to ATPase Drs2p weak similarity to ATPase Drs2p weak similarity to ATPadependent RNA helicases
YMR322c YHR069c YMR288W YER049W YNL240c YBR301W YGL261c YGR294W YIL176c YKL224c YLL025W YLL064c YLR037c YMR325W YOR394W	strong similarity to hypothetical proteins YPL280w, YOR391c and YMR322c strong similarity to hypothetical proteins YPL280w, YOR391c and YDR533c strong similarity to hypothetical S. pombe and human proteins strong similarity to hypothetical S. pombe protein strong similarity to hypothetical S. pombe protein YER049W strong similarity to M. marxianus LET1 protein strong similarity to members of the Srp1p/Tip1p family strong similarity to Dosm1p strong similarity to Osm1p strong similarity to Para rubber tree	YER190W YFL062W YFL063W YFL064c YFL065c YFL066c YGL260W YGR296c YGR296W YHL045W YHL048W YHR217c YHR218W-a YIR040c YJL225c YJR161c		strong similarity to subtelomeric encoded proteins	YER120W YCR044c YGL083W YDR510W YKL124W YLR197W YOL102c YIL080W YBR015c YBR066c  YKL071W YJL126W YCR079W YHR143W YOR353C YER158c YER158c YBR074W YCR051W YNR039c  YMR152W YJL109c YIR002c YMR211W YEL040W	SCS2 SCY1 SMT3 SSH4 SIK1 TPT1 TTP1	suppressor of an inositol auxotrophic and a choline sensitive mutant suppressor of cdc1-1 ts growth defect suppressor of cdc1-1 ts growth defect suppressor of GTPase mutant suppressor of mil2 temperature-sensitive mutation suppressor of shr3 suppressor of toxicity of Gal4-IKB tRNA 2'-phosphottransferase Ty3-2 orf C fragment type II membrane protein weak similarity to A. niger carbon catabolite repressor protein weak similarity to A. parasiticus nor-1 protein weak similarity to A. thaliana nitrilase 3 weak similarity to A. thaliana protein phosphatase 2C weak similarity to a-agglutinin core protein AGA1 weak similarity to adenylate cyclases weak similarity to aminopeptidase Y weak similarity to aminopeptidase Y weak similarity to ankyrins weak similarity to Anapheles mitochondrial NADH dehydrogenase subunit 2 weak similarity to ATPase Drs2p weak similarity to ATPase Drs2p weak similarity to ATPase Drs2p weak similarity to B tubulins weak similarity to B tubulins weak similarity to B. subtilis 1,3-1,4—glucanase
YMR322c YHR069c YMR288W YER049W YNL240c YBR301W YGL261c YGR294W YIL176c YKL224c YLL025W YLL064c YLR037c YMR325W YOR394W YEL047c	strong similarity to hypothetical proteins YPL280w, YOR391c and YMR322c strong similarity to hypothetical proteins YPL280w, YOR391c and YDR533c strong similarity to hypothetical S. pombe and human proteins strong similarity to hypothetical S. pombe protein strong similarity to hypothetical S. pombe protein YER049W strong similarity to members of the Srp1p/Tip1p family strong similarity to Osm1p	YER190W YFL062W YFL063W YFL064c YFL065c YFL066c YGL260W YGR295c YGR296W YHL045W YHL045W YHR217c YHR218W-a YIR040c YJL225c		strong similarity to subtelomeric encoded proteins	YER120W YCR044c YGL083w YDR610W YKL124W YLR197W YOL102c YIL080C YKL071W YJL126W YCR079W YHR143W YOR353c YER158c YBR074W YCR051W YNR039c YMR152W YJL109c YIR002c YMR211W	SCS2 SCY1 SMT3 SSH4 SIK1 TPT1 TTP1	suppressor of an inositol auxotrophic and a choline sensitive mutant suppressor of cdc1-1 ts growth defect suppressor of cdc1-1 ts growth defect suppressor of mif2 temperature-sensitive mutation suppressor of shr3 suppressor of toxicity of Gal4-IKB tRNA 2'-phosphotransferase Ty3-2 of C fragment type II membrane protein weak similarity to A. niger carbon catabolite repressor protein weak similarity to A. niger carbon catabolite repressor protein weak similarity to A. parasiticus nor-1 protein weak similarity to A. thaliana nitrilase 3 weak similarity to A. thaliana protein phosphatase 2C weak similarity to a-agglutinin core protein AGA1 weak similarity to adenylate cyclases weak similarity to adenylate cyclases weak similarity to ankyrins weak similarity to ankyrins weak similarity to ankyrins weak similarity to Arpoheles mitochondrial NADH dehydrogenase subunit 2 weak similarity to ATP-dependent RNA helicases weak similarity to ATP-dependent RNA helicases weak similarity to β tubulins weak similarity to β. subtilis 1,3-1,4—
YMR322c YHR069c YMR288W YER049W YNL240c YBR301W YGL261c YGR294W YIL176c YKL224c YLL025W YLL064c YLR037c YMR325W YOR394W YEL047c YFL059W	strong similarity to hypothetical proteins YPL280w, YOR391c and YMR322c strong similarity to hypothetical proteins YPL280w, YOR391c and YDR533c strong similarity to hypothetical S. pombe and human proteins strong similarity to hypothetical S. pombe protein strong similarity to hypothetical S. pombe protein YER049W strong similarity to Marianus LET1 protein strong similarity to members of the Srp1p/Tip1p family strong similarity to Para rubber tree ethylene-responsive protein 1 and	YER190W YFL062W YFL063W YFL064c YFL065c YFL066c YGL260W YGR296c YGR296W YHL045W YHL048W YHR217c YHR218W-a YIR040c YJL225c YJR161c		strong similarity to subtelomeric encoded proteins	YER120W YCR044c YGL083W YDR510W YKL124W YLR197W YOL102c YIL080W YBR015c YBR066c YKL071W YJL126W YCR079W YHR143W YOR35ac YER158c YER158c YBR074W YCR051W YNR039c  YMR152W YJL109c YIR002c YMR211W YEL040W YNL203c	SCS2 SCY1 SMT3 SSH4 SIK1 TPT1 TTP1	suppressor of an inositol auxotrophic and a choline sensitive mutant suppressor of cdc1-1 ts growth defect suppressor of cdc1-1 ts growth defect suppressor of GTPase mutant suppressor of GTPase mutant suppressor of shr3 suppressor of toxicity of Gal4-IKB tRNA 2'-phosphotransferase Ty3-2 orf C fragment type II membrane protein weak similarity to A. niger carbon catabolite repressor protein weak similarity to A. niger carbon catabolite repressor protein weak similarity to A. parasiticus nor-1 protein weak similarity to A. thaliana nitrilase 3 weak similarity to A. thaliana protein phosphatase 2C weak similarity to a-agglutinin core protein AGA1 weak similarity to adenylate cyclases weak similarity to adenylate cyclases weak similarity to ankyrins weak similarity to Arf1p weak similarity to Anopheles mitochondrial NADH dehydrogenase subunit 2 weak similarity to AST1 and AST2 protein weak similarity to ATP-dependent RNA helicases weak similarity to B. subtilis 1,3-1,4—glucanase weak similarity to B. subtilis CDPdiacylglycerol-serine O-phosphatidyltransferase
YMR322c YHR069c YHR069c YMR288w YER049w YNL240c YBR301w YGL261c YGR294w YIL176c YKL224c YLL025w YLL064c YLR037c YMR325w YOR394w YEL047c YFL059w YNL333w YNR065c	strong similarity to hypothetical proteins YPL280w, YOR391c and YMR322c strong similarity to hypothetical proteins YPL280w, YOR391c and YDR633c strong similarity to hypothetical S. pombe and human proteins strong similarity to hypothetical S. pombe protein strong similarity to hypothetical S. pombe protein YER049W strong similarity to Marking Strong similarity to marking LET1 protein strong similarity to members of the Srp1p/Tip1p family strong similarity to Para rubber tree ethylene-responsive protein 1 and identical to hypothetical protein YFL059w strong similarity to Pep1p	YER190W YFL062W YFL063W YFL064c YFL065c YFL066c YGL260W YGR296c YGR296W YHL045W YHL048W YHR217c YHR218W-a YIR040c YJL225c YJR161c YJR162c		strong similarity to subtelomeric encoded proteins	YER120W YCR044c YGL083W YDR510W YKL124W YLR197W YOL102c YIL080W YBR015c YBR066c YKL071W YJL126W YCR079W YHR143W YOR353c YER158c YBR074W YCR051W YNR039c YMR152W YJL109c YIR002c YMR211W YEL040W YNL203c	SCS2 SCY1 SMT3 SSH4 SIK1 TPT1 TTP1	suppressor of an inositol auxotrophic and a choline sensitive mutant suppressor of cdc1-1 ts growth defect suppressor of cdc1-1 ts growth defect suppressor of mif2 temperature-sensitive mutation suppressor of shr3 suppressor of toxicity of Gal4-IKB tRNA 2'-phosphotransferase Ty3-2 of C fragment type II membrane protein weak similarity to A. niger carbon catabolite repressor protein weak similarity to A. parasiticus nor-1 protein weak similarity to A. thaliana nitrilase 3 weak similarity to A. thaliana nitrilase 3 weak similarity to a. thaliana protein phosphatase 2C weak similarity to a-agglutinin core protein AGA1 weak similarity to adenylate cyclases weak similarity to andrip weak similarity to anklyrins weak similarity to anklyrins weak similarity to Anopheles mitochondrial NADH dehydrogenase subunit 2 weak similarity to ATP-dependent RNA helicases weak similarity to ATP-dependent RNA helicases weak similarity b. S. subtilis 1,3-1,4—glucanase weak similarity b. S. subtilis CDPdiacylglycerol-serine C-phosphatidyltransferase weak similarity to B. subtilis hypothetical protein X
YMR322c YHR069c YMR288W YER049W YNL240c YBR301W YGL261c YGR294W YIL176c YKL224c YLL025W YLL064c YLR037c YMR325W YOR394W YEL047c YFL069W YNL333W YNR065c YNR066c	strong similarity to hypothetical proteins YPL280w, YOR391c and YMR322c strong similarity to hypothetical proteins YPL280w, YOR391c and YDR533c strong similarity to hypothetical S. pombe and human proteins strong similarity to hypothetical S. pombe protein strong similarity to hypothetical S. pombe protein yER049W strong similarity to members of the Srp1p/Tip1p family strong similarity to Para rubber tree ethylene-responsive protein 1 and identical to hypothetical protein YFL059w strong similarity to Pep1p	YER190W YFL062W YFL063W YFL064c YFL065c YFL066c YGL260W YGR295c YGR296W YHL045W YHL045W YHR217c YHR218W-a YIR040c YJL225c YJR161c YJR162c YKL223W YKL225W		strong similarity to subtelomeric encoded proteins	YER120W YCR044c YGL083w YDR610W YKL124W YLR197W YOL102c YIL080c YKL071W YJR126W YCR079W YHR143W YOR353c YER158c YBR074W YOR051W YNR039c YMR152W YJL109c YJR002c YMR211W YEL040W YNL203c YDR336W YOR111W	SCS2 SCY1 SMT3 SSH4 SIK1 TPT1 TTP1	suppressor of an inositol auxotrophic and a choline sensitive mutant suppressor of cdc1-1 ts growth defect suppressor of cdc1-1 ts growth defect suppressor of cdc1-1 ts growth defect suppressor of GTPase mutant suppressor of shr3 suppressor of toxicity of Gal4-IKB tRNA 2'-phosphotransferase Ty3-2 orf C fragment type II membrane protein weak similarity to A. niger carbon catabolite repressor protein weak similarity to A. niger carbon catabolite repressor protein weak similarity to A. thaliana nitrilase 3 weak similarity to A. thaliana protein phosphatase 2C weak similarity to a. thaliana protein AGA1 weak similarity to adenylate cyclases weak similarity to adenylate cyclases weak similarity to anixyrins weak similarity to ankyrins weak similarity to Anopheles mitochondrial NADH dehydrogenase subunit 2 weak similarity to ATPase Drs2p weak similarity to ATPase Drs2p weak similarity to B. subtilis 1,3-1,4—glucanase weak similarity to B. subtilis CDPdiacylglycerol-serine C-phosphatidyltransferase weak similarity to B. subtilis hypothetical protein X weak similarity to B. subtilis hypothetical protein X weak similarity to B. subtilis hypothetical protein X weak similarity to B. subtilis maf protein
YMR322c YHR069c YMR288w YER049w YNL240c YBR301w YGL261c YGR294w YIL176c YKL224c YLL025w YLL064c YLR037c YMR325w YOR394w YEL047c YFL0699w YNL333w YNR065c YNR066c YER089c PTC2	strong similarity to hypothetical proteins YPL280w, YOR391c and YMR322c strong similarity to hypothetical proteins YPL280w, YOR391c and YDR633c strong similarity to hypothetical S. pombe and human proteins strong similarity to hypothetical S. pombe protein strong similarity to hypothetical S. pombe protein YER049W strong similarity to Marianus LET1 protein strong similarity to members of the Srp1p/Tip1p family strong similarity to Para rubber tree ethylene-responsive protein1 strong similarity to Pep1p strong similarity to Pep1p strong similarity to Pep1p strong similarity to Pep1p strong similarity to phosphoprotein phosphatases	YER190W YFL062W YFL063W YFL064c YFL065c YFL066c YGL260W YGR296c YGR296W YHL045W YHL045W YHL045W YHR217c YHR218W-a YIR040c YJL225c YJR161c YJR162c YKL223W YKL225W YKR106W		strong similarity to subtelomeric encoded proteins	YER120W YCR044c YGL083W YDR510W YKL124W YLR197W YOL102c YIL080W YBR015c YBR066c YKL071W YJL126W YCR079W YHR143W YOR353c YER158c YBR074W YCR051W YNR039c YMR152W YJL109c YMR211W YEL040W YNL203c YDR336W YOR336W YOR111W YNR074c	SCS2 SCY1 SMT3 SSH4 SIK1 TPT1 TTP1	suppressor of an inositol auxotrophic and a choline sensitive mutant suppressor of cdc1-1 ts growth defect suppressor of cdc1-1 ts growth defect suppressor of mif2 temperature-sensitive mutation suppressor of shr3 suppressor of toxicity of Gal4-IKB tRNA 2'-phosphotransferase Ty3-2 of C fragment type II membrane protein weak similarity to A. niger carbon catabolite repressor protein weak similarity to A. parasiticus nor-1 protein weak similarity to A. parasiticus nor-1 protein weak similarity to A. thaliana nitrilase 3 weak similarity to A. thaliana protein phosphatase 2C weak similarity to a-agglutinin core protein AGA1 weak similarity to adenylate cyclases weak similarity to ankyrins weak similarity to aminopeptidase Y weak similarity to aminopeptidase Y weak similarity to Aropheles mitochondrial NADH dehydrogenase subunit 2 weak similarity to ATP-dependent RNA helicases weak similarity to ATP-dependent RNA helicases weak similarity to B. subtilis Na-1,4-glucanase weak similarity to B. subtilis CDPdiacylglycerol-serine O-phosphatidyltransferase weak similarity to B. subtilis hypothetical protein X weak similarity to B. subtilis hypothetical protein X weak similarity to B. subtilis naf protein weak similarity to B. subtilis naf protein weak similarity to B. subtilis nitrite reductase (nirB)
YMR322c YHR069c YMR288W YER049W YNL240c YBR301W YGL261c YGR294W YIL176c YKL224c YLL025W YLL064c YLR037c YMR325W YOR394W YEL047c YFL059W YNL333W  YNR065c YNR066c YER089c PTC2	strong similarity to hypothetical proteins YPL280w, YOR391c and YMR322c strong similarity to hypothetical proteins YPL280w, YOR391c and YDR533c strong similarity to hypothetical S. pombe and human proteins strong similarity to hypothetical S. pombe protein strong similarity to hypothetical S. pombe protein YER049W strong similarity to members of the Srp1p/Tip1p family strong similarity to Para rubber tree ethylene-responsive protein 1 and identical to hypothetical protein YFL059w strong similarity to Pop1p strong similarity to protein kinase Kin4p phosphatases	YER190W YFL062W YFL063W YFL064c YFL065c YFL066c YGL260W YGR295c YGR296W YHL045W YHL045W YHR217c YHR218W-a YIR040c YJL225c YJR161c YJR162c YKL223W YKL225W		strong similarity to subtelomeric encoded proteins	YER120W YCR044c YGL083w YDR510W YKL124W YLR197W YOL102c YIL080c YKL071W YJR126W YCR079W YHR143W YOR353c YER158c YBR074W YOR353c YER158c YBR074W YOR051W YNR039c  YMR152W YJL109c YIR002c YMR211W YEL040W YNL203c YDR336W YOR111W YNR074c YNR004W	SCS2 SCY1 SMT3 SSH4 SIK1 TPT1 TTP1	suppressor of an inositol auxotrophic and a choline sensitive mutant suppressor of cdc1-1 ts growth defect suppressor of shr3 suppressor of toxicity of Gal4-IKB tRNA 2'-phosphotransferase Ty3-2 orf C fragment type II membrane protein weak similarity to A. niger carbon catabolite repressor protein weak similarity to A. niger carbon catabolite repressor protein weak similarity to A. thaliana nitrilase 3 weak similarity to A. thaliana protein phosphatase 2C weak similarity to a-agglutinin core protein AGA1 weak similarity to adenylate cyclases weak similarity to afr1p weak similarity to aminopeptidase Y weak similarity to Anopheles mitochondrial NADH dehydrogenase subunit 2 weak similarity to ATP-dependent RNA helicases weak similarity to ATP-dependent RNA helicases weak similarity to B. subtilis 1,3-1,4—glucanase weak similarity to B. subtilis CDPdiacylglycerol-serine C-phosphatidyltransferase weak similarity to B. subtilis hypothetical protein X weak similarity to B. subtilis hypothetical protein X weak similarity to B. subtilis maf protein weak similarity to B. subtilis nitrite reductase (nirB) weak similarity to B. subtilis nitrite reductase (nirB) weak similarity to bovine interferon γ
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## Genetic and physical maps of Saccharomyces cerevisiae

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Genetic and physical maps for the 16 chromosomes of *Saccharomyces cerevisiae* are presented. The genetic map is the result of 40 years of genetic analysis. The physical map was produced from the results of an international systematic sequencing effort. The data for the maps are accessible electronically from the *Saccharomyces* Genome Database (SGD: http://genome-www.stanford.edu/Saccharomyces/).

During the past 40 years, 11 compilations of mapping data for the yeast *Saccharomyces cerevisiae* have been made by R. K. Mortimer and colleagues<sup>1-11</sup>. The last such compilation<sup>11</sup> included mapping data to 1991, and contained for the first time the results of physical as well as genetic mapping methods. Here we present the twelfth, and probably the last, such compilation. These final maps are based on the genetic information accumulated over the years<sup>1-11</sup> and, for the physical mapping data, on an entirely new set of data: the complete genomic sequence of *S. cerevisiae*.

The genetic and physical maps were derived from two entirely different types of data. Genetic distances between genes were determined by tetrad analysis. Distances for gene–gene and gene–centromere linkages are expressed in centimorgans (cM) and were calculated using a maximum-likelihood equation<sup>12</sup> which yields values for map distance, an interference parameter, and error calculations for these two parameters. Mapping results on more than 2,600 named genes are presented. Physical distances are calculated directly from the complete DNA sequence. The precise values of all parameters (both tetrad analysis results and chromosomal basepair coordinates) are available from the SGD.

Associations between open reading frames (ORFs) and corresponding mutations were made using a set of hybridization filters, originally produced by L. Riles and M. Olson<sup>13</sup>, which are now available from the American Type Culture Collection (http://www.atcc.org/). Other such associations were made by complementation experiments using cloned DNA fragments and/or sequence analysis of mutants. The data for some of these associations are published, but the documentation for all of them can be found on SGD.

Now that the entire yeast genome sequence is available, most revisions of the map will consist of associations between a biological function and an ORF. These associations will often involve the study of mutants of the gene. In the past, such an association invariably resulted in the naming of the gene; this process is likely to continue until all of the genes have been associated with a function and have thereby acquired a name. Because the genetic and physical maps are unlikely to change significantly, we see no need for any future publications; rather, we expect the electronic version of the maps to evolve into increasingly accurate guides to *S. cerevisiae* biology.

The maps shown here are also available in a continually updated electronic form from the SGD (http://genome-www.stanford.edu/Saccharomyces/), which will also provide directions to other useful information (gene names, aliases, phenotypes, mapping data, protein information, and curated compilations of published literature about genes).

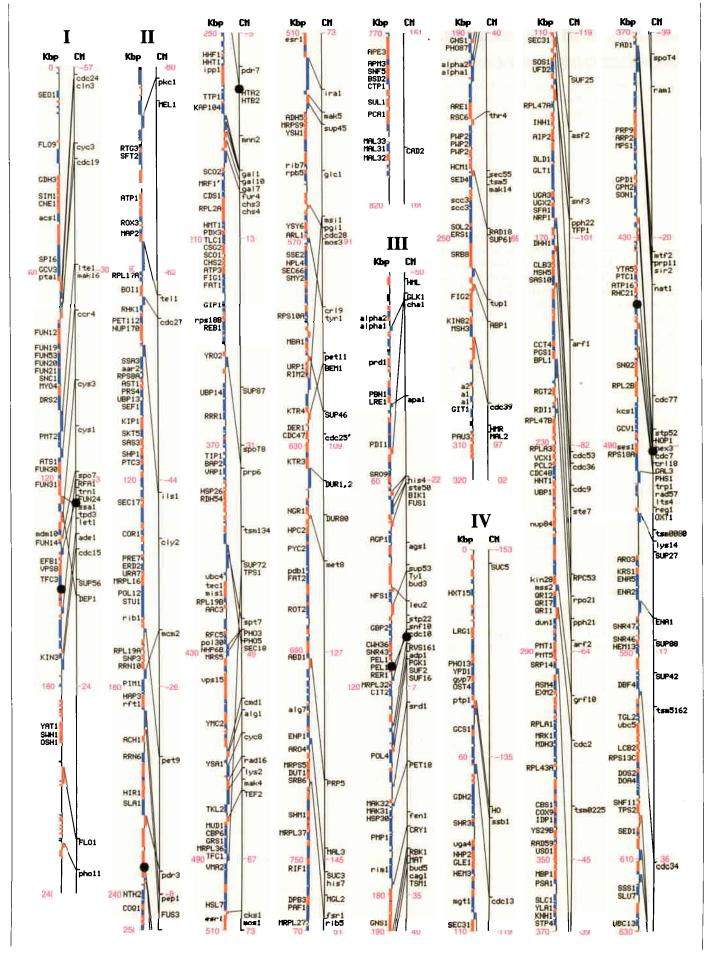
- 1. Hawthorne, D. C. & Mortimer, R. K.  $Genetics\,45,\,1085-1110\,(1960).$
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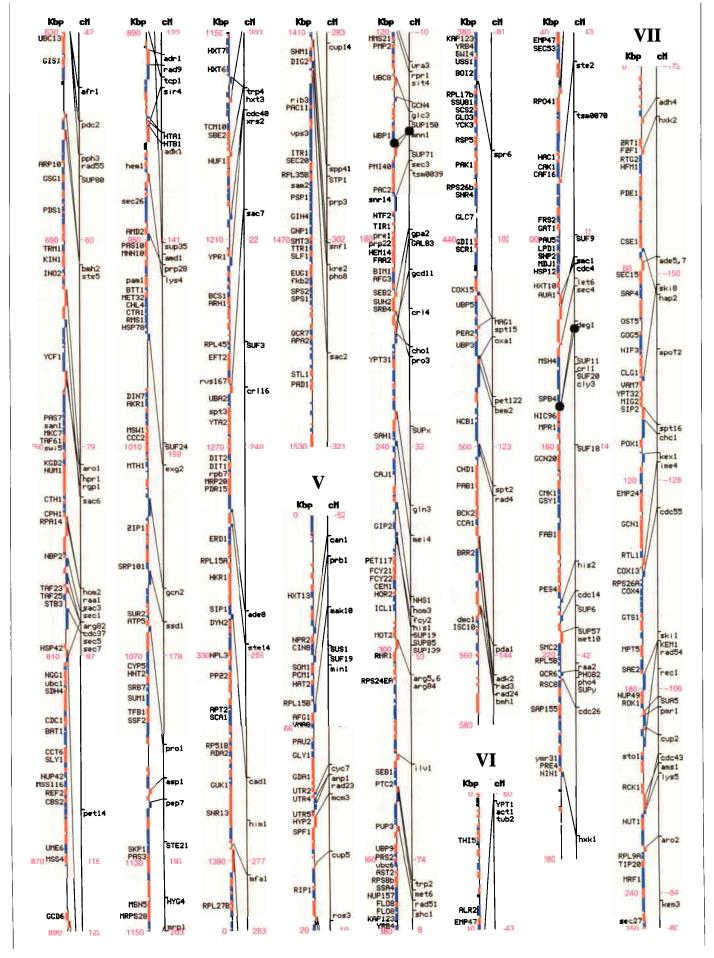
Acknowledgements. We thank all of the yeast researchers, who are too numerous to name individually; F. Dietrich, M. Johnston, E. W. Jones, M. Olson and B. F. F. Ouellette for criticism; A. Goffeau, for encouragement and advice and J. Garrels, D. Lipman, A. Bairoch and H. W. Mewes for their continuing collaboration. S. G. D. is funded by a grant from the National Center for Human Genome Research

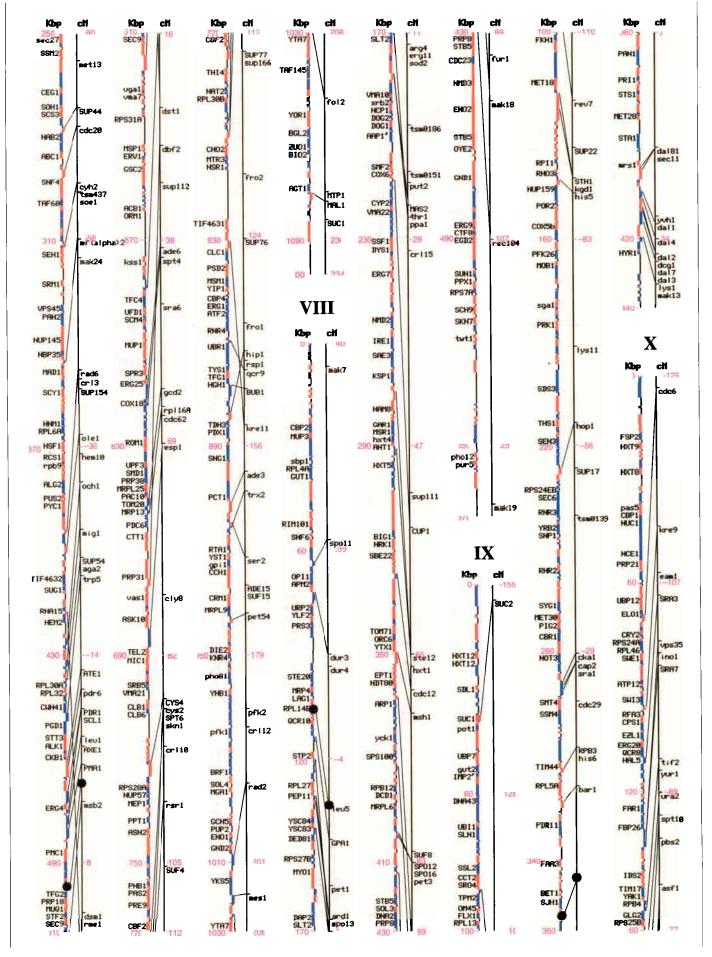
 $Correspondence \ should \ be \ addressed \ to \ J.\ M.\ C.\ (e-mail: cherry@genome.stanford.edu).$ 

Figures I-XVI (overleaf, pages 68-73): Genetic and physical maps, and their correlations, of the 16 Saccharomyces cerevisiae chromosomes. A parallel comparison of the physical map (left, in kilobase pairs) and the genetic map (right, in centimorgans) of each of the 16 chromosomes is illustrated. The information in this figure is available on the Saccharomyces Genome Database (http://genome-www.stanford.edu/Saccharomyces/). The physical map consists of coloured boxes that indicate ORFs. ORFs on the Watson strand (left telomere is the 5' end of this strand) are shown as red boxes, those on the Crick strand as blue boxes. Where it has been defined, the gene name of an ORF is indicated. The genetic map is based on data collected since 1991 by the SGD project, as well as on earlier data<sup>1-1</sup>. Horizontal tick marks on the right of the genetic map line indicate positions of genes. Lines connect genetically mapped genes with their ORF on the physical map. A single name is listed for known synonyms.

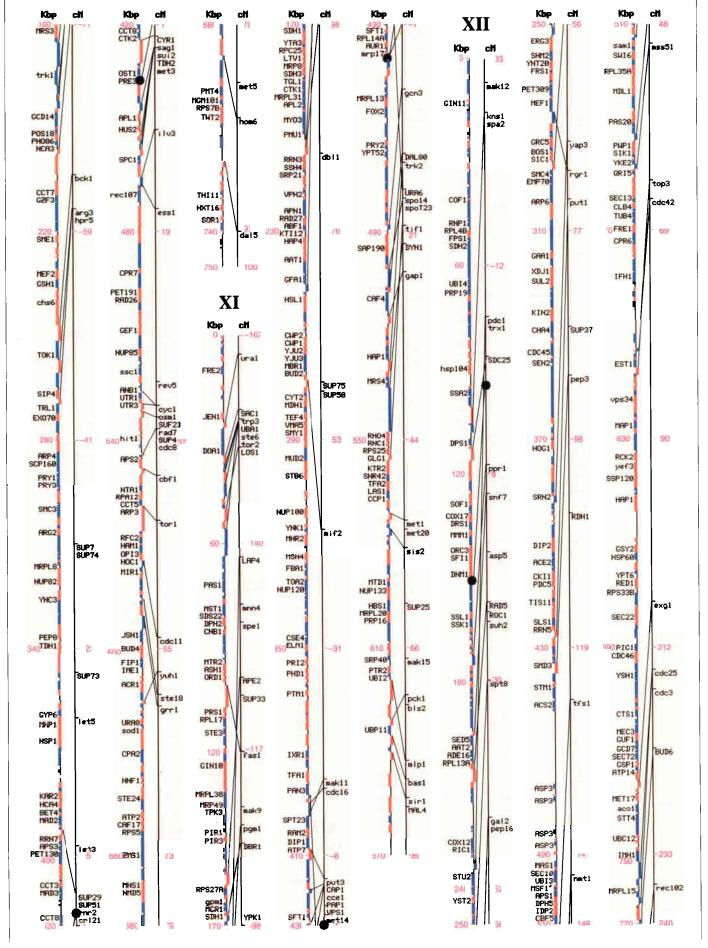




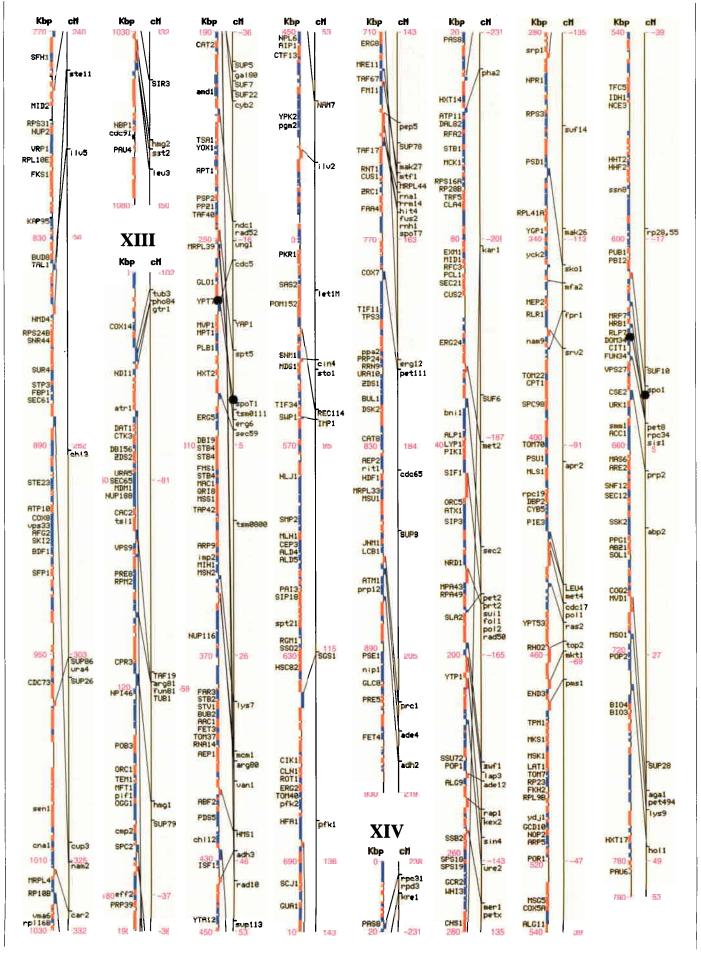




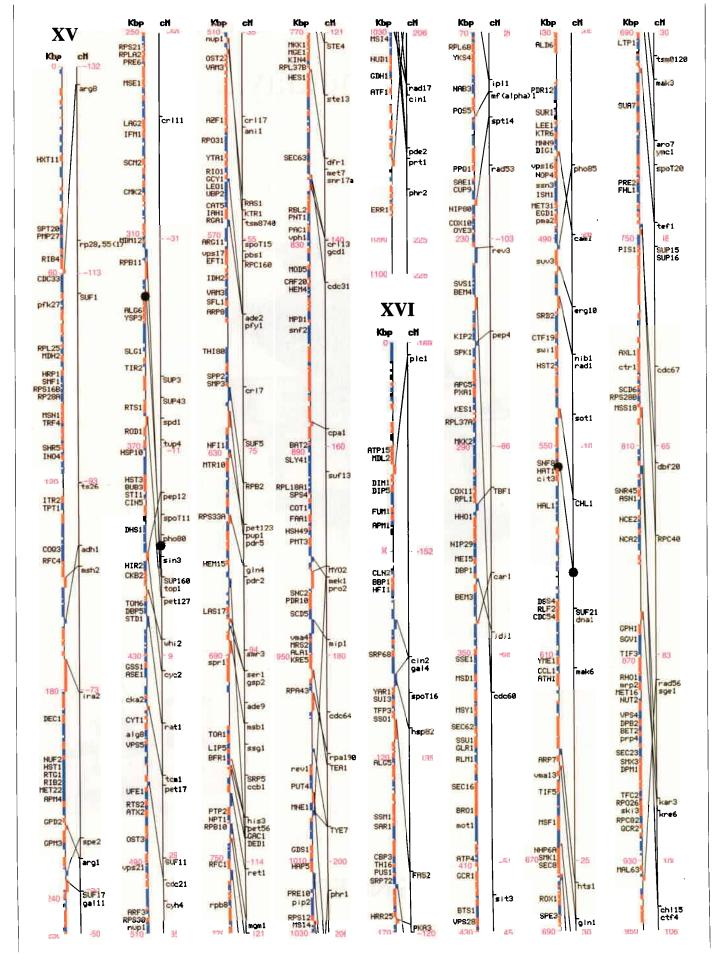




#### maps







# The nucleotide sequence of Saccharomyces cerevisiae chromosome IV

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The complete DNA sequence of the yeast Saccharomyces cerevisiae chromosome IV has been determined. Apart from chromosome XII, which contains the 1-2 Mb rDNA cluster, chromosome IV is the longest *S. cerevisiae* chromosome. It was split into three parts, which were sequenced by a consortium from the European Community, the Sanger Centre, and groups from St Louis and Stanford in the United States. The sequence of 1,531,974 base pairs contains 796 predicted or known genes, 318 (39.9%) of which have been previously identified. Of the 478 new genes, 225 (28.3%) are homologous to previously identified genes and 253 (32%) have unknown functions or correspond to spurious open reading frames (ORFs). On average there is one gene approximately every two kilobases. Superimposed on alternating regional variations in G+C composition, there is a large central domain with a lower G+C content that contains all the yeast transposon (Ty) elements and most of the tRNA genes. Chromosome IV shares with chromosomes II, V, XII, XIII and XV some long clustered duplications which partly explain its origin.

The technique of determining the DNA sequence of large genomes has been unchanged for 21 years¹. Sequencing the yeast genome required considerable organization by the European Union, which initiated the grouping of 35 laboratories to sequence the first yeast chromosome² and coordinate an international effort to sequence the others. Chromosome IV had already been characterized both physically and genetically³.⁴, and our sequence data presented are in good agreement with these preliminary data.

The average base composition of chromosome IV is 37.9% G+C, which is lower than for most of the yeast chromosomes (for example, 38.5% for chromosome III (ref. 2) and 38.3% for chromosome II (ref. 5)). Along the 1,513,914 base pairs of the chromosome there are alternating regions about 50 kilobases long of high and low G+C content (Fig. 1). This periodicity is not clearly associated with a variation in gene density, as has been observed for some other chromosomes<sup>6,7</sup>. The central domain of chromosome IV (coordinates 500,000 to 1,215,000) has a much lower G+C value (37.4%) than the two flanking regions (38.2%); a similar observation has been made for the much smaller chromosome VI(ref. 8).

The low G+C content of the central domain seems to be correlated with the presence of Ty elements. All nine Ty1 or Ty2 elements, including a truncated form of Ty1, are localized between coordinates 450,000 and 1,190,000 (Fig. 1). Yeast transposons seem to insert into specific chromosomal regions<sup>9,10</sup> where they are localized preferentially upstream of tRNA genes, as they might interact with the RNA polymerase III machinery<sup>11</sup>. The density of tRNA genes in the central domain of chromosome IV is twice that in the flanking regions in which no Ty elements are found. A total of 27 tRNA genes are localized on each strand of the chromosome, 17 of which are located in the central domain. Of the 27 tRNA genes, 18 are in the vicinity of long terminal repeats (LTRs). Thus most of the tRNA genes, LTRs and Ty elements,

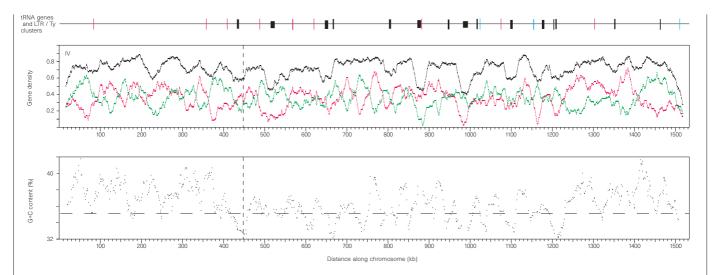


Figure 1 Overall molecular architecture of chromosome IV shows positions of tRNA genes, solo LTR or Ty elements (thin vertical lines), or clusters of them (thick vertical lines), along the chromosome map. Panels show variation of gene density (top) and base composition (bottom) along the sequence-based map of chromosome IV (scale in kilobases from the left telomere). Vertical broken lines indicate the centromere. Gene density is expressed as the probability for each nucleotide to be part of an ORF,

andwas calculated using sliding windows of 30 kb (in steps of 0.5 kb) for the Watson strand alone (red line), the Crick strand alone (green line), and the sum of both (black line). G+C content was calculated from the silent positions of codons using a sliding window of 13 consecutive ORFs; the horizontal broken line indicates average G+C content (%) at silent positions of codons.

together with a lower G+C content, are found in this central domain. In chromosome II the 13 tRNA genes and three Ty elements are in AT-rich regions<sup>5</sup>.

The left telomere of chromosome IV is very similar to other yeast telomeres. Adjacent to the  $C_{1-3}A$  repeat are the usual STR-A, STR-B, STR-C, STR-D and the core X elements (435–904) shared by most of the telomeres<sup>12</sup>. The left end of chromosome IV shares with the right end of chromosome X a large, nearly identical block of sequence similarity more than 19 kilobases long. This duplication includes five ORFs, which code for almost identical products. Indeed the sequences are so similar that we needed to exclude the possibility of contamination of the cosmid contig of chromosome IV by DNA sequences from chromosome X. To confirm our data, we established the genomic sequence of the junction between the duplicated sequence and the rest of the chromosome. Such subtelomeric duplications have often been observed in the yeast genome, suggesting either recent or continuous exchange of genetic information<sup>13</sup>. The right telomere has a less conventional structure with an internal  $TG_{1-3}$  repeat.

Using the classical definition of ORFs (one ATG codon followed by at least 99 sense codons), 776 ORFs were recorded in the chromosome; there are also 20 ORFs shorter than 99 amino acids long, making a total of 796 ORFs. Small ORFs of between 25 and 99 codons were extracted and analysed for different properties (codon usage, homologies and ATG environment) to determine their function<sup>7</sup>; 15 had either a putative translation product that is homologous to proteins of other genes, or a codon adaptation index (CAI) greater than 0.2. Five other short ORFs, longer than 91 amino acids, are thought to be 'questionable'. These results support the choice of the threshold of more than 99 codons<sup>14</sup>, but show that some short ORFs must be considered<sup>15</sup>. Moreover, this evaluation has to take into account that at least 7% of the ORFs can be considered 'questionable'6. Disregarding the retrotransposons, this corresponds to a gene density of one ORF per 2,000 base pairs. The G+C regions correlate roughly, although not precisely, with the regions of increased density. There are approximatively equal numbers of ORFs on the DNA strands (387 on the Watson and 409 on the Crick). However, the gene density is clearly not uniform on a given DNA strand (Fig. 1). This marked prefer ence for an arrangement in which genes are on the same strand has already been observed for other chromosomes<sup>16,17</sup> for which long runs of genes on one strand could be observed. Such gene-rich regions are mainly visible at the two ends of the chromosomes, with more uniform gene density in the central part of the chromosome (550,000 to 1,200,000).

Although not as great as predicted by an approximate calculation<sup>18</sup>, the high number of Ty and LTR elements in that region should give rise to large numbers of genome rearrangements (inversions, deletions and reciprocal translocations), which could explain this difference with the flanking regions. The construction of gene arrangement has led to general features that probably reflect important functional constraints. Thus the size of regions between ORFs is clearly dependent on the orientation of the flanking genes. In the case of divergent promoters, the mean size is 744 base pairs, whereas it is just 324 bp for convergent terminators. An intermediary situation (593 bp) is found for terminator-promoter combinations. This striking difference in inter-ORF size is probably due to the sequence requirements in the promoter regions for the regulation of gene expression. Nevertheless, the mean size of the inter-ORF region in the case of head-to-head gene orientations is small, and suggests that many divergent genes share common regulation signals. The GAL1-GAL10 promoter was the first to be described<sup>19</sup>, but many other candidates for common regulation have been revealed by the systematic genome sequencing.

Based on the canonical sequences known to control the splicing process, 30 introns can be identified in genes coding for proteins<sup>20</sup>. This represents 4% of genes having an intron in their ORF or in the 5′ untranslated region, a figure close to the situation for the genome as a whole. Of these intron-containing genes, 12 code for ribosomal proteins, three for proteins of the actin family, three for proteins involved in the ubiquitin-dependent protein degradation system, and the rest are distributed between genes that do not necessarily have a high CAI.

Although dependent on the criteria used to estimate the significance of sequence similarities, roughly 30% of the 796 ORFs of chromosome IV are orphans<sup>21</sup> with no sequence relatives in the available databases. This is one of the most exciting findings from the systematic sequencing approach of the yeast genome. Future work will tell us whether some of these genes are really 'yeast specific' and why they have escaped detection by the genetic approaches. The number of sequence orphans will no doubt decrease with the arrival of new sequence data<sup>22</sup>. As an example from chromosome IV, the ORF YDL120w, which had no relatives, is homologous to the human gene recently discovered to be involved in Friedreich's ataxia<sup>23</sup>.

Chromosome IV is the longest chromosome in terms of coding sequences, and so might be expected to have features that are scattered on the other chromosomes. One of these features might be the non-uniform organization of the chromosome. The central domain (from 500,000 to

1,250,000) which makes up half of chromosome IV has several distinctive features. First, as with most of the chromosomes, it has more or less regularly spaced regions rich in G+C, but its central domain has a lower G+C content. Second, this central domain contains all of the Ty and most of the LTR elements found on the chromosome. Third, the central domain also contains 18 of the 27 tRNA genes, so its tRNA gene density is twice that of the rest of the chromosome. Finally, the DNA strand distribution of the ORFs is different in the central region when compared with that of the flanking regions. The ORF arrangement of this region might result from a greater genetic plasticity.

Analysis of structural relationships inside the yeast genome might provide an insight into eukaryotic genome organization and evolution. Redundancy is one of the most salient features of the yeast genome structure<sup>24</sup>, and the DNA sequence of the whole yeast genome reveals several types of redundancy, probably originating from different biological processes. The most common form of redundancy involves individual genes that have a homologue in the genome; about 20% of the genes of chromosome IV are in this class. Second, there are clusters of very similar copies of a gene, often arranged in tandem; for example, there are five copies of the ENA1 (or PMR2) gene on chromosome IV. Third, subtelomeric duplications are frequent and involve large regions of chromosomes that are very similar in both coding and non-coding regions<sup>13</sup>. Finally, clustered duplications are characterized by clusters of homologous genes in the same order, usually in the same orientation, and interspersed by long DNA fragments. Such paralogous regions have already been described between chromosomes III and XIV (ref. 25) and between chromosomes V and X (ref. 26). Only in the case of the duplication between chromosomes III and XIV is the gene order conserved. It is 15 kilobases long and contains four genes. The clustered duplications on chromosome IV are made up of at least 336 kilobase pairs, including 49 pairs of homologous genes. Chromosome IV shares large ordered cluster of homologous genes with chromosomes II, V, VIII, XII and XIII (ref. 27). A careful analysis of these duplications will no doubt tell us a great deal about the evolution of the yeast genome. In the largest interchromosomal clustered duplications, involving chromosome IV (coordinates 449,752-569,763) and chromosome II (238,164-407,122), the 18 gene pairs are all transcribed in the same direction. When known, most of the genes from a pair code for proteins with homologous but not identical functions (for example GAL1 and GAL3)19. Homologous genes from a clustered duplication can also be completely identical or totally different in their function. An extreme case of divergence involves YDR037w, which codes for a lysyl tRNA synthetase, and YBR060w\_A, which is part of chromosome II, in which many stop codons interrupt an ORF, of which parts are homologous to YDR037w. Such a pseudogene could not be detected by searching the DNA sequence of chromosome II, as it has very short ORFs and no ATG codon. To our knowledge, this is the most degenerated yeast pseudogene yet discovered. This observation suggests that similar degenerated pseudogenes may have escaped previous analyses, and hence that the total number of pseudogenes may be underestimated.

A pair of genes from a clustered duplication can also differ in the presence of an intron. Both YDR055w and YBRO78w are homologous to the gene *SPS2*, but only YBR078w has an intron, and the CAI of the two genes differs from 0.27 (YDR055w) to 0.61 (YBR078w), suggesting an unusual evolutionary process. The compared analysis of the interspersed DNA fragments is also very informative. For example, chromosome II has a Ty element where an LTR element is present at the equivalent position on chromosome IV, suggesting that the Ty element was lost from chromosome IV after the duplication process.

The greatly different degrees of similarities between the different gene pairs composing a duplicated region indicate that at least some of the duplications have evolved at very different rates, suggesting in some cases that gene conversion processes. A careful quantitative analysis of the relative evolution rates of the different elements will be required to establish a chronological order of the different events. Nevertheless, evidence suggests that a first duplication event has been followed by the dispersal of the duplicated elements by the insertions of DNA fragments of various sizes and gene composi-

tions. Most of these clustered duplications in chromosome IV are localized in the pericentromeric region. The centromere itself is included in the longest duplicated region, which occurs between chromosomes IV (coordinates 450,000-570,000) and II (238,000-407,000). Similar localizations of clusters have already been noticed on other chromosomes<sup>7,17,25</sup>. To explain the proximity of the centromere, it was suggested that the gene dispersion of the initial cluster of duplicated genes might be slower in the centromeric regions than nearer the telomere owing to the adverse effects of rearrangements on chromosome segregation<sup>25</sup>. Alternatively, the centromeric duplications might have been essential steps in the construction of the yeast genome<sup>25</sup>. In agreement with these ideas, the central domain of chromosome IV contains few traces of clustered redundancies, perhaps because of its genetic plasticity. These preliminary observations indicate that the availability of the complete sequence of the yeast genome will allow a greater understanding of the processes involved in creating the genome architecture.

#### Methods

The sequence was assembled from a set of 44 partly overlapping cosmids and lambda phages from two independent contigs of chromosome IV. The 650-kb cosmid contig corresponding to the left part of chromosome IV was constructed mainly from a specific cosmid library obtained from a gel-purified chromosome portion (J. D. H. et al., unpublished), and a few other cosmid clones from this contig came from a library<sup>29</sup>. The rest of the chromosome sequence was established from a cosmid-lambda phage library (L. Riles & M. Olson, unpublished, and ref. 30). The two cosmid contigs were made from two closely related yeast strains: AB972, derived from S288C<sup>30</sup>, and FY1679, a diploid strain issued from the cross between FY23 and FY73, both of which are isogenic with S288C except for the markers indicated. Sequence analysis of a large overlapping fragment (of about 170 kb) confirmed that the strains AB972 and FY1679 are very similar, as the number of base differences was below the estimated error rate. Only the extreme left telomeric regions of the two strains clearly differ, probably in the number of their TG<sub>1-3</sub> repeats (C. B. and C. J., unpublished). The telomeres were isolated independently and sequenced from a plasmid clone generated by integration at the  $TG_{1-3}$  repeats of the telomere, followed by excision of the plasmid and capture of the flanking sequences<sup>13</sup>. Two gaps in the 650-kb left cosmid contig (constructed from the strain FY1679) were filled with lambda clones from the library constructed from AB972. They correspond to the regions 9,756-11360 and 363,100-368,150 . The left 600-kb region was sequenced according to the rules followed by the European consortium and the 20 cosmids and phages were distributed to 18 contractors, whereas the central part was sequenced by the Sanger Centre (EMBL database SCCHRIV, accession no. Z71256); the rest of the chromosome was sequenced by groups from Washington University in St Louis and Stanford University in the United States.

There were very few base differences in the overlapping fragment sequenced in parallel by the Sanger Centre and by the European consortium, demonstrating that both approaches are reliable. However, a verification procedure was necessary because of the greater heterogeneity of the European approach. This was done on  $25\,$ regions of the left part of the chromosome, according to the protocol of G. V. (manuscript in preparation). This allows direct polymerase chain reaction (PCR) sequencing of a 300-bp region of the yeast genome limited by two previously designed oligonucleotides. We could thus correct a sequence in which a bacterial transposon had been inserted during the cloning process but no real sequence error could be detected at this final step of the sequencing project. Sequence errors could only be corrected after examination of the raw sequence data. From these data, the error rate of this part of the yeast chromosome IV sequence presented is less than four errors per 10 kb. In the central part of the chromosome the error rate is estimated as less than one error per 10 kb. Specific strategies were developed to sequence difficult parts of the chromosome. Thus, for example, to finish the regions between the two transposons located in cosmid 8142 (http://www.sanger.ac.uk/ ~yeastpub/svw/sequencing.html), a PCR product covering this region from strain MCYC2576 was sequenced. This strain, a gift from E. Louis, did not contain the transposons

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# The nucleotide sequence of Saccharomyces cerevisiae chromosome V

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Here we report the sequence of 569,202 base pairs of *Saccharomyces cerevisiae* chromosome V. Analysis of the sequence revealed a centromere, two telomeres and 271 open reading frames (ORFs) plus 13 tRNAs and four small nuclear RNAs. There are two Ty1 transposable elements, each of which contains an ORF (included in the count of 271). Of the ORFs, 78 (29%) are new, 81 (30%) have potential homologues in the public databases, and 112 (41%) are previously characterized yeast genes.

As part of an international collaborative effort to sequence the total genome of the yeast *Saccharomyces cerevisiae*, we have deduced the DNA sequence of 569,202 base pairs of yeast chromosome V. We used an overlapping set of recombinant yeast cosmid and lambda clones that together cover the entire chromosome (except for the extreme ends of the telomeres). A line drawing of chromosome V and the identification of the

recombinant DNAs sequenced are shown in Fig. 1. The sequence was broken arbitrarily into 11 slightly overlapping pieces for ease of handling and deposited in Genbank (see Fig. 1 for accession numbers).

Sequencing was accomplished in two phases: the 'shotgun' phase, using dye-primer chemistry, and the 'finishing' phase, using the polymerase chain reaction (PCR) and dye-terminator chemistry. There were no gaps in the sequence at the end of shotgun sequencing and assembly. The assembled, continuous sequence of chromosome V has 569,202 bp, starting from the guanine residue of the <code>Sau3A</code> site on the left vector boundary of the leftmost clone (1160 in Fig. 1). The 569-kilobase sequence is based on the results from 32,631 individual lanes of sequencing gels, or reads. The average depth of coverage was 12.5-fold. The minimum acceptable coverage was three, with at least one read from each strand.

After shotgun sequencing and assembly, problems remained in the sequence at a frequency of (roughly) two per kilobase and were of several types. They included the inability to count unambiguously the number of repeating units, such as poly (dA), and guanine compressions. There were also small regions in which only one of the two strands had been sequenced. These difficulties were resolved during the finishing phase.

After finishing, the 569-kb contig was checked against three external sets of data. First was the use of tetrad segregation data to derive a genetic map for yeast<sup>1</sup>. The chromosome V gene order based on DNA sequence was in complete agreement with the tetrad segregation data. There were two locations on the genetic map (CENV at 151 kb and PRO3 at 200 kb) where closely spaced loci had been mapped against distant markers and not against each other, resulting in ambiguities of relative locus order<sup>1</sup>, which were resolved using the DNA sequence. The gene order across the centromere is GLC3 tRNA-Arg GCN4 CENV MNN1. In the region of PRO3, at 200 kb, the gene order is PRO3 GPA2 GCD11 CHO1 GAL83. Second, our sequence was compared to the *S. cerevisiae* sequences already deposited in Genbank, using both the FASTA and BLAST programs<sup>2,3</sup>. In the rare cases of sequence difference, we re-examined our trace files. Remaining ambiguities were resolved using the same methodology as finishing. Third, we checked our data against the primary *Eco*RI/*Hin*dIII double-digestion fragment maps of the recombinant yeast DNAs<sup>4</sup>. Our sequence was examined for EcoRI and HindIII cleavage sites. Of 534 mapped fragments, there were only five discrepancies, which is a tribute to the care taken in preparing the cleavage sites map<sup>4</sup>. The five apparent discrepancies between the double-digest map<sup>4</sup> and our sequence are: the map had doublets where the sequence predicts singlets after bases 272, 193; 280,936; and 441,102; the map has a fragment that was not found in the sequence after base 414,946; and the sequence is missing a cleavage site after base 506,807.

We examined all six possible reading frames of the 569-kb sequence for ORFs of at least 300 bp that began with a start codon and ended with a stop codon. As a special case, an ORF could be interrupted if there were yeast splice donor/acceptor/branchpoint sequences present at the appropriate intervals. The remaining sequence was examined using FASTA and BLAST for homology to sequences in the public databases. This enabled us to find small ORFs, as well as the centromere, 13 tRNAs, two Ty1 elements (which each contain an ORF), four small nuclear RNAs, many delta and delta-like elements, and the highly conserved X and Y' sequences characteristic of yeast telomeres (see refs 5, 6) at the far left and right ends.

Initially, 271 ORFs were identified in the 569-kb sequence, although this number has changed as evaluation continued. The 271 ORFs make up roughly 70% of the sequence, with an average of 2.1 kb per ORF. The 'average' ORF (1.4 kb) encodes 475 amino acids. Of the ORFs, 112 (41%) have been characterized previously, 81 (30%) have apparent homologues in the public databases, and 78 (29%) are new; six (2%) are spliced. Of the 81 apparent homologues, 55 of these are to other *S. cerevisiae* sequences.

The fractional G+C content of the 569,202 bp of chromosome V is 0.384. The combined ORF DNAs have a fractional G+C content of 0.401, and the combined 'non-ORF' DNA has a G+C content of 0.351.



**Figure 1** The central line representing *S. cerevisiae* chromosome V is marked in kilobase pairs, starts at the left at the guanine of the *Sau*3A site of the leftmost recombinant yeast DNA, and extends to the right to 570 kb. The centromere, *CEN*, is represented by a solid circle at ~151 kb. Above the line, placed across their map positions, are the individual recombinant yeast DNAs that were sequenced; 16 cosmids (thin lines), 8

lambdas (thick lines), and 1 plasmid (very thick line). Genbank accession numbers are placed below the line, above the bars indicating the corresponding map positions. From left to right, Genbank accession numbers are U18795, U18779, U18530, U18778, U18796, U18813, U18814, U18839, U18916, U18917 and U18922. There is some deliberate overlap between Genbank entries to maintain contiguity.

There are only two places on chromosome V where the quality of the sequence is not high. In the first case, at about 312 kb, there are ~50 bp of unique sequence bounded on both sides by poly (dA): poly (dT). Taq polymerase, and the other DNA polymerases tested, frequently terminated within the homopolymer, and seldom reached the short unique sequence. Therefore, we have only a few reads across the unique sequence. In the second case, at about 450 kb, there is a 5-kb stretch that contains many delta and delta-like sequences interspersed with a small amount of unique sequence. The clone containing this segment was shotgun sequenced to an average of 16-fold redundancy, yet there were relatively few reads in this region. Therefore, for PCR amplification, this 5-kb region was divided into many virtual parts, based on the positions of the unique sequences. Several custom primer pairs, and internal sequencing primers, were designed and synthesized for each part<sup>7</sup>. These were used in PCR amplification reactions with total yeast genomic DNA as the template. We have sequenced carefully across this region. For most bases, there is sequence from both strands.

There were three special cases that warrant further attention. First, a point mutation had occurred during either cloning or subsequent propagation in Escherichia coli. In an overlap region shared by two recombinant DNAs (lambda 5898 and cosmid 9867; Fig. 1), the sequence should be the same, but in this case there was one reproducible base difference. Lambda 5898 has a guanine residue where cosmid 9867 has an adenine residue. When total yeast genomic DNA was used as a template for PCR amplification, the product of which was used as a template for dye-terminator sequencing, the base at that position was an adenine. The traces showed no indication of a naturally occurring polymorphism. We therefore conclude that the guanine in lambda 5898 was the result of a mutation. In the second special case, we examined the ORFs for any apparently premature, in-frame stop codon, and found two that were puzzling. The first was the TGA stop codon at position (rounded-off) 352 kb. There are three rightward-reading frames, and this stop codon (TGA) is in the first of these. Following the TGA in this frame, there is a lysine codon (AAA) and a methionine codon (ATG) followed by a long ORF. In the second reading frame there are three stop codons: two (TGA, TAA) are next to each other, the third is five triplets further on; this frame is truly stopped. However, there is a long ORF starting with a methionine codon considerably upstream and ending at the double stop codons TGA, TAA. The third reading frame has many stop codons. The two ORFs share one base: A, the first base (ATG) of the first reading frame and the last base (AAA) of the second reading frame. In general, yeast ORFs are separated by several hundred bases. Except for a -1 frame shift in the first reading frame, there would be one ORF rather than two. However, despite sequencing through this position many times, the sequence, the TGA and the five A bases in a row remained invariant. The second apparently premature stop codon occurred in the ORF that corresponds to FLO8 at  $\sim$ 375 kb. The TAG stop codon between YER108c and YER109c appears not just in the recombinant yeast DNA, but also in PCR amplifications from total yeast DNA. Thus it is possible that FLO8 is not functional in yeast strain AB972. In the third special case, in the entire collection of recombinant yeast DNAs, only lambda 3612 (Fig. 1) covers this region. We found

lambda 3612 to be highly unstable, giving rise to non-random DNA deletions at extremely high frequency. Starting with 30 individual plaques from a primary stock, only one yielded lambda 3612 DNA without a detectable deletion, as judged by *EcoRI/HindIII* double-digestion patterns, but even that gave rise to deleted DNAs upon subsequent growth. Therefore, all of the lambda 3612 sequence came (uncharacteristically) from just one preparation of DNA.

A comparison of the DNA base sequence of chromosome V to that of the other *S. cerevisiae* chromosomes shows that there are two stretches that have similar genes in the same order on two other yeast chromosomes. A portion of the left arm of chromosome V, containing CYC7 and RAD, shows the same relative gene order as chromosome X, but in the opposite orientation, as noted previously<sup>8</sup>. In addition, a 60-kb region of the left arm of chromosome IX contains nine genes or ORFs for which each has an apparent homologue within a 60-kb region of the right arm of chromosome V. The nine putative protein pairs and their calculated similarity (identicality)<sup>9</sup> are: (1) YIL045w/YER054c, 63 (44) %; (2) YIL050w/YER059w, 71 (52) %; (3) YIL051c/YER057c, 87 (70) %; (4) YIL053w/YER062c, 97 (92) %; (5) YIL056w/YER064c, 63 (47) %; (6) tRNA-ser, 100%; (7) YIL057c/YER067w, 85 (67) %; (8) RNR3/YER070w, 90 (82) %; and (9) YIL074c/YER081w, 95 (91) %. On chromosome V itself, the FCY2 protein product<sup>10</sup> and the putative YER060w translation product are 87 (75) % related.

When considering the accuracy of our 569,202-bp sequence of *S. cerevisiae* chromosome V, we must emphasize that (essentially) all of the sequence was determined from recombinant DNA propagated in *E. coli*. Even if our sequence of the recombinant DNAs were 100% accurate, there may be sequence differences between the recombinant DNAs and the yeast genome. We identified one apparent point mutation solely because it occurred within a region common to two recombinant DNAs. Other point mutations, occurring during cloning or propagation in *E. coli*, would probably not be detected.

There is a much more dramatic example of a discrepancy between the sequence of a recombinant DNA and the yeast genome. We deposited our chromosome V sequence in Genbank and SacchDB (http://genomewww.stanford.edu/) in December 1994. On 18 April 1996, we received an e-mail from J.-L. Souciet, J. de Montigny and S. Potier (CNRS, Strasbourg) politely telling us that ~2 kb were missing from our sequence. They had found that, in addition to FCY2 (YER056c; encoding a purinecytosine permease<sup>10</sup>) at ~267 kb and a closely related ORF (YER060w) at ~275 kb, there is also a third closely related ORF in this region (Genbank accession no. X97346) (Fig 2.). Our sequence across the apparent deletion came from two libraries made from lambda 6592. The sequence is 12-fold deep, and there are no traces that diverge from our Genbank sequence. The Genbank sequence is therefore an accurate sequence of this particular recombinant DNA: lambda 6592. We had intended to sequence cosmid 9380. Repeated attempts to prepare 9380 yielded only minute amounts of DNA. We abandoned cosmid 9380, and instead sequenced three lambda DNAs: 4678, 6592 and 4742. From the tiny amount of cosmid 9380 DNA, we constructed (and sequenced) a Sau3A library. The data (traces) from the library of Sau3A-cleaved 9380 DNA were used within the assemblies



Figure 2 The bottom line is a schematic map of yeast chromosome V from 240 kb to 310 kb. Individual, sequenced recombinant DNAs are placed above the line and across the appropriate map positions. Cosmid 9380 covers map positions ~240 kb to 300 kb and overlaps lambda 3612. The latter is the only recombinant DNA in the entire Olson collection<sup>4,14</sup> that covers map positions 300 kb to 310 kb. Because 9380 could only be produced in minute amounts, three lambda DNAs (thick lines) were substituted: 4678, 6592 and 4742. The X marks the position of the ~2 kb deletion in 6592 DNA.

of the three lambda DNAs. There were some data from the 9380 library that were left over, mostly vector without insert, low-quality traces, *etc.*, which we put aside. We searched our 'left-over' 9380 traces for homology to unique sequences in Genbank X97346 and found one excellent (97.3% identity) match for 294 bp (bounded by *Sau*3A sites). We conclude that lambda 6592 has a deletion relative to the yeast genome and that one additional ORF should be added, bringing the ORF total to 272.

To complete the sequence of chromosome V, an insertion of 2,011 bp (Genbank accession number X97346) should be made at base 275,951 of our sequence as has been done in SacchDB. In addition, H. Wedler and R. Wambutt have sequenced the left (Genbank accession no. U73806) and right (Genbank accession no. U34775) telomeres of yeast chromosome V. Within SacchDB, 2,477 bp have been placed to the left of the leftmost base (the G of the leftmost Sau3A site) of our sequence. That G is no longer base 1 but base 2,478. Within the left telomere, there is an ORF, YEL077c, which brings the current ORF total to 273. Concomitantly in SacchDB, 3,181 bp have been placed to the right of our sequence.

Basically, there are two types of errors: random and systematic. If there is a random error in an individual sequence read, we will find and correct that error because we sequenced both strands to high redundancy (average of 12.5-fold). It is much more difficult to identify a systematic error that is inherent in, for example, the dye-primer chemistry, polyacrylamide gel electrophoresis, Taq polymerase, or base-calling software, that systematically misreads or deletes a base(s) within a particular sequence. Tag polymerase seemed to have systematic difficulties synthesizing across short repeating units; not only is the number of repeats often ambiguous, the sequence traces following a repeat are often diminished in signal quality. We believe that this observation reflects an inherent characteristic of Taq polymerase. Of the several DNA polymerases tested in an attempt to solve this problem, Amplitaq FS polymerase (Perkin-Elmer 402079) yielded the best number of good sequence calls, but did not solve the problem completely. However, the problem in counting the short repeating units unambiguously may not be a sequencing problem but in some cases may reflect true biological heterogeneity. A second possible systematic error arises from the well-known guanine compressions. Guanine compressions are usually identified when the base-calling software identifies fewer guanines on one strand than cytosines on the opposing strand. However, if two (or more) guanine compressions are positioned symmetrically on opposing strands, the compression on one strand is compensated by an analogous compression on the other strand. There are no 'extra' cytosines, and the existence of the compressions could be missed.

One reason for sequencing all of the *S. cerevisiae* DNA is that yeast is important as a model organism. A second reason is to test the approaches to, and develop technologies for, large-scale DNA sequencing in preparation for the sequencing of the human genome. In this regard, we would like to describe some important lessons learned during the sequencing of yeast chromosome V. First, 800 kb were shotgun sequenced to achieve 569,202 bp of contiguous sequence, an inefficiency of 40%. Considerable time and money would have been saved if the ends of the recombinant yeast DNAs had been mapped relative to each other (a 'sequence-ready'

contig of cosmid DNAs). Second, a large amount of freezer space was used in archiving recombinant M13 DNAs, a small percentage of which were later used as templates for finishing. An important reason in the delay of finishing was the cost of oligonucleotide primers for PCR. Finishing has been made economical by the availability of low-cost oligonucleotides<sup>7</sup>, so long-term storage of M13 DNAs is no longer necessary. Third, when the Yeast Genome Project was started, the conventional wisdom had that it was necessary to sequence a set of overlapping cosmids. However, we now know that the sequence of DNA as large as bacterial genomes can be assembled using a shotgun approach<sup>11,12</sup>. If we started again, we would purify S. cerevisiae chromosome V directly by pulse-field gel electrophoresis, hydrodynamically shear the DNA to an average size of 1 kb (ref 13) and shotgun clone the sheared DNA directly into the M13 sequencing vector. The yeast genome could probably have been sequenced by the direct shotgun cloning of total genomic DNA to generate one M13 sequencing library. Individual cosmid and lambda clones could have been used to fill holes and resolve ambiguities.

#### Methods

All of the *S. cerevisiae* recombinant DNAs sequenced in this study were constructed in the laboratory of M. Olson<sup>4,14</sup>. With the exception of plasmid 7990, which was derived from two yeast strains<sup>15</sup>, all of the recombinant DNAs were derived from yeast strain AB972. Those recombinant DNAs with number designations less than 8000 are lambdas (except for plasmid 7990), those with numbers over 8000 are cosmids. We sequenced 16 cosmids (8198, 8199, 8229, 8334, 9115, 9132, 9163, 9379, 9537, 9581, 9669, 9747, 9781, 9867, 9871 and 9981), eight lambdas (1160, 3612, 4678, 4742, 5898, 6134, 6592 and 6693), and one plasmid (7990) (Fig. 1). We also obtained some sequence from another five cosmids (8063, 9268, 9380, 9495 which contained a large deletion and 9675) and two lambdas (3955 and 6052). These *S. cerevisiae* recombinant DNAs (except 9495) are available from the American Type Culture Collection.

The 'shotgun' sequencing strategy was to reduce randomly the size of the yeast recombinant DNAs ('inserts') to approximately 1 kb. The inserts were ligated to the M13 sequencing vector by using a 'linker-adaptor' system, which minimizes the formation of chimaeric DNAs. The recombinant M13 'sequencing library' was electroporated into *E. coli* and plated. Individual M13 plaques were picked and grown, and recombinant M13 DNAs were purified. (Our detailed laboratory protocols are freely available on the World-Wide Web at http://sequence-www.stanford.edu.)

The shotgun sequencing used dye-primer chemistry in cycle sequencing reactions, followed by fluorescence detection using an ABI 373A automated sequencer. Most of the sequence data from individual lanes ('traces' or 'reads') were edited automatically using custom software, with borderline cases being edited manually using the TED software<sup>16</sup>. Individual sequence reads were assembled using the XBAP program<sup>16</sup>. The final sequence was determined by editing manually the assembled reads

Where there seemed to be overlapping ORFs, in either the same or in the opposite direction, the conventional assumption was made that yeast seldom uses both overlapping frames. Three criteria were used to determine which was the most likely ORF. First, using both FASTA and BLAST programs, each of the overlapping reading frames was examined for homology to known genes in the public databases; an ORF with homology was chosen over one without. Second, each organism has its own distinctive preference for certain codons over others. This preference can be expressed in arithmetic terms, as it is within the GeneFinder program (L. Hiller and P. Green, 1990–1993; documentation, software and yeast codon usage data files. Genome Sequencing Center, Washington University School of Medicine, St Louis, MO 63108, USA). GeneFinder was used to compare the codon usage for each of the overlapping ORFs. The ORF that more closely matched yeast's codon usage was chosen; in almost all cases, this distinction was unequivocal. Third, the longer ORF was selected. The nomenclature for yeast ORFs is composed of five letter/number combinations: Y (for yeast), E (the fifth letter of the alphabet for V), L or R (for the left or right arm, as defined genetically), a number (counted sequentially from the centromere in both directions), and w or c (for the transcribed strand); for example, the URA3 gene, encoding orotidine-5'-phosphate decarboxylase, is YEL021w.

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# The nucleotide sequence of Saccharomyces cerevisiae chromosome VII

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The complete nucleotide sequence of *Saccharomyces cerevisiae* chromosome VII has 572 predicted open reading frames (ORFs), of which 341 are new. No correlation was found between G+C content and gene density along the chromosome, and their variations are random. Of the ORFs, 17% show high similarity to human proteins. Almost half of the ORFs could be classified in functional categories, and there is a slight increase in the number of transcription (7.0%) and translation (5.2%) factors when com-

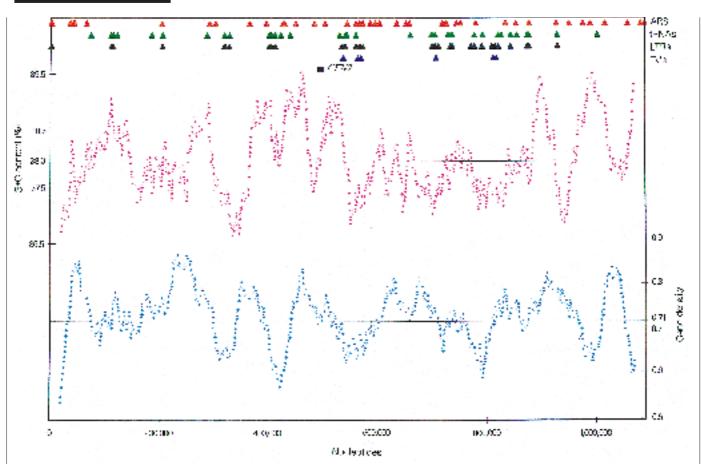


Figure 1 Top, position of genetic elements along chromosome VII. Middle, compositional variation curve; each point represents the average G+C content in a 40-kb sliding window (steps are 500 bp); the horizontal line represents the average G+C (38%). Bottom, gene density is expressed as

the fraction of nucleotides within ORFs versus the total number of nucleotides in sliding windows of 40 kb (steps are 500 bp); the horizontal line represents the average gene density (0.71).

# pared with the complete *S. cerevisiae* genome. Accurate verification procedures demonstrate that there are less than two errors per 10,000 base pairs in the published sequence.

Before the publication in 1992 of the yeast chromosome III sequence<sup>1</sup>, the only available *S. cerevisiae* genome sequence of appreciable size was a contig of 24 kilobases (kb) from chromosome VII (refs 2, 3). A 60-kb physical map covering the left arm of this chromosome between *CEN7* and *TRP5* markers had been built, allowing sequencing and transcriptional mapping of nine ORFs located in the 24-kb region spanning the *PMA1* and *ATE1* loci. Analysis of these data led to the estimation of a minimum number of 5,300 expressed genes in yeast. In this centromeric region a recombination frequency of 1 cM corresponded to an average distance of 3.3 kb, compared with 2.9 kb for the complete chromosome. These extrapolations have been confirmed by the complete 1,090,936 nucleotide sequence of chromosome VII, the fourth longest in *S. cerevisiae*.

Chromosome VII contains 564 ORFs of more than 99 codons, plus eight smaller, previously identified, ORFs. Of these 572 ORFs, 19 are predicted to carry an intron at their extreme 5' end. The *RPL6A* gene is interrupted by two introns, one of which codes for the small nuclear RNA39. Of the 572 ORFs, 152 (26.5 %) had previously been characterized biochemically, and an additional 79 (14 %) had been characterized phenotypically. Of these 231 known genes, disruption phenotypes have been reported in 140 cases, of which 37 are lethal. An additional 61 ORFs (11 %) show a high similarity (FASTA score above 300 or one third of self score) to another ORF of known function. However, if the threshold FASTA score is lowered to 150, which is a significant value in many cases, another 20 ORFs (3.5 %) could be envisaged to be of predictable function, raising the total number of ORFs of known or predictable function to 312 (54.6 %). Of the remaining ORFs, 74 (12.9 %) are similar to protein sequences of unknown function, and 186 ORFs (32.5 %) show weak

or no significant similarity to any other protein sequence in the public data libraries. Finally, the expression of 63 ORFs (11 %) is questionable owing to their partial overlap with other ORFs (44) or to a combination of small size (less than 150 codons) and low codon adaptation index (CAI below 0.110)<sup>4</sup>. However, these criteria are not absolute as at least four expressed ORFs from chromosome VII do not meet them: *AGA2* (87 codons; CAI, 0.089), *SOH1* (127 codons; CAI, 0.096), *SPT4* (102 codons; CAI, 0.109) and *VMA21* (77 codons; CAI, 0.109). Almost 30 % of the ORFs from chromosome VII are redundant, as 166 show high similarity (FASTA score greater than 300 or one third of the self score) with other yeast genes.

The average ORF size is 468 codons, the longest (YGL195w, GCN1) being 2,672 codons. The average distance between ORFs located on the same strand is 514 base pairs when not containing tRNAs or long terminal repeats (LTRs) and six are longer than 2,000 bp. In the case of divergent promotors, the spacing is 553 bp, with two being longer than 2,000 bp. The mean size allocated to convergent terminators is only 304 bp, and one of these is longer than 2,000 bp. The mean G+C content of inter-ORFs regions is 33 %. All of these values are very similar to those found for the complete genome  $^5$ .

An attempt has been made to classify chromosome VII ORFs in functional categories (Table 1). Note that any given protein may belong to more than one category. The percentage of ORFs from chromosome VII in each functional category correlates with the functional distribution of ORFs within the complete genome, with a slightly higher content in the transcription (13 transcription factors) and protein synthesis (18 ribosomal proteins) categories.

The putative transmembrane spans have been computed with the KKD algorithm<sup>6</sup> using a rather low threshold<sup>7</sup> that takes into account not only the fully hydrophobic spans, but also the predicted amphipathic  $\alpha$ -

Table 1 Functional categories of yeast ORFs from chromosome VII			
Functional category	0	RFs	
	Number	Percentage	
Metabolism	55	9.0	
Energy	19	3.1	
DNA synthesis	10	1.6	
Transcription	43	7.0	
Protein synthesis	32	5.2	
Protein destination	18	2.9	
Transport facilitation (permeases)	18	2.9	
Intracellular traffic	17	2.8	
Cell structure	19	3.1	
Organelle assembly	11	1.8	
Signal transduction	5	0.8	
Cell division	24	3.9	
Cell rescue	12	1.9	
Retrotransposons	13	2.1	
Unclassified	318	51.8	
Total	614	••••••	

helices which, when present in a bundle, can contribute to the formation of a polar channel within the lipid bilayer. Of the 572 ORFs, 359 (63 %) show no predicted transmembrane spans or are known to be soluble, 79 (14 %) carry at least three putative spans or are known to be membrane bound, and 134 (23 %) have one or two predicted hydrophobic  $\alpha$ -helices, a feature which does not necessarily mean that they are membranebound. All ORFs have been submitted to PSORT analysis<sup>8</sup> to predict their subcellular localization. If we consider a high certainty score to be at least 0.8 for a given localization, and a low one to be less than 0.5 for all other possible localizations, only 76 ORFs match these criteria: 37 ORF products predicted to be in the nucleus, 16 in the endoplasmic reticulum, nine in the mitochondria, nine in the plasma membrane, two in the vacuole, two in the peroxisome, and one secreted outside the cell. For the 23 chromosome VII proteins of known subcellular localization, the PSORT prediction was correct in 14 cases (61 %). Note that three of the six ORFs that exhibited an erroneous nuclear localization were ribosomal proteins which are known to carry a nuclear localization signal to allow the biosynthesis of the ribosome particles<sup>9</sup>.

By applying the program PYTHIA $^{10}$  to search for simple repeats within a gene, we detected at least 19 genes with regularly repeated nucleotides corresponding to repeated amino acids in the encoded proteins. Some of these regions are composed of single amino-acid repeats, including 21 aspartates (in YGL227w), 13 aspartates (YGL058w, RAD6), 11 and 8 glutamines (YGL066w), 18 asparagines (YGR233c), 15 asparagines (YGL014w), 10 asparagines (YGL013c, PDR1), 23 serines (YGR023w) or 16 serines (YGR130c). We also identified more complex repeats, such as (T S/N ATTT A/E S X $_{4}$ )<sub>11</sub> in YGR296w (=Y'), (QQQP) $_{9}$  in YGL122c (NAB2), (DEEE) $_{3}$  in YGL164w, (AQ) $_{14}$  in YGL181w (GTS1), (TSSS) $_{9}$  in YGL028c, or (HN) $_{5}$  in YGL178w (MPT5).

A systematic search for similarities with human proteins was performed for the 572 ORFs of yeast chromosome VII. A total of 95 ORFs (16.6 %) show a very significant similarity (FASTA score higher than 300 or higher than one third of self score) with human proteins, of which these 79 (13.8%) correspond to known yeast proteins whose function is often closely related to the function of the human homologue. Similarities of some of the 16 previously unknown ORFs (2.8 %) with human proteins are shown in Table 2.

Several chromosome VII ORFs show a high degree of similarity with interesting proteins from other organisms. These include: YGL236c, similar to the glucose-inhibited division (gidA) protein of the bacterium *Escherichia coli*; YGL201c, similar to the intestinal DNA replication protein of the rat *Rattus norvegicus*; and YGL054c, similar to the Cni protein necessary for anterior–posterior and dorsal–ventral patterning in the fruit fly *Drosophila melanogaster*.

Another interesting feature of *S. cerevisiae* chromosome VII is the existence of a pseudogene, which has been confirmed by direct polymerase chain reaction (PCR) sequencing on the yeast genome. This pseudogene,

Table 2 Similarity of yeast chromosome VII ORFs of unknown function with human proteins

Yeast ORF	Human protein		
YGL150c	SNF2a transcription activator that cooperates with the oestrogen and retinoic acid receptors		
YGL125w	methylenetetrahydrofolate reductase		
YGL106w	calmodulin		
YGL003c	probable cell-division control protein CDC 55		
YGR034w	new ribosomal protein similar to the human ribosomal protein L26		
YGR043c	transaldolase		
YGR217w	first putative calcium channel in yeast similar to the human voltage-dependent L-type calcium channel a1 subunit		
YGR231c	prohibitin, which inhibits DNA synthesis and regulates proliferation		
YGR256w	phosphogluconate dehydrogenase		

The similarity threshold is a FASTA score higher than 300 or higher than one third of self score.

YGL259w, contains two frameshifts, and only one of the three ORFs is longer than 99 codons. However, all three parts show a high similarity with YIR039c, a hypothetical aspartyl proteinase. Another curious feature is the presence of three ORFs in the same frame separated by two stop codons. The rightmost one, YGL238w, corresponds to the *CSE1* chromosome segregation gene. The leftmost ORF, YGL241w, shows 17% identity over 1,053 amino acids with *CSE1*, whereas the central ORF shows no similarity with this protein. Finally, a possibly unique feature in the yeast genome is the tail-to-tail arrangement of the *SMD1* (YGR074w) and *PRP38* (YGR075c) genes, with their respective ORFs terminating on opposite strands without any intervening nucleotide between the stop codons<sup>11</sup>. This region, as well as the *CSE1* region, have been verified by direct PCR sequencing on the yeast genome.

Chromosome VII contains six yeast retrotransposons: three Ty1s, one Ty2, one Ty3 and a pseudo-Ty, which contains, in addition to the normal frameshift separating the Ty1A and Ty1B coding sequences, two frameshifts splitting both ORFs in two parts. Of 35 tRNA genes identified, eight are interrupted by introns. All LTRs on chromosome VII are associated with a tRNA (for review, see ref. 12), except for the two Ty5 LTRs located close to the left telomere; however, 12 tRNAs are not associated with LTRs. The positions of tRNAs, Tys, LTRs and putative ARS consensus have been compared to G+C content and gene density along the chromosome (see Fig. 1). No clear correlation could be identified regarding the location of these genetic elements. Furthermore, no statistical correlation exists between the G+C content and the gene density curves (correlation coefficient, 0.04) when highly overlapping, neighbouring sliding windows (98.7 % overlap) are used. These G+C content and gene density variations are not significant, as the same analysis performed on several random mixes of the original sequence yields similar G+C content and gene density variations. A similar graph was obtained using non-overlapping neighbouring windows along the sequence after removal of Ty and LTR elements. In this case, a good correlation was found between the G+C content of the genes and the gene density (correlation coefficient, 0.98), as well as between the G+C content of silent positions of codons in genes and the gene density (correlation coefficient, 0.66). Finally, there is no significant difference in the G+C content of the coding regions on each strand: 40.07 % G+C and 305 ORFs on the Watson strand, and 39.95 % G+C and 267 ORFs on the Crick strand.

The physical map of chromosome VII has been constructed independently from the genetic map using the meganuclease I-SceI to produce *in vitro* nested fragmentations of the chromosome<sup>13,14</sup>. The cosmids chosen for sequencing were screened from two genomic libraries<sup>14</sup> and completed using a few cosmids from the physical map constructed by L. Riles (unpublished). The left telomere has been cloned<sup>15</sup> and the right telomeric sequence was obtained from a PCR fragment amplified from a strain carrying the pEL61 plasmid<sup>15</sup> integrated in the subtelomeric region.

The quality of the sequence of chromosome VII was assessed using dif-

ferent approaches. As well as partial overlaps between the regions sequenced by two laboratories, putative frameshift checking, alignment of the sequence with previously published data and a few random resequencing verifications were performed on cosmid subclones. A new method for verifying specific regions of the sequence was developed for this chromosome (G. V. et al., manuscript in preparation) and applied to several other chromosomes. The extrapolation from the number of discrepancies observed in the overlaps (102,049 nucleotides, 9.4 %) to the whole sequence suggests that the nucleotide sequence of chromosome VII is 99.974 % accurate. The quality of the coding regions, where frameshifts are quite easy to check, is probably much higher than that of the intergenic regions. Indeed, the quality assessment procedure led to the correction of a total of 90 errors mainly located in the coding regions. A total of 56,344 bp (5.2 %) have been resequenced, and the comparison with the original data makes it possible to estimate that about 120 errors remain in the chromosome VII sequence. Parts of the sequence were published independently<sup>16-30</sup> before assembly of the contig and application of the final quality controls; several other manuscripts are in the press.

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# The nucleotide sequence of Saccharomyces cerevisiae chromosome IX

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Large-scale systematic sequencing has generally depended on the availability of an ordered library of large-insert bacterial or viral genomic clones for the organism under study. The generation of these large insert libraries, and the location of each clone on a genome map, is a laborious and time-consuming process. In an effort to overcome these problems, several groups have successfully demonstrated the viability of the whole-genome random 'shotgun' method in large-scale sequencing of both viruses and prokaryotes<sup>1-5</sup>. Here we report the sequence of Saccharomyces cerevisiae chromosome IX, determined in part by a whole-chromosome 'shotgun', and describe the particular difficulties encountered in the random 'shotgun' sequencing of an entire eukaryotic chromosome. Analysis of this sequence shows that chromosome IX contains 221 open reading frames (ORFs), of which approximately 30% have been sequenced previously. This chromosome shows features typical of a small Saccharomyces cerevisiae chromosome.

The sequence derived for chromosome IX is 439,886 nucleotides in length, and 71.6% codes for proteins or predicted proteins. There are 219 non-overlapping ORFs equal to or greater than 100 amino acids long, and a further two ORFs (YIL060W and YIL059C) that overlap; these are short, and both have a low codon adaptation index (CAI). Although it is unlikely that both are coding, one could not be selected above the other as more likely to encode a protein. A single Ty3-2 retrotransposon containing three ORFs is present on the left arm of chromosome IX (between bases 205,217 and 210,644), leaving 218 S. cerevisiae-derived ORFs encoded on this chromosome, of which 116 are on the Crick strand, and 102 (+ 3 transposon ORFs) are on the Watson strand. Of these, 66 (30.3%) have been sequenced previously. A further 68 (31.2%) have some similarity to genes in S. cerevisiae and other organisms for which some functional information is available. However, 74 (33.9%) of the predicted genes on this chromosome cannot be assigned even a putative function based on sequence similarity. These can be divided into two groups: those that show no similarity to current database entries (53, 24.3%), and those that are similar to predicted genes of unknown function (21, 9.6%). The remaining 10 (4.6%) are putative pseudogene ORFs.

The average length of a chromosome IX ORF is 476 codons, with an average of one ORF every 1,993 base pairs. The largest ORF on chromosome IX is YIL129C, which encodes a hypothetical protein of 2,376 amino acids. The YIL129C protein is similar to another hypothetical protein encoded on *Caenorhabditis elegans* chromosome III (EMBL database, accession numbers CEF21H11, U11279 and ORF F21H11.2) over a region of 2,009 amino acids. In total, 20 chromosome IX ORFs are longer than 1,000 codons. Short *S. cerevisiae* genes with no homology are difficult to detect<sup>6</sup>. On chromosome IX, five ORFs with less than 100 codons have been identified, but future analysis will probably reveal additional short coding regions. Less than 4% of the ORFs on chromosome IX are predicted to be spliced; eight ORFs contain introns. None of the tRNA genes on this chromosome are spliced.

Ten ORFs have been identified as contributing to five putative pseudogenes. These ORFs have very good homology to genes or predicted genes, but are separated from an adjacent ORF with homology to the same protein by internal stop codons or frameshifts. These areas have been sequenced on *S. cerevisiae* genomic DNA, and the frameshifts and stop codons confirmed. However, at least two pseudogene ORFs, YIL168W and YIL167W, probably constitute the single gene *SDL1*, which codes for a serine dehydratase<sup>7</sup>. This gene is not present elsewhere in the *S. cerevisiae* genome and is not essential in *S. cerevisiae*. A second putative pseudogene is highly similar to hexose transporter genes, and may also simply prove to be mutated in AB972 rather than being a true pseudogene. All putative pseudogenes are located near the telomeres of the chromosome.

For this and other *S. cerevisiae* chromosomes, the intergenic distance between two adjacent ORFs varies depending on their orientation with respect to each other. Of the adjacent ORFs on chromosome IX, 95 are arranged in tandem, 54 are divergent and 55 convergent. For ORFs arranged in tandem the intergenic distance averages 472 basepairs; ORFs with divergent promoters average 619 bp; and ORFs with convergent terminators average 421 bp. This is consistent with the greater information content required for transcription initiation and regulation than for transcription termination.

Chromosome IX also contains ten tRNAs, five solo delta elements, one solo sigma element, two sigma elements flanking a transposon, and a single solo tau element.

Reports describing the features of the other small yeast chromosomes suggest that they have used a variety of strategies to achieve a certain minimum length<sup>8-10</sup>, and this seems to be the case for chromosome IX. Its

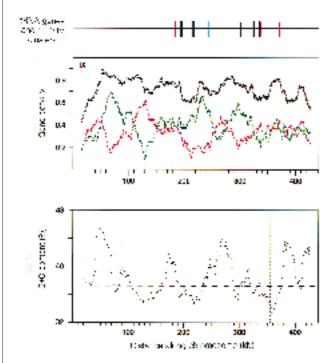


Figure 1 Overall molecular architecture of chromosome IX. The top line indicates positions of tRNA genes, solo long terminal repeat (LTR) or Ty elements (thin vertical lines) or clusters of them (thick vertical lines) along the chromosome map. The panels show variation in gene in gene density (top) and base composition (bottom) along the sequence-based map of chromosome IX (scale in kilobases from left telomere). Vertical broken lines indicate the centromere. Gene density is expressed as the probability for each nucleotide to be part of an ORF, and was calculated using sliding windows of 30 kb (steps of 0.5 kb) for the Watson strand alone (red line), the Crick strand alone (green line), and the sum of both (black line). G+C richness (%) was calculated from the silent positions of codons using a sliding window of 13 consecutive ORFs (horizontal broken line indicates average percentage G+C at silent positions of codons, 35.8%)

right telomeric region is gene poor, with only 25.3% of the sequence contributing to ORFs over approximately the last 15 kilobases of the chromosome. Chromosomes I and VI, the two smallest yeast chromosomes, also have a low coding density in their telomeric regions. Ten ORFs on chromosome IX are thought to contribute to five putative pseudogenes, all of which are located in the telomeric regions (four in the left telomeric region and one in the right). Four of these putative pseudogenes have a high degree of similarity to sequences repeated elsewhere in the yeast genome (the remaining putative pseudogene may be a mutated copy of SDL1, as discussed previously). Two of these occur in a 21-kb region of the chromosome IX left telomere, which is duplicated almost exactly on the chromosome X left telomere. Comparison of these two pseudogene ORFs with the equivalent regions on chromosome X shows that one region is interrupted by a frameshift on that chromosome, but the second is a single ORF. The putative pseudogene on the right arm of the chromosome is highly similar to a single ORF on chromosome XIII. The centromere<sup>11</sup> of chromosome IX is located towards the right end of the chromosome between bases 355,627 and 355,744.

Sequencing has revealed the definitive chromosomal position for all genes on chromosome IX. The resulting physical map correlates well with the genetic map<sup>12</sup> for this chromosome. Local variations in the ratio of cM to kb occur throughout this chromosome. For example, the region bounded by the genes *REV7* and *HOP1* has a significantly lower ratio of 0.3, indicating that recombination events in this area are less frequent than for the chromosome as a whole.

A cluster of genes on this chromosome occurs within its smaller, right arm between bases 399,775 and 415,615 (YIR023W to YIR032C). Six of the ten ORFs in this region are involved in the allantoin degradation pathway<sup>13,14</sup>.

Evidence of several interchromosomal duplications occurs on chromosome IX. As well as the large region common to the left telomeres of chromosomes IX and X already described, a smaller region at the right telomere shows good homology with the telomeres of several other chromosomes. There are also several other internal chromosomal regions with long-range homology to other chromosomes. The largest of these is an area common to chromosomes IX and XIV, occurring at 89,233–186,363 and 478,568–616,076, respectively, and containing 15 homologous ORFs. Smaller interchromosomal duplications have also occurred, including a region at 230,272–258,279 repeated on chromosome V at 273,881–305,178 and a region at 46,201-69,525 repeated on chromosome XI at 617,636–639,600.

A further long-range feature previously observed for  $S.\ cerevisiae$  is a variation in the percentage G+C content along the length of its chromosomes  $^{15}$ . In most cases the G+C composition for the third base of each codon has been analysed, as this is less influenced by biases in amino acid composition. For several chromosomes a periodic variation in G+C content has been observed. A plot of third-position G+C composition for chromosome IX (Fig. 1) shows that, as for other chromosomes, G+C content varies along its length. Consistent with previous analyses, the region around the centromere of the chromosome has low G+C content; the highest content occurs in peaks separated by about 100 kb.

The occurrence of first-, second- and third-codon position G+C composition was analysed for individual ORFs, as well as G+C composition in intragenic regions and the total G+C content of the chromosome (Fig. 2). This was superimposed on a chromosome map showing individual ORFs, as the usual method for plotting G+C composition uses a large window to calculate the average third-position G+C content of several adjacent ORFs, making it difficult to ascertain whether high G+C composition is a general trend in a particular region or derives from a single ORF. This method correctly predicted the peaks in third-position G+C content already described for chromosome III (data not shown).

In regions producing peaks of G+C content several adjacent reading frames show higher than average third-position G+C. Specific areas noted include 1–6, 52–67, 93–97, 175–180, 266–276, 308–313, 380–385 and 421–424 kilobases, with up to six ORFs contributing to each region. The areas of high G+C content are much more pronounced in chromosome III, with many more reading frames over a much longer distance contributing

to the two main peaks on each of the chromosome arms (results not shown).

As expected, the G+C content in intergenic regions is, on average, lower than that for coding DNA. However, it is not uniformly low, and local areas of high G+C content can be observed in some non-coding areas. The largest of these regions have been examined in detail for potential coding sequence. Although any ORFs present in these areas could conceivably be coding, they are all short, and standard methods for predicting coding sequences suggest that this is unlikely. A BLASTX search does not show any significant similarity to other *S. cerevisiae* ORFs, indicating that these areas are not remnants of ancient pseudogenes. Other possibilities have not yet been fully investigated.

Very few genes show high G+C content in position 2 of their codons. However, YIL169C, a putative glycoprotein, and YIR019C (STAI), a glucoamylase gene, show high second-position G+C content. Both genes code for proteins with a biased amino-acid composition. YIR019C is surrounded by regions low in G+C, but coincides with a high G+C peak on a plot of overall G+C content (results not shown), showing that a single gene can cause a peak on these plots. The role of these differences in base composition found in all yeast chromosomes has not been determined, although high G+C content might promote DNA replication or recombination.

The chromosome IX sequencing project served to highlight the difficulties involved in a whole-chromosome 'shotgun' project. This approach is described in detail in the Methods section. The purity of the starting chromosomal DNA is critical to avoid redundant sequencing effort and to minimize problems in assembly. Contamination of the chromosome IX preparation with DNA from other chromosomes resulted in a large number of single reads in the database that were not from that chromosome, but which increased the complexity of sequence assembly, slowing down both assembly and subsequent manipulation of contigs. Re-running the PFG-purified chromosome on a second pulsed-field gel has been shown to improve significantly the purity of the DNA preparation<sup>16</sup>. Data from the whole-chromosome 'shotgun' helped to fill the gaps in the cosmid and lambda libraries, but on their own were difficult to manage. The cosmid clones provided a framework on which to build data from the whole-chromosome shotgun.

#### Methods

The chromosome IX sequencing project was initiated using a lambda clone library generated by M. Olsen and L. Riles<sup>17</sup>. This was an inefficient approach because of short insert sizes (20 kb) and relatively large overlaps (about 5 kb) between lambda clones. Few cosmids were available at the time, so the approach of randomly 'shotgun' sequencing the entire chromosome was attempted.

Yeast genomic DNA was electrophoresed on pulsed-field gels<sup>18</sup>. To increase the purity of the chromosomal preparation, yeast plugs were excised early in the run after chromosome IX had entered the gel, reducing the background DNA level. Degradation of the material of higher molecular weight occurs with prolonged running of the gel and is the likely cause of contamination of material of lower



Figure 2 G+C composition of chromosome IX (drawn to scale). The top graduated line represents the chromosome split into 50-kb segments, with ORFs indicated below this as coloured boxes. ORFs located on the Watson strand are shown above those on the Crick strand. ORFs encoding previously identified genes are shown in red, those with similarities to known genes in yellow, those with similarities to hypothetical proteins in orange, and those with no significant similarities in green; pseudogene ORFs are shown in blue. tRNA genes are shown as white boxes, as are transposonderived ORFs, with LTRs shown in dark blue (delta), turquoise (tau) and

pink (sigma). Below this, variations in G+C composition (calculated using a sliding window of 200 bases) are shown as bars, with gradations of red varying from 35% to 45% (P.R., unpublished data); areas lower than 35% G+C are white, and those over 45% are red. Five bars of G+C variation are shown: the lowest bar shows total G+C content; the second shows G+C content in intergenic regions alone; and the G+C composition in each of the three bases of each codon are shown above this, with the central of the five bars representing first-position G+C, the next representing second-position G+C, and the top bar showing third-position G+C content.

molecular weight. The chromosome IX band was excised under long-wave ultraviolet transillumination to minimize DNA damage. Chromosomal DNA was purified by melting and phenol extraction, sonicated and end repaired. Two libraries were prepared: fragments 1.4-2 kb in length were cloned into M13mp18, and fragments 6-9 kb long were cloned into the phagemid vector pBS. Over 10,000 independent M13 clones were sequenced and assembled into a database using the program XBAP19. Sequencing strategy and methods used for sequence assembly are as described<sup>19-25</sup>. The lambda-clone consensus sequences were also entered into this database, which contained several thousand contigs at this stage, most of which contained a single gel read. We concluded that the chromosome IX DNA preparation was approximately 30% contaminated with DNA from other chromosomes, and that this was the source of most single-read contigs. This contamination, together with repetitive sequences in the database, caused many problems with the data assembly.

To overcome this problem, all single-read contigs were removed from the working copy of the chromosome IX database and collected in a secondary database. As further data was generated, the secondary database was periodically rescreened, and single reads were re-entered if they found matches in the primary database. This reduced the number of reads in the primary database to approximately 7,000, which represented coverage of the chromosome five times over. The database still contained several hundred contigs. At this stage a cosmid library covering most of chromosome IX became available<sup>17</sup>. The chromosomal 'shotgun' data were 'seeded' with reads from cosmid clones selected to give coverage over regions not previously sequenced by lambda clones. This approach also allowed the chromosome to be split up into manageable sections to solve double-stranding and compression problems. A minimal 'shotgun' of 300-500 reads was performed on each cosmid clone. Data from these cosmids were entered into the chromosome IX 'shotgun' database to contiguate the entire chromosome, and into separate cosmid databases for ease of handling, together with overlapping reads from the whole-chromosome shotgun. Each cosmid-sized project was contiguated, double stranded and all compressions

Three regions of the chromosome remained unrepresented in either cosmid or lambda libraries: the left and right telomeres, and a region near the centre of the chromosome flanked by lambda clones 6569 and 3299. The right telomere was sequenced by primer walking using a plasmid clone<sup>26</sup>. The left telomere was finished using data from the whole-chromosome 'shotgun' and some primer walking from polymerase chain reaction (PCR) products generated from PFGE-purified chromosome IX DNA. The gap near the centre of the chromosome was filled using data from the whole-chromosome 'shotgun' and by sequencing a 1 kb fragment generated by PCR from genomic DNA. The gap between the lambda clones 6569 and 3299 was approximately 7 kb.

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# The nucleotide sequence of Saccharomyces cerevisiae chromosome XII

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The yeast *Saccharomyces cerevisiae* is the pre-eminent organism for the study of basic functions of eukaryotic cells<sup>1</sup>. All of the genes of this simple eukaryotic cell have recently been revealed by an international collaborative effort to determine the complete DNA sequence of its nuclear genome. Here we describe some of the features of chromosome XII.

The nucleotide composition of the chromosome, which is 38.48% G+C overall, and gene density vary across the chromosome. This has been observed for other yeast chromosomes<sup>2-6</sup> (Fig. 1). There are three main regions deficient in G+C, centred at approximately 150, 685 and 1,043 kilobases; one of these, as expected, coincides with the centromere. There is only one main peak of high G+C content, at approximately 473 kb, centred over the rDNA repeats. There does not seem to be any regularity in the variation in nucleotide composition, as may be the case for some other yeast chromosomes<sup>3</sup>.

Like other yeast chromosomes, 72% of chromosome XII is predicted to code for protein (considering only two copies of the rDNA cluster). The sequence contains 534 open reading frames (ORFs) of 100 or more sense codons (excluding the 13 ORFs contained within yeast transposable elements), distributed roughly equally on the two strands (255 on the Watson (top) strand and 279 on the Crick (bottom) strand. The average ORF size is 485 codons. The largest gene in the chromosome, YLR106c, containing 4,910 codons, is the largest in the yeast genome. The average distance between ORFs is 545 base pairs for the 121 divergently transcribed genes (promoters abutting), 282 bp for the 120 convergently transcribed genes (terminators abutting), and 493 bp for the 208 genes that are transcribed in the same direction (promoter abutting terminator). Of the ORFs, 17 (3.2% of the total) contain introns, all of which are at the extreme 5' end of the gene (except for *YLR464w*, a probable pseudogene). Two genes (YLL057c and YLR388w) may contain introns in the 5'untranslated region of their mRNA. As expected, about half of the intron-containing genes (9) encode ribosomal proteins.

Only 170 (31.8%) of the genes were previously identified. Of the 364 newly identified genes, 34 (6.4% of the total genes) are obviously similar to proteins of known function, and 54 (10.1%) are weakly similar to proteins of known function. Thus a function is known or can be predicted for 48.3% of the encoded proteins. A further 69 genes (12.9%) encode proteins similar to proteins of unknown function; 207 (38.8%) of the predicted proteins are not similar to other proteins.

Included in the predicted ORFs are 55 that are 'questionable', that is, they consist of fewer than 150 codons and have a codon adaptation index (CAI)<sup>8</sup> of less than 0.110, or they overlap with another ORF. Of the 40 questionable ORFs that overlap with another ORF, the true gene can be predicted for 27 of these pairs, which include either a gene whose product is known (16 pairs) or whose predicted product is similar to another protein in the databases (11 pairs). There are therefore 13 overlapping ORFs that are suspect, although which of these ORFs is actually a gene awaits experimental determination.

Chromosome XII contains 22 tRNA genes, of which 7 are predicted to contain introns. Most of the tRNA genes are widely separated, although there are two clusters of three tRNA genes, each in a region of 9 kb to 13 kb (725,746–734,874 and 784,352–797,247). As expected<sup>9</sup>, many (12) of the tRNA genes are near yeast retrotransposons (Ty elements) or their isolated long terminal repeats (LTRs). Three known small nuclear RNAs, *SNR6*, *SNR30* and *SNR34* are encoded on chromosome XII. Four of the six retrotransposons on chromosome XII are of the Ty1 type and two are Ty2 elements. There are several complete or partial 'solo' retrotransposon LTRs, including nine delta elements, four sigma elements, and a tau element.

The subtelomeric regions of chromosome XII are typical <sup>10</sup>. The left subtelomeric region contains a 'core X' element, and subtelomeric repeats STR-D, C, B and A, along with two tandem Y' elements (short versions). The right subtelomeric region contains a core X element, the STR elements listed above, and 3–4 tandem Y' (long version) elements. The sequence of the first 1.5 and the last Y' elements were fused to give two copies of the Y' element in the presented sequence. Proximal to the core X are shared homologies with several other telomere regions. As with several other chromosomes, both chromosome ends contain members of the

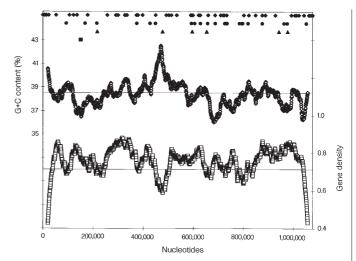


Figure 1 Top, non-coding elements of chromosome XII including autonomously replicating sequence (ARS) (filled diamonds); tRNA (filled circles); Ty element (filled triangles); centromere (filled square). Middle, G+C content as a percentage (open diamonds). Bottom, gene density (open squares).

#### PAU/TIP/SRP gene family 11.

Chromosome XII is estimated to contain 100–200 copies of the 9,137 base pair rDNA repeat <sup>9,12–14</sup>. Only one complete copy (the leftmost repeat in Fig. 2) and one nearly complete copy of the rDNA (the rightmost repeat in Fig. 2) are represented in the assembled sequence. In some strains these repeats seem to be interrupted by non-rDNA sequence<sup>14</sup>.

The boundaries of the rDNA repeats are in non-transcribed regions downstream of the 35S rDNA (the left, or centromere-proximal, boundary) and 5S rDNA (the right, or centromere-distal, boundary) <sup>15</sup>. The structure of the left boundary of the rDNA (nucleotide 21,811 in Fig. 2) is straightforward; the right boundary<sup>16</sup> is more complicated. Immediately to the right of the rDNA repeats are several copies of a 3.6-kb repeat (one of which is interrupted by a Ty element) that includes the *ASP3* gene<sup>17</sup> and ends with a nearly complete 5S rDNA gene (5S<sup>var</sup> in Fig. 2). The precise number of copies of this 3.6-kb repeat in the genome is not known. The rightmost rDNA repeat ends in a 5S rDNA that adjoins a 3.6-kb repeat. Thus this rightmost rDNA repeat is lacking the 759 bp of sequence between the end of 5S rDNA and the end of the rDNA repeat (equivalent to nucleotides 30,186–30,947 in Fig. 2). The structure of the right rDNA junction differs in other yeast strains<sup>15</sup>.

The 5S rDNA gene in the 3.6-kb repeats lacks the non-transcribed regions of the gene. It begins two nucleotides upstream of the 5' end of 5S rRNA, and is missing the last four nucleotides of the 5S rRNA. These genes are labelled '55<sup>var'</sup>, in Fig. 2 to indicate that they are incomplete. Immediately downstream of this gene is a run of 10 T residues that is reminiscent of the transcription termination sequence of RNA polymerase III (there are 29 T residues downstream of the 5S rDNA gene in the rDNA repeats). Because this gene seems to be missing the promoter and much of the terminator, it might represent a reverse-transcribed copy of the 5S rRNA that integrated into the genome. Nevertheless these genes produce 5S rRNA transcripts<sup>18</sup>.

One possible explanation of the structure of the right junction is that a reverse-transcribed copy of 5S rRNA is inserted into the genome near the right border of the rDNA cluster. This gene could then have been part of a 3.6-kb duplication. It is then easy to imagine a recombination event between an intact 5S rDNA gene in one of the rDNA repeats and a 5S<sup>var</sup> rDNA in one of the 3.6-kb repeats that generated the right rDNA junction we sequenced. Other explanations for the origin of this junction have been proffered<sup>16</sup>.

To speed the completion of the sequence of this large chromosome, two groups collaborated on its sequencing. The rDNA repeats on chromosome XII served as a convenient point to divide the effort: the EU sequencing network <sup>19</sup> determined the sequence of the chromosome to the

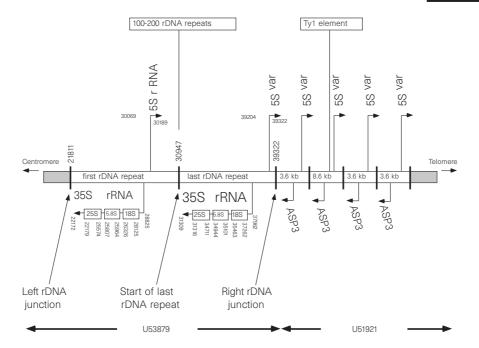


Figure 2 Diagram of the rDNA repeats and surrounding sequence, as assembled for cosmids YSCL9634 (left, GenBank accession no. U53879) and YSCL9362 (right, GenBank accession no. U51921). The numbers shown are the nucleotide coordinates for cosmid YSCL9634. The left rDNA junction (U53879 coordinate 21,811) begins at nucleotide 451,418 of chromosome XII; the right rDNA junction (U53879 coordinate 39,322) is at nucleotide 468,929. The sequence includes 1.92 rDNA repeats, representing the leftmost and rightmost copies in the genome. The remaining

100-200 rDNA repeats in the genome are represented as an insertion at coordinate 30,947. Only one complete 5S rDNA gene (in the left rDNA repeat) is included in this sequence (nucleotides 30,069-30,189); the 5S rDNA genes in the 3.6-kb repeats are variant genes. The 5S rDNA gene in the last rDNA repeat (nucleotides 39,204-39322) includes all 5' non-translated sequences (like the normal 5S rDNA in the first repeat), but is missing sequences downstream of the 5S rRNA transcript (like the 5S rDNA genes in the 3.6-kb repeats).

left of the rDNA repeats; the sequence to the right was determined at the Washington University Genome Sequencing Center. The sequence of both strands of the entire 1,078,171 base-pair chromosome (but including only two copies of the rDNA repeats) was determined, nearly all the way to the telomeres.

The 781,865 nucleotides determined at Washington University came from 24 partly overlapping cosmid and two lambda clones<sup>20</sup>. The sequence of each clone was determined by a 'shotgun' strategy followed by directed sequencing<sup>2</sup>. The sequence of each clone was submitted to GenBank, and the entire non-overlapping sequence was assembled, analysed and annotated<sup>2–5</sup>.

The 460,166 nucleotides to the left of the rDNA were determined by the EU network from a set of cosmid clones constructed from gel-purified chromosome XII DNA and mapped specifically for this purpose<sup>21</sup>. Sequencing was done by a directed approach that combines the advantages of primer walking (low redundancy) and 'shotgun' sequencing (use of a single primer)<sup>22</sup>. The sequence was determined from 'shotgun' sublibraries of 1-kb fragments of the cosmids that were then ordered by hybridization fingerprinting<sup>22</sup>. The sublibraries were arrayed on high-density filters, and sorted into smaller groups by hybridization with restriction fragments of the cosmids . Detailed mapping information was obtained by hybridizations with both oligodeoxynucleotides and pools of clone inserts amplified by the polymerase chain reaction (PCR).

The sequence of the left telomere region, including the  $TG_{1-3}$  sequence at the very end of the chromosome, was obtained from clones generated by integrating then excising a plasmid at the telomere, with capture of the flanking sequence<sup>10</sup>. The right telomere sequence was obtained by cycle sequencing of an anchored PCR product of the last Y' element from a strain whose chromosome end was specifically marked by unique vector sequence<sup>23</sup>. The sequence of the very end of the Y' element (about 130 bp short of the end of the chromosome) was not determined.

Only the sequence of the leftmost rDNA repeat (see Fig. 2) and about 300 nucleotides across the junction of the first and second repeat was

determined. It was assembled appropriately to give the two rDNA repeats presented in Fig. 2 and in the database (GenBank accession no. U53879). The right junction sequence was not present in the cosmid closest to the rDNA on the right (YSCL9362; GenBank accession no. U51921), nor in two phage lambda clones that were mapped to this region. The structure of the junction was inferred from our ability to obtain a product of the expected size (the size of a 3.6-kb repeat) in PCR using an oligonucleotide primer in the 3.6-kb repeat (lying just to the right of 55<sup>var</sup>) and a primer unique to the rDNA repeat (lying just to the left of 5S rDNA). Our sequence was assembled from these results, and found to match the sequence of the previously determined junction <sup>16</sup>.

The complete, assembled, non-overlapping sequence of chromosome XII can be obtained at: http://speedy.mips.biochem.mpg.de/mips/yeast/and http://genome-www.stanford.edu/Saccharomyces/.

Verification of 71,072 bp of sequence determined by the EU network (64,001 bp of overlaps between cosmids sequenced independently, and 7,071 bp of selected region that were resequenced) revealed five mistakes per 10 kb, but most errors were clustered in just a few regions. Only 14 differences were found in 175,891 nucleotides that were sequenced independently by both groups; six of these were sequencing errors, leading to an error frequency of only one mistake per 29 kb. The origins of the remaining eight discrepancies were determined by sequencing PCR products of the genome of the two strains used to generate the clones. Seven of the differences are due to changes that arose in the clones, presumably during propagation in *Escherichia coli*; only one results from differences between the two yeast strains (which are isogenic, but were propagated separately for many years) used to generate the two sets of clones. Thus the number of errors in the sequence is equivalent to the number of errors resulting from propagation of the DNA in E. coli and yeast. 

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# The nucleotide sequence of Saccharomyces cerevisiae chromosome XIII

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Systematic sequencing of the genome of Saccharomyces cerevisiae has revealed thousands of new predicted genes and allowed analysis of long-range features of chromosomal organization. Generally, genes and predicted genes seem to be distributed evenly throughout the genome, having no overall preference for DNA strand. Apart from the smaller chromosomes, which can have substantially lower gene density in their telomeric regions<sup>1-3</sup>. there is a consistent average of one open reading frame (ORF) approximately every two kilobases. However, one of the most surprising findings for a eukaryote with approximately 6,000 genes was the amount of apparent redundancy in its genome. This redundancy occurs both between individual ORFs and over more extensive chromosome regions, which have been duplicated preserving gene order and orientation<sup>4-6</sup>. Here we report the entire nucleotide sequence of chromosome XIII, the sixth-largest S. cerevisiae chromosome, and demonstrate that its features and organization are consistent with those observed for other S. cerevisiae chromosomes. Analysis revealed 459 ORFs, 284 have not been identified previously. Both intra- and interchromosomal duplications of regions of this chromosome have occurred.

Chromosome XIII of *S. cerevisiae* is 924,430 base pairs long, and contains 459 ORFs. Eight of these are TyA and TyB ORFs from four Ty1 retrotransposons present on chromosome XIII in strain AB972, two of

which are located on each arm of the chromosome, and these are excluded from further analyses. The average gene density on this chromosome is one ORF for every 1,997 base pairs of DNA, which correlates well with that observed for other *S. cerevisiae* chromosomes, with 74.2% of DNA on this chromosome contributing to ORFs. An average chromosome XIII ORF is 494 codons long.

Of the 451 S. cerevisiae ORFs on chromosome XIII, 167 (37.0%) encode previously identified proteins. A further 281 (62.3%) predicted genes have not been previously sequenced; 121 (26.8%) of these ORFs have similarities to genes for which some biochemical information is available. However, several of this category of ORF have their best protein similarity to a protein of unknown function. A total of 160 ORFs (35.5%) encode predicted proteins that are not significantly similar to proteins of known function. Because of the rapidly advancing progress of other systematic sequencing projects, many of these ORFs have homology to hypothetical proteins both in yeasts and higher organisms. A total of 51 predicted genes have similarity only to predicted proteins of unknown function. Although the majority are most similar to another S. cerevisiae hypothetical protein (50.9%), several have their best homology to an ORF identified in systematic sequencing of the yeast Schizosaccharomyces pombe<sup>7</sup> (11.8%), or to predicted proteins in the nematode Caenorhabditis elegans8 (17%). Thus they are members of gene families whose function is currently unknown. There were no significant protein sequence similarities for 109 ORFs, of which 11 are thought to be questionable ORFs based on their length, codon adaptation index (CAI) value and positional base preferences.

During the systematic sequencing of other chromosomes, several putative pseudogenes were identified<sup>1.9</sup>. These consisted of ORFs separated by a stop codon or frameshift from upstream or downstream sequences that shared a common homology to a single *S. cerevisiae* ORF. Most of these pseudogenes identified occur close to the telomeres of chromosomes. Three ORFs on chromosome XIII (YMR084W, YMR085W and YMR326C) have been classified as putative pseudogene ORFs. Of these, only YMR326C is located close to one of the chromosome telomeres; all three have strong similarity to sequences found elsewhere in the *S. cerevisiae* genome. These frameshifts have been confirmed by sequencing genomic DNA.

The average intergenic distance between adjacent ORFs depends on their relative orientation. This is certainly the case on chromosome XIII, in which 204 ORFs are arranged in tandem with an average intergenic distance of 450 base pairs. Of these, 110 are divergent and are an average 616 bp apart, and 111 are convergent and an average of 260 bp apart. This is consistent with a greater sequence requirement for the regulation of gene expression from promoter elements than for transcription termination.

Of the 451 ORFs on chromosome XIII, 24 (5.3%) are predicted to contain introns. There seems to be no preference for DNA strand, with 229 genes coded on the Watson strand and 222 on the Crick strand. There is no evidence of any significant clustering of related genes. However, there are several instances in which two very similar ORFs occur close to one another in tandem; for example, YMR169C and YMR170C/ALD2 (aldehyde dehydrogenases), and YMR006C and YMR008C/PLB1 (lysophospholipases).

The longest ORF on chromosome XIII is *HFA1*, (which is homologous to *FAS3*), a putative acetyl-CoA carboxylase that had been sequenced previously (2,123 codons). A total of 39 ORFs on this chromosome are more than 1,000 codons in length. *S. cerevisiae* genes of less than 100 codons with no homology are difficult to detect On chromosome XIII, 10 ORFs shorter than 100 amino acids in length have been identified. The smallest of these is YMR248C, which is just 55 amino acids long, and may be spliced to a second small ORF immediately upstream. The smallest ORF on this chromosome that encodes a previously characterized protein is *COX7*, which is 59 amino acids long and encodes cytochrome oxidase polypeptide VII (ref.12).

Chromosome XIII encodes 21 predicted tRNA genes, of which six are spliced. In addition to the four Ty1 retrotransposons, several long terminal repeat (LTR) sequences are present, providing evidence of previous trans-

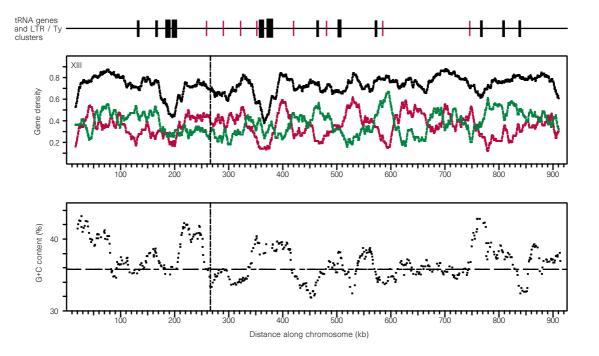


Figure 1 Overall molecular architecture of chromosome XIII. Variation in gene density (top) and base composition (bottom) along the sequence-based map of chromosome XIII (scale in kilobases from left telomere). Veritical broken lines indicate the position of the centromere. Gene density is expressed as the probability for each nucleotide to be part of an ORF. It was calculated using sliding windows of 30 kb (steps of 0.5 kb) for the Watson strand alone (red line), the Crick strand alone (green line), and the

sum of both strands (black line). Percentage of G+C was calculated from the silent positions of codons using a sliding window of 13 consecutive ORFs (horizontal broken line indicates average percentage G+C% at silent positions of codons as 35.8). Top line, positions of tRNA genes, solo LTR or Ty elements (thin small vertical lines), or clusters of them (thick small vertical lines) along the chromosome map.

position events on this chromosome. Of the 30 LTRs (whole or partial) identified on this chromosome, 29 are in close proximity to tRNA genes. There are 24 delta elements, with eight of these flanking the four retrotransposons and 16 solo elements. A further five LTRs resemble tau elements, and there is evidence of a single sigma element.

The telomeres of chromosome  $\bar{XIII}$  are highly similar to the telomeres of several other S. cerevisiae chromosomes. Adjacent to the terminal  $C_{1-3}A$  telomeric repeat at the left telomere is a Y' element, which is separated from a core X element by the subtelomeric repeats STR-D, STR-C, STR-B and STR-A<sup>13</sup>. The right telomere of chromosome XIII conforms to this structure but does not contain a Y' element. The right telomere shares a region of 4 kb in which the sequence is almost identical to that found at the right telomere of chromosome XV (EMBL database, accession no. SC23472). The centromere of chromosome XIII is located between bases 268,031 and 268,150; it conforms to the consensus sequence derived from the centromeres of other S. cerevisiae chromosomes  $^{14}$ .

Comparison of the positions of genes on chromosome XIII with their corresponding genetically mapped loci<sup>15</sup> shows that, as for most *S. cerevisiae* chromosomes, the two are generally in agreement. Several genes are incorrectly positioned on the genetic map in comparison with the sequence-derived map; for example, *van1* is much closer to the left telomere of chromosome XIII than expected. Small inversions are evident, for example between *UPF1* and *ADH3*, but no gross discrepancies have occurred as observed for chromosome XI (ref. 16). *MEL6* has been mapped to this chromosome, but in the *S. cerevisiae* strain S288C, from which AB972 was derived, this locus is missing. Also, the locus *SUP8* has been only tentatively assigned to the tRNA(Tyr) at base 837928 as a second tRNA(Tyr) is present on the left arm of the chromosome.

Chromosome XIII contains both intra- and interchromosomal duplications of both single ORFs and more extensive regions. The largest intrachromosomal duplication consists of two regions approximately 40 kb to 50 kb in length containing six homologous genes in the same order and orientation with respect to each other; the duplication has occurred between the left and right arms of the chromosome. This encompasses the region from base 32,334 to 73,917 and 790,207 to 840,147. Smaller instances of tandem gene duplication have also occurred within chromosome XIII; for example, YML125C and YML124C (*TUB3*) are similar to YML087C and YML085C (*TUB1*) on the short arm of the chromosome.

The largest interchromosomal duplication observed has occurred between a 200 kb region on the right arm of chromosome XIII and an equivalent region on the left arm of chromosome XI (in the opposite orientation). On chromosome XIII the region spans bases 303,238 to 502,733 and is bounded by ORFs YMR016C and YMR118C, on chromosome XI the coordinates of this repeat occur between bases 179,672 and 357,489. Of a total of approximately 90 genes, 17 show significant similarity and are in the same order and orientation on each chromosome. Further evidence of large scale duplications exists, including two separate regions on both chromosome IV and XVI.

Chromosome XIII has been analysed for variations in base composition, as described in ref. 9. The percentage G+C content in the third position of each codon varies throughout the length of chromosome XIII (Fig. 1), as observed through long-range analysis of other *S. cerevisiae* chromosomes. Detailed analysis at the level of individual ORFs (Fig. 2) shows that, as for chromosome IX, regions of high third-position G+C are shorter and contain fewer ORFs that regions of chromosome III that are rich in G+C. Comparison with chromosome IX shows that regions of high G+C are slightly less evident on chromosome XIII. This is also seen when plotting total G+C content for these two chromosomes: peaks of high G+C are generally lower in magnitude for chromosome XIII (results not shown).

Local areas of high G+C composition have also been observed in several of the intergenic regions of this chromosome, for example regions at approximately 119, 306, 541 and 653 kb are G+C rich. It is possible that these intergenic regions of high G+C may contain previously unidentified, small *S. cerevisiae* genes. These areas do not appear to correlate with sequences of high coding potential. However, this does not exclude the

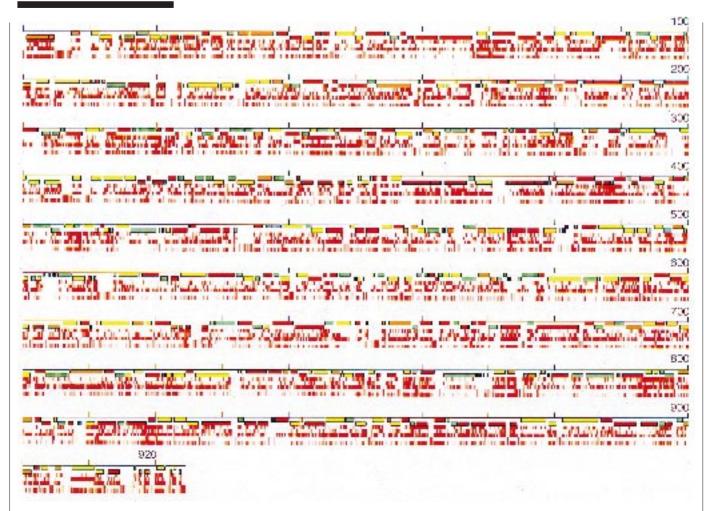


Figure 2 G+C composition of chromosome XIII. Chromosome XIII and its features are drawn to scale. The top graduated line represents the chromosome split into segments of 100 kb, with ORFs indicated below this as coloured boxes. ORFs located on the Watson strand are shown above those on the Crick strand. ORFs encoding previously identified genes are shown in red, those with similarities to hypothetical proteins in orange, and those with no significant similarities in green; pseudogene ORFs are shown in blue. tRNA genes and transposon-derived ORFS are shown in white boxes, with LTRs shown in dark blue (delta), turquoise (tau) and pink

possibility that coding sequences exist in these areas. No similarities to other *S. cerevisiae* ORFs were found using the program BLASTX, indicating that these areas rich in G+C are not pseudogene remnants. Other possibilities for these G+C peaks in intergenic regions have not yet been fully investigated.

Few ORFs show a high incidence of high G+C content in the second position of their codons. The most pronounced example on chromosome XIII is YMR317W, which encodes a protein rich in serine and threonine residues, and is located close to the right telomere of the chromosome.

Analysis of other *S. cerevisiae* chromosomes has demonstrated that, in general, areas high in G+C content correlate with high gene density, and that regions around chromosome centromeres and telomeres appear to be G+C poor<sup>4-6,16</sup>. This is also the case for chromosome X111. However, the significance of these areas of high and low G+C content is not yet clear.

Two of the genes located on chromosome XIII have human homologues that have been implicated in certain forms of cancer. *MLH1* encodes a DNA mismatch repair protein that is very similar to a human protein defective in some forms of hereditary non-polyposis colon cancer<sup>17</sup>. In *S. cerevisiae*, null mutants of this gene are viable, but show an elevated rate of spontaneous mutations and an increased instability of simple repeat sequences<sup>18,19</sup>. A second gene, *SGS1*, is homologous to the human *BLM* gene, which is involved in Bloom's syndrome<sup>20</sup>. Both the

(sigma). Below this, variations in G+C composition (calculated using a sliding window of 200 bases) are shown as bars, with gradations of red varying from 35% to 45% G+C content (P. R., unpublished data). Areas of less than 35% are shown in white, with those over 45% red. Five bars of G+C variation are shown, the lowest bar shows total G+C content; above this a second shows G+C content in intergenic regions alone. The G+C composition in each of the three bases of each codon are shown above this, with the central of the five bars representing first position G+C, the next representing second position G+C, and the top bar showing third position G+C.

human and yeast genes encode DNA helicases. Mutations in the human gene confer a predisposition to many types of cancer and also cause other clinical defects<sup>20</sup>. In *S. cerevisiae*, null mutants are viable, but again show genomic instability<sup>21,22</sup>. Future analysis of these and other *S. cerevisiae* genes should assist the understanding of the molecular mechanisms underlying many human diseases.

Chromosome XIII is the largest S. cerevisiae chromosome to be sequenced by a single laboratory. Analysis shows that its features are typical of large S. cerevisiae chromosomes.

#### Methods

Sequencing. Chromosome XIII was sequenced using a cosmid-based strategy that uses DNA isolated from the S288C-derived strain AB972. Methods used for sequence generation and assembly have been described in detail elsewhere R23. Cosmids were chosen from the map generated by L. Riles and M. Olson (personal communication), giving rise to two large contigs with a central gap. This was filled using lambda clones L-6543 and L-6223. The two chromosome telomeres, pEL161H (left) and pEL175H (right), were provided as plasmid clones Pb. L. Louis. Two further lambda clones, L-4987 and L-7056, were sequenced to complete the left end of the chromosome. Sequence from pEL161H overlapped L-4987, so no further gap filling was required at the left telomere of chromosome XIII. However, at the right telomere a gap between cosmid clone 9924 and plasmid pEL175H remained, and

was filled using long-range polymerase chain reaction (PCR) from S. cerevisiae genomic DNA. The sequence generated for this chromosome extends into the  $C_{1-3}A$  telomeric repeat sequences on both chromosome arms, although the exact number of these repeats has not been determined. Sequencing was considered to be finished when each base had been sequenced on both strands and all ambiguities had been resolved.

Analysis. For each completed clone, a consensus of the nucleotide sequence was generated in the Staden sequence assembly package XBAP<sup>25</sup>, flanked by short regions of sequence overlapping neighbouring clones. This sequence was analysed primarily within the DIANA (Display and Analyse) package (T. Horsnell and B. B., unpublished), a sequence editor with a graphical interface. ORFs equal to or greater than 100 codons in length were marked and trimmed to their first methionine. Each ORF was screened against the SWIR database, a non-redundant compilation of the protein databases Swiss-Prot<sup>26</sup>, TrEMBL<sup>27</sup> and WormPep, using the program FASTA<sup>28</sup> with limited optimization. The consensus sequence for each clone was screened against SWIR using BLASTX<sup>29</sup>, and EMBL/EMNEW using BLASTN<sup>29</sup>, to detect small ORFs less than 100 amino acids in length, other genome features, and local similarity. Some features were specifically identified; Prosite<sup>30</sup> amino-acid motifs (regular expression searching), transposon LTRs (GCG Wordsearch/Segments) and tRNAs (tRNA scan). Individual annotated clones were submitted to the EMBL database within days of being finished. The complete chromosomal sequence was built from overlapping clones and also submitted to the EMBL database as a single record (accession no. SCCHRXIII, Z271257).

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# The nucleotide sequence of Saccharomyces cerevisiae chromosome XIV and its evolutionary implications

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In 1992 we started assembling an ordered library of cosmid clones from chromosome XIV of the yeast Saccharomyces cerevisiae. At that time, only 49 genes were known to be located on this chromosome<sup>1</sup> and we estimated that 80% to 90% of its genes were vet to be discovered. In 1993, a team of 20 European laboratories began the systematic sequence analysis of chromosome XIV. The completed and intensively checked final sequence of 784,328 base pairs was released in April, 1996 (ref. 2). Substantial parts had been published before 3-22 or had previously been made available on request. The sequence contained 419 known or presumptive protein-coding genes, including two pseudogenes and three retrotransposons, 14 tRNA genes, and three small nuclear RNA genes. For 116 (30%) protein-coding sequences, one or more structural homologues were identified elsewhere in the yeast genome. Half of them belong to duplicated groups of 6-14 loosely linked genes, in most cases with conserved gene order and orientation (relaxed interchromosomal synteny). We have considered the possible evolutionary origins of this unexpected feature of yeast genome organization.

Figure 1 shows the map of cosmid, lambda and plasmid clones and of polymerase chain reaction (PCR) fragments from two unclonable regions which were used to determine the sequence of chromosome XIV. The final positions of genes listed in the 1992 map<sup>1</sup> are also presented changing the order of closely linked genes in only three regions. The assembled contig consists of 784,328 bp. The sequence of 180,983 bp (23%) was independently determined twice on both strands. These control sequences included 28 overlapping regions of cosmid and lambda clones (117,891 bp) as well as 108 selected regions, mainly at termini of open reading frames (ORFs), resequenced either on cosmids (54,540 bp) or by genomic PCR (8,552 bp). A total of 27 sequence mistakes were corrected. We estimate that the final sequence carries less than one error in every 10 kilobases, an estimate confirmed by a recent independent control analysis using 83 randomly picked genomic clones of chromosome XIV (G. Valle, unpublished data). Among the 40 kb sequenced, four deviations from our final sequence were noted: three single base-pair changes with neutral effects on coding regions (probably resulting from strain or clone differences), and only one confirmed sequence mistake. The left end of the chromosome carries telomeric repeat sequence (see below) and it is

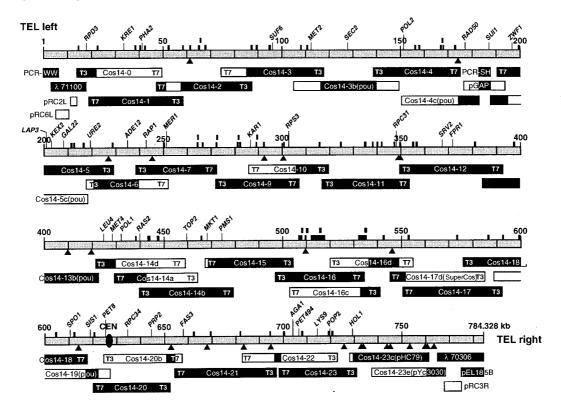


Figure 1 Physical map of subclones of chromosome XIV used for systematic DNA sequence analysis and final locations of originally genetically mapped genes<sup>1</sup>. Position of cosmid clones (cos), lambda clones (λ), plasmid clones (p) and genomic PCR fragments (PCR) are drawn as overlapping bars. Sequenced regions are shown in black. The 108 short regions selected for verification analyses are shown as small bars (resequenced cosmid clones) or triangles (sequenced genomic PCR fragments) along the contig. All clones were derived from S288C strains, except plasmid pGAP (carrying a spontaneus nonsense mutation in the toxic YNL247w), which originates from strain A364a<sup>36</sup>. Most cosmid clones with chromosome XIV DNA were isolated from cosmid libraries provided by B. Dujon<sup>37</sup> and R. Stucka<sup>38</sup>, and mapped by a modified chromosome fragmentation approach<sup>39,40</sup>. Several clones extending into or bridging remaining gaps were isolated by colony screening using non-radioactively labelled restriction fragments as hybridization probes. Two cosmid clones (14-17d and 14-23c) and both lambda clones carrying telomere DNA were obtained from L. Riles<sup>41</sup> and the right telomere clone pEL185 was provided by E. Louis<sup>42</sup>. A more detailed description of the mapping strategy will be published elsewhere (K. Ham-

berg et al., manuscript in preparation). The complete sequence can be retrieved from the EMBL database, accession nos Z71277-Z71692 or from the Martinsrieder website<sup>2</sup>. Different parts were sequenced in different laboratories: 1-6035 (R. Wambutt); 3,203-17,700 (B. Obermeier); 13,990-22,212 (A. Goffeau); 18,699-58,748 (C. Gaillardin); 47,022-51,246 and 57,523-87,525 (R. J. Planta); 85,152-132,424 (N. N. Glansdorf); 130,724-187,891 (J. H. Hegemann); 183,004-187900 (P. Philippsen); 187,809-192,153 (F. Del Rey); 192,154-195,234 (A. Jimenez); 190,506-229,360 (G. Valle); 220,854-239,907 (A. Düsterhöft); 238,582-273,742 (A. Goffeau); 271,932-319,898 (H. Domdey); 317,148-353,960 (C. Herbert); 349,559-393,039 (M. Jacquet); 384,059-421,858 (G. Valle); 421,188-443,100 (J.-L. Revuelta & F. Del Rey); 443,001-456,300 (A. Jimenez); 456,201-479,289 (J. P. G. Ballesta); 468,833-504,727 (P. Philippsen); 496,969-541,433 (M. Crouzet); 536,275-549,131 (C. Herbert); 545,180-592,214 (A. Düsterhöft); 575,858-617,912 (A. Urrestarazu); 617,105-622,324 (M. Crouzet); 620,016-652,539 (G. Volckaert.); 650,830-653,557 (R. J. Planta.); 651,995-654,446 (A. Düsterhöft); 654,389-731,357 (T. M. Pohl); 729,267-768,530 Düsterhöft); 764,973-784,328 (A. Urrestarazu); 774,980-784,145 (C. Gaillardin).

ORF Chr.XIV*	ORF Chr.VI*	% identity/	Biochemical or biological function (gene na	
3-17.3 kb <sup>†</sup>	6-15.5 kb	stretch of amino acids	Chr. XIV ORF	Homologue in cluster duplication
/NL336w	YFL062w	94.2% overall	unknown	unknown
NL335w	YFL061w	100 % overall	fungal cyanamide hydratase homologue	fungal cyanamide hydratase homologue
NL334c	YFL060c	99.1% overall	unknown, probable membrane protein	unknown, probable membrane protein
NL333w	YFL059w	99.7% overall	unknown	unknown
/NL332w	YFL058w	99.7% overall	thiamine regulated protein homologue	thiamine regulated protein (THI5)
/NL331c	YFL057-56c	87.0%/226 aa‡	probable aryl-alcohol reductase	probable aryl-alcohol reductase
ORF Chr.XIV	ORF Chr.XV (A)	% identity/		
88.7-106.7 kb	25.3-142.6 kb	stretch of amino acids		
/NL318c	YOL156w	38.4%/510 aa	hexose transporter (HXT14)	glucose transporter (LGT3)
/NL307c	YOL128c	41.6%/316 aa	Ser/Thr/Tyr protein kinase (MCK1)	probable Ser/Thr protein kinase
/NL302c	YOL121c	99.3% overall	ribosomal protein (RPS 16A)	ribosomal protein (RPS 16B)
/NL301c	YOL120c	100% overall	ribosomal protein (RP28B)	ribosomal protein (RP28A)
/NL299w	YOL115w	54.1%/556 aa	topoismerase I related protein (TRF5)	topoisomeras I related protein (TRF4)
/NL298w	YOL113w	61.2%/317 aa	Ser/Thr protein kinase (CLA4)	probable Ser/Thr protein kinase
/NL293w	YOL112w	53.2%/417 aa	unknown	unknown
/NL290w	YOL094c	34.4%/317 aa	replication factor C subunit (RFC3)	replication factor C subunit (RFC4)
/NL283c	YOL105c	43.4%/302 aa	similarity to yeast chitinase	unknown
ORF Chr.XIV	ORF Chr.IV	% identity/		
252.1-307 kb	44.1-80.4 kb	stretch of amino acids		
/NL209w	YDL229w	99.3% overall	heat shock protein (SSB2)	heat shock protein (SSB1)
/NL204c	YDL226c	30.5%/177 aa	sporul.spec.zinc finger protein (SPS18)	prolif.spec.zinc finger protein (GCS1)
/NL197c	YDL224c	36.5%/581 aa	regulator of cell size (WHI3)	unknown
NL194c	YDL222c	52.0% overall	unknown, probable membrane protein	unknown, probable membrane protein
NL183c	YDL214c	42.6%/479 aa	Ser/Thr protein kinase (NPR1)	probable Ser/Thr protein kinase
/NL176c	YDL211c	24.3%/292 aa	unknown, probable membrane protein	unknown, probable membrane protein
			process moniplano protein	production
ORF Chr.XIV	ORF Chr.VIII	% identity/		
109-410 kb	390.3-341.4 kb	stretch of amino acids		
NL173c	YHR146w	27.4%/351 aa	pheromone-response G protein	unknown, probable G protein
/NL162w	YHR141c	100% overall	ribosomal protein (RPL41A)	ribosomal protein (RPL41A)
/NL160w	YHR139c	45.0%/307 aa	secreted glycoprotein (YGP1)	sporulat.spec. wall maturation (SPS 100)
/NL156c	YHR133c	40.5%/205 aa	unknown	unknown
	YHR135c			
/NL154c		70.9%/499 aa	casein kinase I isoform (YCK2)	casein kinase I (YCK1)
/NL144c	YHR131c	36.2%/464 aa	unknown	unknown
/NL130c	YHR123w	53.8% overall	diacylglyc.choline-P transferase (CPT1)	ethanolamin P-tranferase (EPT1)
/NL121c	YHR117w	49.3%/651 aa§	import recept.mito outer memb.(TOM70)	mitochondrial outer membrane protein
/NL116w	YHR115c	55.4%/424 aa	unknown	unknown
ORF Chr.XIV	ORF Chr.XV (B)	% identity/		
119-466 kb	529-486.8 kb	stretch of amino acids		
/NL108c	YOR110w	65.0%/273 aa	unknown	unknown
/NL106c	YOR109w	58.5%/979 aa	inositol phosphatase homologue	probable phosphatase
/NL104c	YOR108w	88.5%/601 aa	2-isopropyl malate synthase (LEU4)	2-isopropyl malate synthase homologue
/NL098c	YOR101w	55.8%/303 aa	GTP-binding protein (RAS2)	GTP-binding protein (RAS1)
/NL096c	YOR096w	87.9% overall		
			ribosomal protein S7 homologue	ribosomal protein (RP30)
/NL095c	YOR092w	55.3%/445 aa	unknown, probable membrane protein	unknown, probable membrane protein
/NL093w	YOR089c	56.9%/209 aa	GTP-binding protein (YPT53)	GTP-binding protein (VPS21)
NL090w	YOR089c	56.9%/209 aa	GTP-binding protein (RHO2)	GTP-binding protein (VPS21)
NL087w	YOR086c	54.5% overall	unknown, probable membrane protein	unknown, probable membrane protein
ORF Chr.XIV				
JRF Chr.XIV	ORF Chr.IX	% identity/		
178.6-597.6 kb	89.3-202.1 kb	stretch of amino acids		
NL079c	YIL138c	54.1%/159 aa	tropomyosin (TPM1)	tropomyosin (TPM2)
NL074c	YIL135c	23.2%/375 aa	unknown	unknown
NL069c	YIL133c	90.3% overall	ribosomal protein (RP23)	ribosomal protein (RP22)
/NL068c	YIL131c	52.1%/190 aa	unknown, fork head domain (FKH2)	unknown, fork head domain (FKH1)
NL066w	YIL123W	62.9%/415 aa	ß-glucosidase homologue (SUN4)	homologue of aging gene UTH1
NL065w	YIL121w	47.7%/342 aa	cycloheximid resist.protein homologue	antibiotic resitance protein homologue
NL065w	YIL120w	43.0%/351 aa	cycloheximid resist.protein homologue	antibiotic resitance protein homologue
/NL058c	YIL117c	37.3%/126 aa	unknown	unknown
NL055c	YIL114c	49.5% overall	outer mito membrane porin (OMP2)	OMP2 homologue
NL053w	YIL113w	48.8%/162 aa	protein phosphatase (MSG5)	protein-Tyr phosphatase homologue
NL052w	YIL111w	63.6% overall	cytochrome c oxidase (COX5A)	cytochrome c oxidase (COX5B)
/NL049c	YIL109c	61.8%/566 aa	unknown	unknown
/NL047c	YIL105c	54.3%/639 aa	unknown	unknown
/NL037c	YIL094c	35.8%/296 aa	isocitrate dehydrogenase (IDH1)	isopropyl malate dehydrog, homologue
/NL029c	YIL085c	55.7%/476 aa	mannosyl transferase homologue	mannosyl transferase homologue
/NL020c	YIL095w	41.2%/636 aa	probable Ser/Thr protein kinase	probable Ser/Thr protein kinase
ORF Chr.XIV	ORF Chr.III	% identity/		
23.4-753.7 kb	101.7-301.8 kb	stretch of amino acids		
NL004w	YCL011c	39.4%/409 aa	poly(A)bdg.protein homologue (TOM34)	probable TEL associated protein (GBP2)
			citrate synthase (CIT1)	
NR001c	YCR005c	81.4%/441 aa	, ,	peroxysomal citrate synthase (CIT2)
NR002c	YCR010c	77.7% overall	unknown, probable membrane protein	unknown, probable membrane protein
NR013c	YCR037c	48.1%/489 aa	unknown, probable membrane protein	probable phophate transporter (PHO87)
NR019w	YCR048w	52.5%/459 aa	sterol acyltransferase (SAT1)	cholesterol acyltransferase (ARE1)
NR023w	YCR052w	29.5%/353 aa	unknown	unknown
NR026c	YCR067c	45.4%/388 aa	GTP-GDP exchange factor (SEC12)	ER protein (SED4)
NR028w	YCR069w	33.2%/304 aa	peptidyl-prolyl isomerase homologue	peptidyl-prolyl cis-trans isom.(SCC3)
NR031c	YCR073c	53.6%/1172 aa	MAPKKK high osm.sign.transd. (SSK2)	MAP kinase kinase kinase (SSK22)
NR034w	YCR073w-a	76.9% overall	multicopy sup of los1-1 (SOL1)	GIcN-6-P deaminase homologue (SOL2)
NR047w	YCR091w	72.4%/424 aa	probable Ser/Thr protein kinase	probable Ser/Thr protein kinase (KIN82)
			·	
/NR048w	YCR094w	65.4% overall	unknown	unknown
YNR065-66c	YCR099-101c	64.8%/637 aa¹	peptidase Y sorting protein (pseudogene)	peptidase Y sorting (PEP1 homologue)

Degrees of homology were extracted from pairwise FASTA alignments of deduced protein sequences and are listed as percentage identity per stretch of amino acids. \*Y' is included in Fig. 2 in the cluster duplication but is not listed in this table. †Coordinates of clusters.

Overall homology between YNL331c and the sum of YFL056c and YFL057c (pseudogene in chromosomeVI?).

<sup>§</sup>Gaps introduced by the alignment algorithm may result in homology stretches slightly longer than the protein sequences.

Overall homology of the pseudogene (YNR065-YNR066c) to the sum of YCR099c, YCR100c and YCR101.

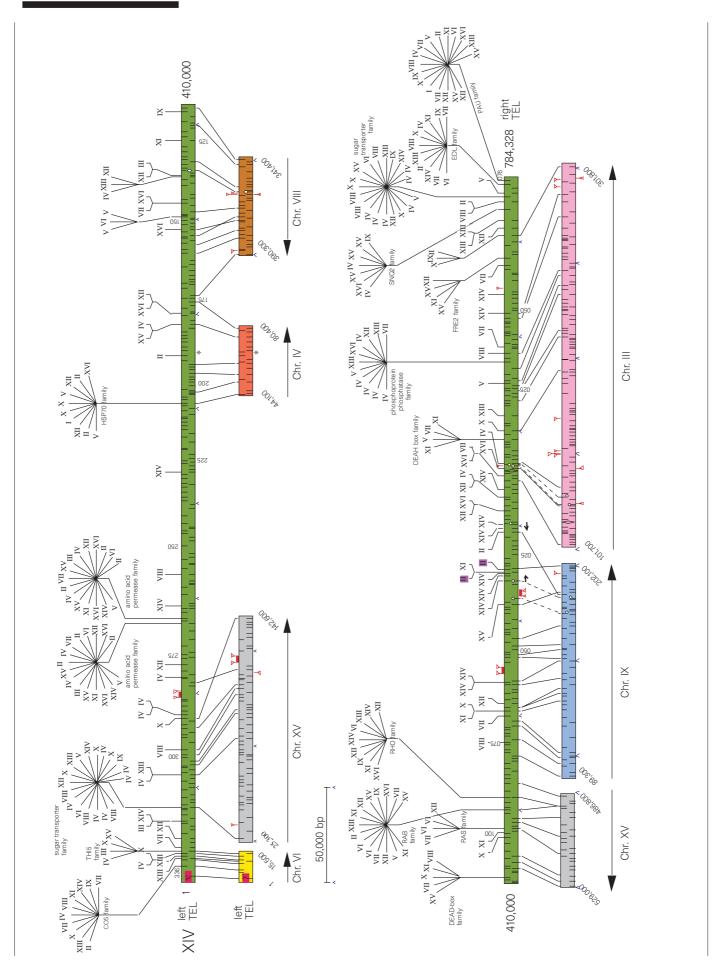


Figure 2 Map of chromosome XIV ORFs that are members of either multigene families or of pairs, triplets or quadruplets of structurally related S. cerevisiae ORFs. The green bar represents both strands of chromosome XIV, with centres of all ORFs (excluding Ty and four short telomere ORFs) drawn as vertical lines; 215 are coded by the upper strand and 195 by the lower strand. Vertical lines with open circles mark selected tRNA genes. Three-digit numbers beneath or above the green bar refer to the systematic ORF nomenclature starting with 1 at either side of the centromere (white dot at 628 kb). Lines above or below the green bar indicate ORFs with structural homologues elsewhere in the genome (at least 30% identity in 150 amino acids, or, in a few cases, 25% in 300 amino acids). Lines extending into branches mark multigene families, with roman numbers indicating members on different chromosomes (order of decreasing homology to the chromosomes XIV ORF from left to right or clockwise, respectively). Coloured bars below chromosome XIV display seven syntenic or partly syntenic segments of other chromosomes with accumulations of ORFs structurally related to and arranged similarly to chromosome XIV ORFs. Broken lines in three of these clusters connect positions of pairs of functionally identical tRNA genes. The star at 280 kb indicates a functional ARS element on chromosome XIV (Ref. 36) which seems to be positionally conserved on chromosome IV. Further details of these cluster duplications are given in Table 1. The red bar of the left telomere represents the ubiquitous Y' element found at many ends of S. cerevisiae chromosomes<sup>43,44</sup>. Red triangles mark positions of solo delta sequences (remnants of Ty elements) and red bars flanked by triangles indicate Ty elements. The two black arrows at 570 kb and 600 kb indicate an intrachromosomal highly conserved inverted repeat, involving in each repeat element one tRNA<sup>lle</sup> gene and two new ORFs (YNL034w-YNL035w and YNL019c-YNL018c, respectively). The two marked chromosome II homologues and the corresponding chromosome XIV ORFs at 575 kb represent the two copies of the duplicated histone H3-H4 gene pair. As indicated there is an additional homologue to histone H3 on chromosome XI (CSE4), probably the yeast homologue of the human CENP-A gene<sup>45</sup>

possble that this end is a few hundred base pairs longer than indicated in Figure 1.

A systematic search of the chromosome XIV contig revealed 414 ORFs with 100 and more codons, including overlapping ORFs but excluding ORFs located within longer ORFs on either the same or the complementary strand. Chromosome XIV also has at least seven ORFs with less than 100 codons, of which four are known genes (MFA2, TOM7, ATX1 and PBI2) and three show significant homology to known genes. A systematic nomenclature was given to all ORFs (excluding the six ORFs of the three Ty retrotransposons), indicating the organism (Y), the chromosome (N), the chromosome arm (L or R), the coding strand (Watson, w or Crick, c), and increasing numbers starting at the centromere; examples include YNL001w and YNR001c.

A simultaneous search for introns (using the EXPLORA program<sup>23</sup>) revealed 16 intron-carrying genes, in two of which, (YNL066w and YNL065w) the introns are located in the non-translated 5' region<sup>24,25</sup>. EXPLORA failed to locate an additional, experimentally verified intron in ORF YNL044w, because it has an unusual 5' splice sequence (EMBL database, accession nos X97400 and X97401).

Two pairs of adjacent ORFs (YNR065c and YNR066c; and YNR068c and YNR069c) were separated only by a stop codon; this was confirmed in both cases by genomic PCR. These pairs are rare examples of yeast pseudogenes, as highly conserved copies lacking internal stop codons are present on other chromosomes. Like their functional homologues these pseudogenes should be considered as single ORFs. Taking this into account, 419 ORFs are located on chromosome XIV, including six Tyelements and 23 questionable ORFs (short ORFs overlapping longer ones). The ORF density, not counting questionable ORFs, is one ORF per 1.98 kb (a total of 396 ORFs in 784 kb), and the average ORF size is 1.5 kb. These numbers are very similar to corresponding numbers obtained with other *S. cerevisiae* chromosomes. The ORF density (the ratio of ORF nucleotides to total nucleotides) fluctuates between 0.6 and 0.9. These fluctuations do not correlate with fluctuations in G+C content; five of

eight ORF density peaks coincide with regions of highest G+C content (39.4-40.0%) and the other three with regions of lowest G+C content (36.6-37.7%)

How many of the 396 non-questionable ORFs are new? Presently, functions are known, at least partly, for 149 ORFs (38%), based on detailed experiments or very high sequence homology to known genes<sup>2,26</sup>. Most of these are involved in metabolism, cell growth, cell division, translation, transcription and intracellular transport, with a few involved in energy production, metabolite transport, protein modification, signal transduction, and stress response. Of the 247 new ORFs, some functional predictions can be made for 43 (11%), owing to homologies to characterized genes in S. cerevisiae or other organisms. Presumptive products coded by these 43 ORFs include: a human breast cancer-associated autoantigen homologue; a genetically linked cluster of three proteins (transporter, epimerase and reductase) for potential utilization of an unidentified mono- or oligosaccharide; four proteins with homology to prokaryotic ribosomal proteins; three protein kinases; three GTP-binding proteins; two protein phosphatases; two translation factors; two drug- resistance proteins; one actin homologue; one zinc finger; one peptidyl-prolyl isomerase; and ten with presumptive metabolic activities, such as cyanamide hydratase, mannosyl transferase, isocitrate dehydrogenase and inositol phosphatase. Further details can be found on the Martinsrieder website<sup>2</sup>.

The functions of the other 204 ORFs (51%) cannot yet be predicted. One third of these code for presumptive membrane proteins, and more than four transmembrane domains are predicted for 18. Of the 204 new ORFs, 12 have homology to human expressed sequence tags (EST)<sup>27, 28</sup> with FASTA scores of 200–760. Remarkably, two of the 23 questionable ORFs (YNL228w and YNL114c) also have significant homology to human EST sequences.

We used FASTA comparisons of all chromosome XIV ORFs (except the highly repetitious Y' and Ty ORFs) to all S. cerevisiae ORFs in order to establish the extent of gene duplications, and found that 116 ORFs shared structural homology with one or more ORFs elsewhere in the genome. For this search, structural homology was defined as over 30% identity in a stretch of 150 amino acids (in some cases, 25% identity in a stretch of at least 300 amino acids). Of these 116 ORFs, 67 belong to pairs of homologues, 32 to groups consisting of three or four homologues, and 17 are members of multigene families. ORFs from all chromosomes contribute to this picture of sequence homology (Fig. 2). The list of homologies based on FASTA analyses also revealed several regions of chromosome XIV with accumulations of homologous ORFs originating from distinct regions of six other chromosomes, and showing, with only a few exceptions, conserved gene orders and gene orientations. One of these apparently ancient duplications, involving ORFs of the left arms of chromosomes IX and XIV, respectively, had previously been reported 19,29. Duplications involving several genes had been described up to that time, mainly for relatively short subtelomeric and centromeric regions<sup>30–34</sup>.

The extent of these types of duplications became apparent after the complete sequence information of the *S. cerevisiae* reference strain S288C was released². With respect to chromosome XIV, so-called gene cluster duplications were found in seven regions of 17 kb to 130 kb. The precise locations of the 67 pairs of ORF homologues in these seven cluster duplications are shown in Fig. 2, together with all other chromosome XIV ORFs for which structural homologues were found; five pairs of positionally conserved duplicated tRNA genes are also indicated. Probably half of these structural homologies among different chromosomes would have remained undetected in classical DNA hybridization experiments.

Complementary to the graphical display of the seven cluster duplications, we have determined the degree of homologies for each ORF pair and, if known or predictable, their functions (Table 1). ORFs displayed from left to right in Fig. 2 are listed from top to bottom in the table. An automated means of finding and displaying structurally homologous segments in genomes several million base pairs long involves the screening of sliding windows of 500 bases between pairs of chromosomes<sup>35</sup>. This very efficient method was also applied to chromosome XIV, and most of the ORF pairs participating in cluster duplications were detected (K. Heumann, unpublished data). However, this automated approach still

requires manual editing to find all details of cluster duplications, such as multigene families, potentially inverted ORF members, more than averagely diverged ORFs, and tRNA genes.

The 17-kb subtelomeric cluster duplication between chromosomes XIV and VI (cluster duplications 14-6) consists entirely of highly conserved ORF pairs (average 96.6% amino-acid identity) and shows stringent synteny. The intergenic regions are also highly conserved, suggesting that the duplication of the six ORFs is a relatively recent event on an evolutionary timescale.

Most of the ORF pairs in the other six cluster duplications are much less conserved, and their promotor and terminator regions lack significant homologies, suggesting that they are ancient duplication events. Five of the highly conserved ORF pairs of these ancient duplications code for ribosomal proteins (average 95.3% amino-acid identity), one for two members of the 70K heat-shock protein family (99.3% amino-acid identity), one for two forms of iso-propyl malate synthase (88.5% amino-acid identity) and one for two forms of citrate synthase (81.4% amino-acid identity) (Table 1). Excluding these ORF pairs, which are apparently under high selection pressure to preserve their sequence information, the average homology of ORF pairs was determined for each of the cluster duplications. ORF pairs in cluster duplications CD14-15B and CD 14-3 (average 56% amino-acid identity) seem to be less diverged than ORF pairs in CD14-15A, CD14-8, CD14-9 (average 47.5% amino-acid identity) and CD14-4 (average 37% amino acid identity). However, there are too few ORF pairs to draw conclusions about different temporal orders for the cluster duplications involving chromosome XIV.

Could the six ancient cluster duplications, at the time of their creation, have looked similar to the recent cluster duplications between chromosomes XIV and VI, with perfect synteny of all ORFs? And could they have been shaped over evolutionary time by base-pair changes, insertions of new ORFs, deletions of some of the originally duplicated ORFs, inversions of single or groups of ORFs, and translocations to yield the present picture of 'relaxed synteny'? This is certainly possible if the now visible arrangements indeed originated from duplications of gene clusters, perhaps by long-range gene conversions or chromosome duplications. However, it remains possible that the evolutionary history of S. cerevisiae involved fusion of two ancient forms of yeast cells with smaller genomes already displaying sequence divergencies and some level of relaxed synteny and that, for most of the duplicated ORFs, one copy was lost over time because of a lack of selective advantage for *S. cerevisiae* to keep more than

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# The nucleotide sequence of Saccharomyces cerevisiae chromosome XV

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Chromosome XV was one of the last two chromosomes of Saccharomyces cerevisiae to be discovered<sup>1</sup>. It is the third-largest yeast chromosome after chromosomes XII and IV, and is very similar in size to chromosome VII. It alone represents 9% of the yeast genome (8% if ribosomal DNA is included). When systematic sequencing of chromosome XV was started, 93 genes or markers were identified, and most of them were mapped<sup>2</sup>. However, very little else was known about chromosome XV which, in contrast to shorter chromosomes, had not been the object of comprehensive genetic or molecular analysis. It was therefore decided to start sequencing chromosome XV only in the third phase of the European Yeast Genome Sequencing Programme, after experience was gained on chromosomes III, XI and II (refs 3-5). The sequence of chromosome XV has been determined from a set of partly overlapping cosmid clones derived from a unique yeast strain, and physically mapped at 3.3-kilobase resolution before sequencing. As well as numerous new open reading frames (ORFs) and genes encoding tRNA or small RNA molecules, the sequence of 1,091,283 base pairs confirms the high proportion of orphan genes and reveals a number of ancestral and successive duplications with other yeast chromosomes.

The DNA sequence of 1,091,283 nucleotides contains 560 ORFs, of at least 100 sense codons, that are not entirely included within a larger one (our standard basic definition; see ref. 4). If those corresponding to Ty or Y' elements are excluded, and intron predictions are considered (see below), 551 different ORFs remain. To these were added eight known genes shorter than 100 codons (*BAT2, CRS5, RPB10, RPS30B, RPS33A*,

SME1, TOM6 and the CPA1 leader), and a pseudogene 581 codons long (YOL153c) that contains two in-frame ochre codons. It is considered here because its putative translation product has significant homology with the Gly-X carboxypeptidase encoded by CPS1, and because, in another yeast strain, the two stop codons are replaced by two glutamine codons CAA<sup>6</sup>. Note that, in the present sequence, YOR031w (CRS5) also contains an inframe ochre codon instead of the CAA codon found in other strains (the reality of the stop codon was verified by direct sequencing on yeast DNA). Other interesting but more complex cases of pseudogenes found in chromosome XV will be described elsewhere. Also note that YOL040c has been considered here (coordinates 253,147–253,575) instead of the larger antisense ORF within which it is entirely included because it corresponds to a known gene (RPS21).

The sequence also reveals 526 short ORFs (from 50 to 99 sense codons) not entirely included within larger ones, six of which are already considered above. In this size range, it is obviously difficult to distinguish actual genes from random occurrences. Using high codon bias (CAI > 0.2) and absence of a partial overlap with larger ORFs as predictive criteria, only six candidates remained. One of these shows very significant homology with the 60 codon-long gene HOR7 of chromosome XIII. This ORF, named YOL052ca, has been added to the above list, bringing the grand total to 561. Of these ORFs 33 (5.9%) are 'questionable', based on their short size and low CAI (see ref. 4), and 18 of them partly overlap other ORFs, increasing their suspicious character.

The longest ORF of chromosome XV is YOL081w (the *IRA2* gene) with 3,079 codons. The two shortest ORFs, if the 25 amino-acid leader peptide of the *CPA1* gene is ignored, are YOR045w (*TOM6*) and YOL052ca, with 61 codons each. The average size of chromosome XV ORFs is 457 codons, very close to the figure observed for the entire yeast genome<sup>7</sup>. In total, 33 pairs and 5 trios of partly overlapping ORFs are found; 25 pairs are antiparallel, excluding the possibility of sequencing errors. Among the parallel pairs, YOR012w and YOR013w are suggestive of a frameshift error, or a pseudogene, as their products share homology with the amino terminus and the carboxy terminus of the product of YDR391c, respectively.

The overall density for protein-coding genes is 70.6%, slightly lower than the average for the whole yeast genome subtracted from rDNA<sup>7</sup>. Variations are observed along the chromosome, with two short regions showing gene density above 85% (centred around ~200 kb and ~950 kb, respectively; see Fig. 1). These regions also correspond to areas of high G+C content. As is generally observed in yeast, the two subtelomeric regions show low gene density.

The entire chromosome shows no significant strand coding bias, but important local variations are observed, with seven short regions (of  $\sim$ 30–50 kb each) showing a clearcut excess of ORFs on the Watson strand; eight others have an excess on the Crick strand (Fig. 1). Orientation of neighboring ORFs is random for the whole chromosome, with 150 diverging pairs, 149 converging pairs, and 261 tandemly arranged pairs (123 on the Watson strand, and 138 on the Crick strand). The longest tandem array contains 11 successive ORFs (YOR104w to YOR114w, coordinates 517,639–538,451).

A total of 13 introns have been identified, most of which occur in short ORFs with high codon bias. Chromosome XV introns are short, as is typical for yeast, ranging in size from 135 to 527 nucleotides (average 334 nucleotides). They have an average G+C content of 34.9%, significantly lower than that of the entire chromosome (38.2%) or its ORFs, (39.5%). Note that the possible occurence of introns in the 5' untranslated region of the pre-mRNA molecules has not been examined systematically for lack of discriminative criteria among the numerous occurrences of the intron consensus 5'-GYMHGH-N1-TACTAAC-N2-YAG-3' in the sequence (294 occurences if N1 and N2 are set shorter than or equal to 400 and 50 nucleotides, respectively, or more than 600 for limits of 1,000 and 180 nucleotides).

The 20 tRNA genes recognized correspond to 12 different amino acids and 22 different codons. Six tRNA genes contain introns. All tRNA genes are significantly richer in G+C content (47–63%) than the average yeast genome sequence. The frequent duplication of tRNA genes in yeast is

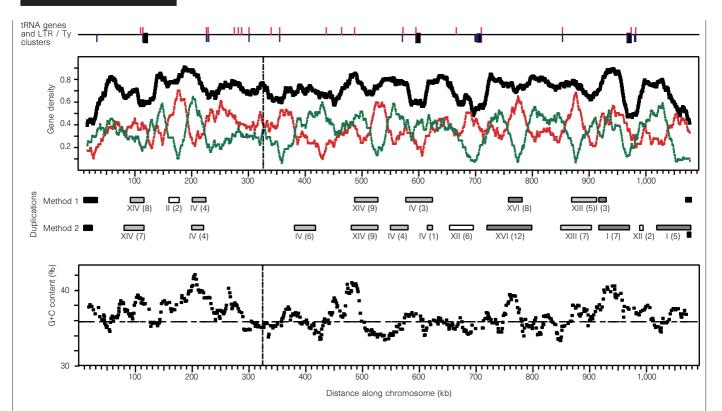


Figure 1 Variation in gene density (top) and base composition (bottom) along the sequence of chromosome XV (scale in kilobases from left telomere). Vertical broken lines indicate position of the centromere. Gene density is expressed as the probability that each nucleotide is part of an ORF, calculated using sliding windows of 30 kb (steps of 0.5 kb) for the Watson strand alone (red line), the Crick strand alone (green line), and their sum (black line). The Watson strand is oriented 5' to 3' from left to right on the chromosome map<sup>4</sup>. G+C content was calculated from silent codon positions using a sliding window of 13 consecutive ORFs (horizontal broken line indicates

average G+C content at these positions; 35.7%). Top line, positions of tRNA genes (thin bars above line), solo LTR (thin bars below line), and complete Ty elements (thick bars below line). Middle, positions of major 'ancient' chromosomal duplications. Blocks represent extent of clusters (method 1), or arrays of ORF pairs (method 2), as defined in text, with indication of the matching chromosome and the number of ORFs involved (in parentheses). Note that several blocks corresponding to a given chromosome are often intermingled with those corresponding to another. Blocks in subtelomeric position (filled) match with several distinct chromosomes.

noticeable on chromosome XV alone, with four gly-tRNA genes (tG(GGY)OL1 and tG(GGY)OL2 are identical in sequences, and tG(GGG)OR1 is similar to the previous two), three pro-tRNA genes (identical in sequences except for their introns), two thr-tRNA genes, and two asn-tRNA genes, respectively identical in sequences; there are also two met-tRNA genes, but they differ in sequence. Duplicated tRNA genes are always found within different sequence environments (including different associated long terminal repeats (LTRs); see below). The tRNA genes are distributed throughout the chromosome (Fig. 1), as is generally the case for yeast which, unlike other organisms, does not show large clusters of tRNA genes in its genome.

Seven genes encoding small known RNA molecules were recognized from the sequence. One of these, *snR17A*, which encodes the U3 snRNA, contains an intron and is duplicated elsewhere in the yeast genome<sup>8</sup>. The downstream part of the gene encoding snR35 partly overlaps the downstream part of an ORF of unknown function, YOR222w, the product of which shares similarity with ADP-ATP carrier proteins.

Four complete Ty elements (two Ty1 and two Ty2), 20 solo LTRs or remnants of them (12 delta, 6 sigma and 2 tau elements), and one Y' element were found. Solo LTRs, or complete Ty elements, are almost always located immediately upstream of tRNA genes (Fig. 1). Only one solo LTR element and one Ty1 stand alone. Consistent with general trends<sup>9</sup>, the two Ty2 elements are found at 'old' sites occupied by several solo LTRs associated with tRNA genes; the same is true for only one of the two Ty1 elements. Conversely, only 11 of the 20 tRNA genes have one or more LTR element upstream of their 5' end, the closest element always being within 200 base pairs of the tRNA gene (sigma elements are only 16–18 nucleotides upstream of tRNA genes).

In total, RNA-coding genes and transposons occupy only 1% of the chromosome XV sequence.

There remain 309,627 base pairs (28.4% of the chromosome) that we will call here 'intergenic regions'. Such regions contain, for a small part, structural chromosomal elements such as the centromere (coordinates 326,592–326,706), the telomeric  $(C_{1-3}A)_n$  repeats (coordinates 1–113 and 1,091,264-1,091,283) and two subtelomeric core X elements and their associated repeated elements (STR) (coordinates 114-847 and 1,083,914-1,084,611). But intergenic regions primarily contain promoters, terminators and transcriptional regulatory elements of the proteincoding genes, most of which have not yet been identified. Intergenic regions believed to contain promoter elements based on the orientation of flanking ORFs are noticeably longer (791 nucleotides on average between diverging ORFs) and are richer in G+C (36.2%) than intergenic regions containing putative terminators (421 nucleotides and 28.7% G+C). The presence of flanking RNA-coding genes does not alter this trend. The sequence also reveals 63 ARS consensus elements (5'-WTTTAYRTTTW-3') the activity of which remains to be examined; 39 of these occur in intergenic regions.

Chromosome XV contains few simple sequence iterations. The longest dinucleotide repeat is an alternating poly(AT) stretch of 20-mers (coordinates 45,691–45,730) within the intergenic region that separates the converging ORFs YOL149w (*DCP1*) and YOL148c (*SPT20*). Only 19 other cases exist of either dinucleotide repeats of at least 10-mers (all are alternating poly(AT) or mononucleotide repeats of at least 20-mers (all poly(A) or poly(T)). Similarly, few trinucleotide repeats are found, the longest being a 20-mer of the triplet CAA occurring within an ORF of unknown function, YOR267c, and encoding a poly-glutamine stretch. Six

Cosmids or DNA	Coordinates on final chromosome	Overlap	Strategy*	Reference
telomeric plasmid / pEOA363	1-32687		S, A	
pEOA179 / pEOA461	24486-97824	8202	N, A, M	6, 14, 16, 17, 18, 20
pEOA417	96924-140942	901	S, M	26
pEOA228	139031-178337	1912	S, A	28.29
pEOA1044	177014-210234	1324	N, W, A	in the press
pUOA1217	209185-235991	1050	SS, M	22
pUOA1344	222408-256233	13584	S, W, A	
pEOA321	253576-287613	2658	N, A	in the press
pEOA215	286637-323078	977	S, R	
DEOA156	321732-352202	1347	S, P, A	30
pEOA303 / pEOA270	350740-408356	1463	S, A	
pEOA272	391560-427841	16799	S, A	
pEOA213 / pEOA217	415169-477887	12673	SS, M	in the press
11 cosmids <sup>†</sup>	476475-606002	1413	S, W, A	27 and in the press
pEOA477 / pUOA1258	604545-660867	1458	SS, W, M	15, 21
pUOA533 / pEOA378 / pEOA241	655864-741096	5004	S,R	
pEOA423 / pEOA048	739215-799188	1882	S, A	8, 11
pUOA1302	795488-832262	3701	SS, W, M	in the press
pUOA1337	823760-861431	8503	S, A	19
pEOA487	859329-895527	2103	SS, W, M	in the press
pEOA284	892246-927955	3282	SS, A	24
pUOA502 / pEOA232	927738-957182	218	S, A	23
pEOA138	955761-996055	1422	S, M	25
5 cosmids <sup>‡</sup>	992145-1081258	3911	SS, W, M	•••••
Right PCR	1080794-1091283	465	P	

S, shotgun of cosmid or part thereof (SS); N, nested deletions; W, walking primer; P, PCR fragments; M, manual gels; A, automatic fluorescent; R, direct membrane blotting

other cases of trinucleotide repeats of at least 10-mers are found. Polymorphic variations in trinucleotide repeats have been described in yeast 10. An example of such variations is given by two ORFs of unknown function, YOR229w and YOR230w, that represent an ancient and diverged tandem duplication (67% sequence identity), with an insertion of a long imperfect trinucleotide repeat in YOR229w that is absent from YOR230w<sup>11</sup>.

Iterations of a few longer sequence motifs are also present. The clearest example is probably the near-perfect repeat of the 39 nucleotide-long unique sequence 5'-GAGCCTGATTCTGTGGCAGAAGATGAACCGGAGACTGAT-3', which occurs nine times between positions 30,935 and 31,309, at the beginning of YOL155c, an ORF of unknown function shows similarity to glucan-1,4- $\alpha$ -glucosidase. The repeats determine a serine-rich amino-acid sequence. At the end of the same ORF (coordinates 28,905–29,279), another near perfect repeat of a unique long sequence, 5'-CAGTAGTGTATGWYTTNGGRGAARCASTRGTTKCKG-3', occurs four times. In both cases, degenerated copies of the unique sequence are also found beyond the main repeats.

Of the 561 identified ORFs, 212 (37.8%) correspond to known and functionally characterized genes; all of the others are new. By sequence comparison of their products with general databases, 34 of these (6.1% of the total) show significant homology to proteins of known biochemical and/or physiological function of either yeast or other organisms, and 69 others (12.3% of the total) show weak homology. There are 246 ORFs with products that have either no significant homologue (187 cases or 33.3% of total, among which 28 are questionable) or are homologous to proteins that are themselves of unknown function (59 cases or 10.5% of the total).

Using previously defined criteria<sup>12</sup>, 239 ORF products (42.6% of total) are predicted to contain at least one transmembrane span, 170 of which are of unknown function. Two proteins have 12 predicted spans (SCM2, the product of YOL020w, and ALG8, the product of YOR067c), and 43 others have five predicted transmembrane spans or more (only 15 of them are functionally characterized).

Duplications are frequent in the yeast genome, and take several different forms that suggest distinct mechanisms of formation. Comparison of the chromosome XV sequence with the entire yeast genome (including chromosome XV), reveals 12 'clusters' of duplicated sequences that may represent ancestral chromosomal duplications subsequentely modified. Such clusters range in size from 12 kb to 49.5 kb, and contain two to nine ORFs, making a total of 297.5 kb of the chromosome XV sequence (27% of total) that is duplicated on at least eight other chromosomes. Duplications with chromosomes IV and XIV are each represented by two clusters intermingled along the chromosome XV map, suggesting successive events of chromosome duplication or rearrangements. Among the four clusters that contain tRNA genes, there are two cases where homologous tRNA genes are conserved at equivalent positions on the other chromosome, further supporting, in such cases, the hypothesis of ancestral chromosomal duplications.

For chromosome XV, duplications were also examined using a second approach based on the systematic comparison of predicted translation products of all yeast ORFs against all others, followed by sequence alignments and estimation of their significance compared to randomizations, and to the overall distribution of similarity values for the entire yeast genome. A total of 193 different ORFs of chromosome XV (34.4%) were found to have at least one significant homologue in the yeast genome (including 28 pairs on the chromosome XV itself). Half of these have several homologues, forming gene families with various degrees of divergence. Among these, 35 ORFs, nearly all in a subtelomeric location, are members of large families with five partners or more (one of them has up to 26 partners). Large gene families include HXT genes, PAU genes and *RAS* genes, with more than 15 members each in the entire yeast genome. The chromosome XV ORF homologues include 426 different ORFs from the other chromosomes (7.8% of the yeast genome). Distribution of duplicated ORFs along chromosome XV using this method gives roughly the same results as the first method (Fig. 1).

Chromosome XV contains several local ORF duplications in tandem or inverted orientations. Those showing the highest degree of sequence

<sup>&</sup>lt;sup>†</sup>pEOA347, pUOA522, pEOA246, pEOA264, pEOA273, pEOA306, pEOA265, pEOA106, pEOA338, pEOA986 and pEOA1081.

<sup>\*</sup>pEOA387, pEOA360, pEOA343, pEOA434 and pEOA390.

conservation are the tandem YOR229w and YOR230w already mentionned (63% amino-acid identity), and the inverted repeat YOR010c (*TIR2*) and YOR009w (62% identity). Other local duplications show significantly greater sequence divergence, suggesting more ancient events; they are represented by the tandems YOL083w and YOL082w (35% identity), YOR285w and YOR286w (37% identity), and YOL048c and YOL047c (38% identity, the latter ORF containing an intron). There also exists some 'local' duplications including pairs of ORFs, such as YOR162c and YOR172w (44% identity), or YOR381w and YOR384w (37% identity), that are separated by a few unrelated ORFs. They have also diverged, and may correspond to ancient local duplications that subsequently received intervening DNA.

When this work started, 81 genes or markers were genetically mapped to chromosome XV, and 12 others were assigned to it but unmapped<sup>2</sup>. Seven of the unmapped genes and 55 of the mapped genes could be unambiguously assigned to ORFs or tRNA genes of the present sequence on the basis of previous partial sequence data, use of probes or gene function. Two genes, *ts26* and *PTP1*, originally mapped to chromosome XV, belong to chromosomes XII and IV (YLR268w and YDL230w, respectively). One gene, *TIR2* which corresponds to YOR010c, was originally named *SRP1*, creating confusion with YNL189w on chromosome XIV. Other than that, the original genetic map agrees fairly well with the present data, except for some local inversions of gene order, mostly around the centromere (*TOP1* and *SIN3* are on the left arm, *PEP12* is on the right) and in subtelomeric regions (*MEK1*, *PHR1* and *RAD17*), as is also observed for other chromosomes.

The chromosome XV sequence, like that of other yeast chromosomes, has been interpreted using criteria that are essentially predictive for ORFs, but are comparative with previously described sequences for other genetic features such as RNA-coding genes, Ty elements and the various chromosomal elements. It follows that the number of predicted ORFs is probably overestimated by a few percent compared with the number of actual protein-coding genes, whereas the identification of the other features should be considered as a minimum. Clear-cut identification of the questionable ORFs is not possible without independent experimental evidence, but it is suggested that they represent ~6% of all predicted ORFs. The a posteriori comparison of the predicted ORF products with general protein database entries forms the basis for the notion of 'orphan' genes<sup>7</sup>. Orphans are those protein-coding genes, predicted from the genomic sequence, that fail to show significant homology (at the chosen threshold value) when their translation products are compared to gene product sequences translated from all other genomic sequences present in public databases, whether they correspond to S. cerevisiae or any other organism. As is the case for other yeast chromosomes, a large fraction (33%) of chromosome XV ORFs are orphans without any significant structural homologue; while another 10.5% are orphans with structural homology to one or several other S. cerevisiae orphan(s). It is not surprising that, as with other genes, orphans can be duplicated in the yeast genome, or form diverged gene families. But what is more interesting is the significant deficit of these compared with the overall number of gene families in yeast. Of the 193 chromosome XV ORFs that are duplicated or parts of gene families, only 50 are orphans, compared with 83 predicted (43% of the 561 ORFs). The deficit of orphans among gene families (and the correlated excess of functionally characterized genes) is exactly opposite to the classical expectation from standard genetic screenings based on negative mutant phenotypes, which should tend to ignore isofunctional duplicated genes. One possible explanation for the bias observed may be that molecular methods, in contrast to classical genetic screenings, tend to facilitate the isolation of gene families that are structurally but not functionally related. Systematic functional analysis of the yeast genome, which is expected to follow the completion of the genomic sequence, should help to solve this important question.

#### Methods

The sequence of chromosome XV was assembled from 46 cosmids covering the entire length of the chromosome except its left and right telomeres, which were sequenced from a rescued plasmid and a polymerase chain reaction (PCR) genomic product, respectively (Table 1). The cosmid map will be described separately. Because chromosome XV comigrates in PFGE with chromosome VII (which is only 348 bp shorter), the technique of chromosome fragmentation based on the insertion of unique artificial I-SceI sites<sup>13</sup> played a key role in the physical mapping of these two chromosomes.

Each segment of the chromosome was sequenced on both strands using the methods and strategies indicated in Table 1. Overlaps between sequences submitted by different laboratories range from 218 bp to 16,799 bp (average 3,765 bp). In nearly all cases, overlapping sequences were also entirely determined on both strands by each laboratory and were found to be 100% identical. Only three differences were found in a total of 90,360 bp. After re-examination of the sequences, only one real divergence remained (an A to G transition), probably resulting from a mutation in one of the sequenced cosmids. The present chromosome sequence includes an A at position 400,735 but a G is equally probable. This uncertainty affects YOR036w (*PEP12*), by changing a codon CAG (Gln) to CGG (Arg).

After assembly, the entire sequence was verified as follows. A total of 201 short segments (259 bp–400 bp long) were selected after examination of the sequence using, as criteria, the possible occurrence of frameshifts, compressions (particularly in G+C-rich regions), and the presence of oligomeric stretches of mono- or dinucleotide repeats. Selected segments were attributed anonymously to four different laboratories and resequenced following the protocol of G. V. (unpublished). In total, 64,370 bp were verified revealing 21 original errors (13 nucleotides omitted, 3 nucleotides in excess, and 5 substitutions). Taken together with overlaps between different laboratories, 14.2% of the chromosome (154,730 bp) has thus been sequenced twice independently. The average sequence accuracy is 99.98%. This figure is probably an underestimate, however, as verifications were directed to suspicious regions. Parts of the present sequence were published independently by the sequencers before assembly of the contig and application of final quality controls<sup>6,8,11,14–30</sup>. Several other manuscripts are also in the press.

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# The nucleotide sequence of Saccharomyces cerevisiae chromosome XVI

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The nucleotide sequence of the 948,061 base pairs of chromosome XVI has been determined, completing the sequence of the yeast genome. Chromosome XVI was the last yeast chromosome identified<sup>1</sup>, and some of the genes mapped early to it, such as *GAL4*, *PEP4* and *RAD1* (ref. 2) have played important roles in the development of yeast biology. The architecture of this final chromo-

some seems to be typical of the large yeast chromosomes, and shows large duplications with other yeast chromosomes. Chromosome XVI contains 487 potential protein-encoding genes, 17 tRNA genes and two small nuclear RNA genes; 27% of the genes have significant similarities to human gene products, and 48% are new and of unknown biological function. Systematic efforts to explore gene function have begun.

There are 487 open reading frames (ORFs) on chromosome XVI, and 10 Ty-related ORFs. Of these ORFs, 17 have an intron, and ORF RPL6B (YPL198w), which encodes a ribosomal protein, has two introns. ORFs were identified using the working definition that they commence with an ATG and have at least a further 99 contiguous sense codons<sup>3</sup>, and were analysed using established procedures<sup>4,5</sup>. Before systematic sequencing, there were 73 genes<sup>6</sup>, with 47 genes and their relative positions defining the genetic map, and an additional 26 genes located on the physical map. An additional 92 genes have formal genetic names, some of which had been previously cloned but not mapped to this chromosome or have been studied following their identification by systematic sequencing, for a total of 165 known genes. Thus only 33% of the total ORFs found on chromosome XVI had been identified before the completion of the sequence. Other genetic elements include: 17 tRNAs (9 of which are within 500base pairs of a long terminal repeat (LTR) element of a retrotransposon; 5 Ty retrotransposons; 15 delta elements including partial elements; 4 sigma and 2 tau elements; and 2 snRNAs.

The number of ORFs of known function is 194 (40%), of which 76 are functionally characterized proteins; 88 are known proteins that are not fully characterized; 26 have similarity to proteins of known biochemical and physiological function; 6 are homologous to proteins of known biochemical function; and 55 have a weak homology to known proteins. These weak similarities alone are insufficient to confidently assign function. This leaves 236 ORFs of unknown function (48%), of which 50 have homologues of unknown function, and 186 have no similarity to known proteins. There are 36 questionable ORFs, all of which partly overlap another ORF. All have a low codon adaptation index (CAI) of not greater than 0.18, are short (with an average length of 132 codons), and have no known homology with other proteins or are associated with no known phenotype. For four of these ORFs in two pairs (YPL034c and YPL035c, and YPR038w and YPR039w) it is unclear which, if any, are biologically meaningful. There are few apparent pseudogenes but these include YPL276w and YPL275w, which occur together in the genome as a frameshifted pair, both with homology to a formate dehydrogenase. This arrangement has been confirmed by direct sequencing of genomic DNA. Whether this region represents a mutation specific to strain S288C awaits experimental determination.

Functional categories have been compiled for chromosome XVI ORFs: 214 (43%) are classified in some form and 283 remain unclassified. The chromosome is sufficiently large to have a broad representation of all of the predominant functional groups. Detailed global genome classification and statistics for these functional assignments are tabulated and have been discussed elsewhere 7.8.

A robust amino-acid sequence motif is the presence of a predicted transmembrane domain, a region of a protein that spans a lipid bilayer. There are 181 ORFs with one or more predicted transmembrane domains on chromosome XVI (37%)<sup>9</sup>, a number close to that seen on chromosomes II and III (refs 3, 10). Of these, 68 are known functionally in some form, and this percentage of known membrane proteins (38%) is similar to that of all known ORFs. Most of these membrane-protein encoding ORFs contain one or two predicted transmembrane domains (99 and 39, respectively); 15 proteins have 7 or more predicted transmembrane domains, and Ypl006p has 13.

An immediate way to use the sequence information is to examine experimentally ORF function, and the Canadian group is compiling systematic transcript and gene-disruption data. For a section encoding 89 ORFs in the region spanned by YPL085w to YPR017c, 61 transcripts were detected in haploid cells grown on rich medium at 30°C. This level of ORF expression is similar to that seen on chromosomes I and III (refs 5, 11). Of the 117 genes on chromosome XVI that have been disrupted, 36

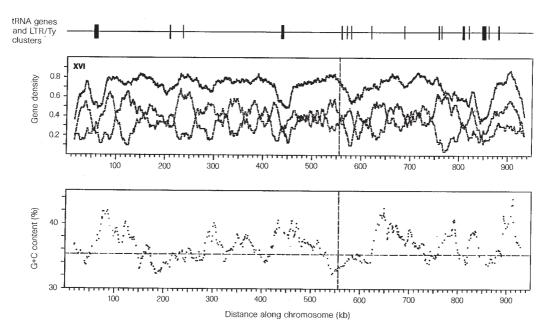


Figure 1 Molecular architecture of chromosome XVI. Top line shows positions of tRNA genes, solo LTR or Ty elements (thin vertical lines) or clusters of them (thick vertical lines) along the chromosome. Panels: variation of gene density (top) and base composition (bottom) along chromosome XVI (scale in kilobases from left telomere). Vertical broken lines

indicate position of the centromere. Gene density determined as for chromosome XV is shown for the Watson (medium line) or the Crick (thin line) strands, and the sum of both (thick line). G+C content was calculated as for chromosome XV (horizontal broken line).

(31%) are 'essential' for vegetative growth. Although this fraction is higher than the approximately 12% estimated for the entire genome<sup>12</sup>, or found on chromosome I (ref. 5), it still represents only 7% of the ORFs on the chromosome. The final proportion of essential genes on chromosome XVI awaits a complete disruption set. This information is displayed and will be updated (web sites URL http://www.mips.biochem.mpg.de and URL http://genome-www.stanford.edu).

Several ORFs deserve mention, some because of size, some because they were anticipated but not previously found, and others because they occur in metazoans with phenotypes or functions that appear characteristic of the larger multicellular eukaryotes, and whose unexpected presence in yeast affords some insight into function. There are 130 ORFs (27%) with significant similarity to products or predicted products of human genes. Four ORF products (PAL1, PHO85, ROX1 and RAD1) are similar to products of the human genes ALD, RET, SRY and XPF (ERCC4) that, when altered by mutation, lead to X-linked adrenoleukodystrophy, multiple endocrine neoplasia 2A, gonadal dysgenesis, and xeroderma pigmentosum, respectively<sup>13,14</sup>. The largest ORF is YPR117w, specifying a 2,489codon putative membrane protein of unknown function. Just one other ORF, SEC18 (YPL085w), has more than 2,000 codons, and only 38 ORFs (8%) are larger than 1,000 codons. Identifying very small ORFs presents special problems<sup>3,15</sup> and just six identified ORFs on chromosome XVI are less than 100 codons. The smallest known functional ORF, ATP15 (YPL271w), has 62 codons and encodes an F1-ATP synthase epsilon subunit<sup>16</sup>. Other small ORFs undoubtedly exist on the chromosome, and remain to be uncovered by functional analysis.

YPL127c encodes an apparent H1 histone, a protein previously not thought to be present in yeast. Plant and animal H1 histones are known to be involved in the higher-order assembly of nucleosomes but, despite considerable work, the precise role of H1 histone remains unclear<sup>17,18</sup>. Disruption of this single-copy yeast gene indicates that it is not essential for mitotic growth<sup>32</sup>. A detailed analysis of the possible role of this H1 histone in chromosome assembly, stability and the regulation of gene expression can now be explored.

YPR048w encodes a cytochrome P450 protein with similarity to human nitric oxide synthase, NOS. Human NOS is an amino-acid oxidoreductase that oxidizes the terminal N of arginine to give citrulline and nitric oxide. Nitric oxide (NO) in mammals behaves as a hormone, and is

involved in many processes including vasodilation and neurological activities<sup>19</sup>. The involvement of NO in yeast metabolism had not previously been imagined. One possibility is that it acts to regulate cell signalling through interaction with small GTP-binding proteins<sup>20</sup>.

We found that 74.57% of the chromosomal DNA is involved in the coding of ORFs. These 497 ORFs have an average size of 474 codons, close to the average values seen for other large chromosomes<sup>3,4,15</sup>. Of the 487 ORFs that are not Ty related, 251 are on the Watson strand and 236 are on the Crick strand, with no apparent strand bias3. There is, on average, an ORF every 1,908 bp over the chromosome. The positioning of ORFs relative to each other seems random: 111 ORFs are divergent, 118 are convergent, and 195 are tandemly arranged. Of the remaining ORFs, 38 are next to a non-ORF element, and in 12 cases two non-ORF elements are adjacent. With regard to intergenic spacing, the average length between tandemly arranged ORFs is 534 bp, for divergent ORFs it is 569 bp, and for convergent ORFs it is 340 bp. Only one region is apparently devoid of ORFs or other genetic entities for 3 kilobases or more: a subtelomeric 3,863 bp gap between YPL275w and YPL274w. There are no large noncoding regions comparable to those found in the subtelomeric regions of chromosomes I and VIII (refs 5,21).

There are no clustered gene families<sup>5</sup> on chromosome XVI and, as found with other yeast chromosomes, there is little apparent functional clustering of genes. There are two exceptions: a 'syntenic' pair, *CIT3* (YPR001w) and YPR002w, conserving the arrangement of the mmgD and mmgE genes in *Bacillus subtilis* (GenBank accession no. U29084); and two adjacent cyclin genes, *CLB2* (YPR119w) and *CLB5* (YPR120c), an arrangement that is duplicated on chromosome VII as *CLB1* (YGR108w) and *CLB6* (YGR109c), and which forms part of a larger duplication between these two chromosomes (see below).

The G+C periodicity on chromosome XVI varies about an average content of 38.1% (Fig. 1). Gene density also fluctuates along the chromosome, although it shows little correlation with G+C periodicity. Overall the G+C content of coding regions is 39.5%, and for non-coding regions is 33.29%. The centromere lies in a region of low G+C content, and the Ty and tRNA element clusters lie in regions of low gene density; such long-range compositional variations have been discussed elsewhere<sup>22</sup>.

The centromere of chromosome XVI spans nucleotide residues 555,952–556,069, between *HAT1* and *CIT3*, making the chromosome

close to being metacentric. Both telomeres seem to be typical in structure. There are 47 potential origins of DNA replication that match the 11-bp ARS element consensus, although the actual autonomously replicating sequences (ARS) used in replicating the chromosome remain to be determined experimentally.

Like much of the yeast genome, regions of chromosome XVI are duplicated. There are some large-scale DNA duplications spanning 25 kb or more<sup>23,24</sup>. The largest of these is on a 129-kb section of the right arm of chromosome XVI, nucleotide coordinates 731,001-860,000, where regions are duplicated onto a 129.5-kb section on the right arm of chromosome VII (nucleotide coordinates 648,001-777,500). Although removed from the comparison that identified this duplication, the region on chromosome XVI is rich in repetitive elements and contains three Ty elements, five additional LTRs and six tRNA genes. Such DNA duplications form large regions of partial gene synteny between these two chromosomes. An example is a section from nucleotide 834,000 to 860,000 on chromosome XVI and from 762,422 to 777,500 on chromosome VII. In the chromosome XVI interval from YPR154 to YPR159, four of the six genes, two delta elements and two tRNA genes, are syntenic with their chromosome VII counterparts, YGR136 to YGR143, with the exception of a tandem Ty1 element inserted between YPR158 and YPR159 on chromosome XVI. It has been suggested<sup>25</sup> that the origin of the KRE6 (YPR159w)/SKN1(YGR143w) pair in this region resulted from some event involving duplication through transposition of the retrotransposon or tRNA elements. The origin of these major cluster homology regions remains unclear but probably consisted of more than one event; the subject is discussed elsewhere at a global genome level<sup>7</sup>. Evidence for duplications can also be found at the ORF level; 125 of the ORFs on chromosome XVI have one or more counterpart with significant similarity in the yeast genome. In addition to duplications, chromosome XVI also contains members of larger gene families, with at least 38 ORFs having similarity to two or more yeast ORFs. An example is KTR6 (YPL053c), a member of a family of nine mannosyltransferase-encoding genes located on eight different chromosomes<sup>26</sup>.

Establishment of the genetic and physical maps were critical precursors to obtaining the nucleotide sequence of the chromosomes. The genetic map of chromosome XVI is 251 cM in length, giving an average cM/kb value of 0.26, the smallest seen for a yeast chromosome, and close to that previously reported<sup>27</sup>. It indicates that a chromosome XVI bivalent has, on average, ten crossovers per meiosis. Although the genetic map is generally correct, there are several discrepancies with the positions found on the sequenced chromosome. Of the 46 genes mapped genetically through the phenotypes of alleles, 14 (*spoT16*, *rad53*, *nib1*, *sot1*, *SUF21*, *dna1*, *mak6*, *tsm0120*, *ymc1*, *spoT20*, *SUP15*, *SUP16*, *cdc67* and *rad56*) remain to be identified on the sequenced chromosome.

Determination of the nucleotide sequence of chromosome XVI completes the sequence of the yeast genome, allowing a genome-wide analysis of a small and experimentally amenable eukaryotic organism. Such systematic studies should enhance our knowledge of cell function, and help us to understand the structure and function of eukaryotes with larger genomes.  $\hfill \Box$ 

#### Methods

Chromosome XVI was sequenced using a set of overlapping cosmid and lambda clones based on a previous chromosome XVI physical map<sup>28</sup> (L. Riles and M.V. Olson, personal communication) from the S288C-derived strain AB972. Two gaps on the right arm and both telomeres were sequenced using polymerase chain reaction (PCR) products amplified from genomic DNA<sup>29</sup>. Individual cosmids representing the portion mapped by the EU group were sequenced by contracting laboratories using a variety of subcloning, sequencing and assembly methods<sup>3, 4</sup>. Explanations of the cloning, sequencing, assembly and quality control methods used by the other groups have been described<sup>21,30</sup>. The telomeres were sequenced using specially devised procedures<sup>31</sup>. Assembly of the completed chromosome sequence was made in Martinsried or Montreal as described<sup>3-5,15</sup>. Determination of overlapping sequence between groups indicated that seven differences were found and resolved in 81

kb of sequence. This allowed us to estimate the accuracy of the sequence to be conservatively within the three errors per 10 kb average for the yeast genome<sup>7</sup>.

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