

## H<sub>2</sub>O<sub>2</sub>-specific genes

Gene name	Annotation
SPAC1F8.04C	putative chlorohydrolase/deaminase; putative guanine deaminase
SPCC663.08C	putative short chain dehydrogenase
SPBC609.04	MFS multidrug efflux transporter
SPCC663.06C	putative short chain dehydrogenase protein
SPBC409.13	6,7-dimethyl-8-ribityllumazine synthase; DMRL synthase family
SPBC359.02	putative alanine racemase
SPCC18B5.02C	cinnamoyl-coa reductase pseudogene
trr1/caf4	thioredoxin reductase
SPCC576.02	putative hydantoin racemase
SPAC513.06C	probable dimeric dihydrodiol dehydrogenase
SPCC24B10.20	hypothetical short chain dehydrogenase
meu8	putative betaine aldehyde dehydrogenase; meiotic expression up-regulated
SPBC16A3.17C	MFS efflux transporter of unknown specificity
SPCC1450.13C	riboflavin synthase alpha chain
SPBC1604.01	conserved hypothetical protein
SPAC1F7.12	oxidoreductase similar to pyridoxal reductase
bfr1/hba2	MFS brefeldin A efflux transporter
SPAC22G7.08	putative serine/threonine protein kinase
SPAC23G3.03	putative peptide monooxygenase
SPCC1281.07C	protein with glutathione-S-transferase domain
SPAC1B3.15C	MFS transporter of unknown specificity
obr1	brefeldin a resistance protein
SPBC1652.01	may bind Pst1 histone deacetylase B; by similarity to <i>S. cerevisiae</i> SIN complex protein (transcriptional regulator of RNA polymerase II)
SPBC17D11.03C	hypothetical protein; similar to <i>S. cerevisiae</i> YJR111C
SPAPB8E5.04C	putative phosphatidylglycerol/phosphatidylinositol transfer protein; similar to <i>S. cerevisiae</i> YDL046W- unknown function
suc22	ribonucleoside-diphosphate reductase small chain; similar to <i>S. cerevisiae</i> RNR2
SPAC29B12.14C	NCS1 uracil transporter
SPCC1223.09	uricase
sec7b	putative golgi secretory protein; contains Sec7 domain; putative guanine nucleotide exchange factor; similar to <i>S. cerevisiae</i> Sec7p -component of non-clathrin vesicle coat required for protein trafficking within the Golgi
SPAC1B3.06C	methyltransferase- UbiE family
SPAC3C7.02C	hypothetical protein; similar to <i>S. cerevisiae</i> YPL004C
rec6	meiotic recombination protein rec6
SPAC6G10.03C	hypothetical protein; similar to <i>S. cerevisiae</i> YGR110W- which is induced during aerobic growth; contained Pfam abhydrolase motif, alpha/beta hydroalse fold
SPACUNK4.10	putative 2-hydroxyacid dehydrogenase
SPAC222.08C	putative pyridoxine (vitamin B6) biosynthetic enzyme; similar to glutamine aminotransferases by similarity to yeast sno1,2 and 3
SPAC2E1P3.04	peroxisomal copper amine oxidase
SPAC21E11.04	putative transcriptional regulatory protein
SPCC663.07C	short chain dehydrogenase pseudogene
SPAC9.10	APC amino acid transporter
SPBC947.06C	MFS multidrug efflux transporter

SPBC1271.05C	Zinc finger zf-AN1 protein
SPBC725.01	aspartate aminotransferase, mitochondrial
SPBC409.12C	hypothetical protein; sequence orphan
SPAC23G3.02C	putative peptide synthetase; with 3 phosphopantetheine attachment sites
SPAC1F3.09	hypothetical protein; similar to <i>S. cerevisiae</i> YGR093W
SPBC29A3.01	putative P-type copper ATPase
SPBC359.05	ABC multidrug or ion efflux transporter
pyp3	protein-tyrosine phosphatase; regulates mitotic cyclin dependent kinase cdc2p
SPBC3H7.09	conserved hypothetical protein; zf-DHHC
lys3	saccharopine dehydrogenase
SPAC2E12.03C	hypothetical protein; similar to <i>S. cerevisiae</i> YDR090C; contains Pfam-B_30810; predicted N-terminal signal sequence; contains 7 predicted transmembrane helices
SPBC887.15C	integral membrane protein, putative Hydroxylase involved in sphingolipid metabolism by similarity to yeast sur2
SPCC4F11.04C	putative transferase; possibly involved in the production of sphingolipids
SPAC869.02C	probable flavohemoprotein
SPAC56E4.03	putative aminotransferase
SPBC19C2.04C	putative ubiquitin carboxyl-terminal hydrolase

#### **CESR genes that are super-induced in response to H<sub>2</sub>O<sub>2</sub>**

SPAC23D3.05C	alcohol dehydrogenase pseudogene
SPBC1773.06C	alcohol dehydrogenase
SPAC5H10.02C	hypothetical protein; similar to <i>S. cerevisiae</i> YPL280W
SPAC15E1.02C	hypothetical protein; sequence orphan; contains 3 predicted transmembrane helices
SPBC215.11C	putative oxidoreductase; aldo-keto family
SPAC139.05	probable succinate semialdehyde dehydrogenase
SPBC2A9.02	putative dyhydroflavanol-4-reductase
SPAC23C11.06C	hypothetical protein; similar to <i>S. cerevisiae</i> YNL115C; contains 5 predicted transmembrane helices
SPCC1393.12	hypothetical protein; sequence orphan
SPAC19G12.09	putative aldose reductase
SPAC4H3.03C	putative family 15 glycosyl hydrolase
isp6	sexual differentiation process protein; putative subtilase-type proteinase