Expression Analysis: Pivot Tab

	1511 total	1511 total	1511 total	1511 total	1511 total	1511 total	1511 total
Descriptions	Avg Diff	Abs Call	Diff Call	Avg Diff Change	B=A	Fold Change	Sort Score
AFFX-MurIL2_at	-295.4	A					
M16762 Mouse interleukin 2 (IL-2) gene, exon 4							
AFFX-MurIL10_at	148.3	A					
M37897 Mouse interleukin 10 mRNA, complete cds							
AFFX-MurIL4_at	-12.5	A					
M25892 Mus musculus interleukin 4 (Il-4) mRNA, complete cds							
AFFX-MurFAS_at	107.7	A					
M83649 Mus musculus Fas antigen mRNA, complete cds							
AFFX-BioB-5_at	2584.1	P					
J04423 E coli bioB gene biotin synthetase (-5, -M, -3 represent transcript regions 5 prime, Middle, and 3 prime respectively)							
AFFX-BioB-M_at	3327.2	P					
J04423 E coli bioB gene biotin synthetase (-5, -M, -3 represent transcript regions 5 prime, Middle, and 3 prime respectively)							
AFFX-BioB-3_at	3669.1	P					
J04423 E coli bioB gene biotin synthetase (-5, -M, -3 represent transcript regions 5 prime, Middle, and 3 prime respectively)							
AFFX-BioC-5_at	7387.3	P					
J04423 E coli bioC protein (-5 and -3 represent transcript regions 5 prime and 3 prime respectively)							
AFFX-BioC-3_at	7087.4	P					
J04423 E coli bioC protein (-5 and -3 represent transcript regions 5 prime and 3 prime respectively)							
AFFX-BioDn-5_at	2580.8	P					
J04423 E coli bioD gene dethiobiotin synthetase (-5 and -3 represent transcript regions 5 prime and 3 prime respectively)							
AFFX-BioDn-3_at	8164.5	P					
J04423 E coli bioD gene dethiobiotin synthetase (-5 and -3 represent transcript regions 5 prime and 3 prime respectively)							
AFFX-CreX-5_at	4327.1	P					
X03453 Bacteriophage P1 cre recombinase protein (-5 and -3 represent transcript regions 5 prime and 3 prime respectively)							
AFFX-CreX-3_at	6407.7	P					
X03453 Bacteriophage P1 cre recombinase protein (-5 and -3 represent transcript regions 5 prime and 3 prime respectively)							
AFFX-BioB-5_st	-47.8	A					
J04423 E coli bioB gene biotin synthetase (-5, -M, -3 represent transcript regions 5 prime, Middle, and 3 prime respectively)							
AFFX-BioB-M_st	-728.7	A					
J04423 E coli bioB gene biotin synthetase (-5, -M, -3 represent transcript regions 5 prime, Middle, and 3 prime respectively)							
AFFX-BioB-3_st	-524.8	A					
J04423 E coli bioB gene biotin synthetase (-5, -M, -3 represent transcript regions 5 prime, Middle, and 3 prime respectively)							
AFFX-BioC-5_st	-956.2	A					
J04423 E coli bioC protein (-5 and -3 represent transcript regions 5 prime and 3 prime respectively)							
AFFX-BioC-3_st	171.7	A					
J04423 E coli bioC protein (-5 and -3 represent transcript regions 5 prime and 3 prime respectively)							
AFFX-BioDn-5_st	-135.0	A					
J04423 E coli bioD gene dethiobiotin synthetase (-5 and -3 represent transcript regions 5 prime and 3 prime respectively)							
AFFX-BioDn-3_st	454.7	A					

J04423 E coli bioD gene dethiobiotin synthetase (-5 and -3 represent transcript regions 5 prime and 3 prime respectively)
AFFX-CreX-5_st 164.5 A
X03453 Bacteriophage P1 cre recombinase protein (-5 and -3 represent transcript regions 5 prime and 3 prime respectively)
AFFX-CreX-3_st -656.0 A
X03453 Bacteriophage P1 cre recombinase protein (-5 and -3 represent transcript regions 5 prime and 3 prime respectively)
AFFX-DapX-5_at 153.4 A
L38424 B subtilis dapB, jojF, jojG genes corresponding to nucleotides 1358-3197 of L38424 (-5, -M, -3 represent transcript regions 5 prime, Middle, and 3 prime respectively)
AFFX-DapX-M_at 394.9 A
L38424 B subtilis dapB, jojF, jojG genes corresponding to nucleotides 1358-3197 of L38424 (-5, -M, -3 represent transcript regions 5 prime, Middle, and 3 prime respectively)
AFFX-DapX-3_at -244.3 A
L38424 B subtilis dapB, jojF, jojG genes corresponding to nucleotides 1358-3197 of L38424 (-5, -M, -3 represent transcript regions 5 prime, Middle, and 3 prime respectively)
AFFX-LysX-5_at -56.5 A
X17013 B subtilis lys gene for diaminopimelate decarboxylase corresponding to nucleotides 350-1345 of X17013 (-5, -M, -3 represent transcript regions 5 prime, Middle, and 3 prime respectively)
AFFX-LysX-M_at -463.5 A
X17013 B subtilis lys gene for diaminopimelate decarboxylase corresponding to nucleotides 350-1345 of X17013 (-5, -M, -3 represent transcript regions 5 prime, Middle, and 3 prime respectively)
AFFX-LysX-3_at 574.4 A
X17013 B subtilis lys gene for diaminopimelate decarboxylase corresponding to nucleotides 350-1345 of X17013 (-5, -M, -3 represent transcript regions 5 prime, Middle, and 3 prime respectively)
AFFX-PheX-5_at -269.5 A
M24537B subtilis pheB, pheA genes corresponding to nucleotides 2017-3334 of M24537 (-5, -M, -3 represent transcript regions 5 prime, Middle, and 3 prime respectively)
AFFX-PheX-M_at -298.0 A
M24537B subtilis pheB, pheA genes corresponding to nucleotides 2017-3334 of M24537 (-5, -M, -3 represent transcript regions 5 prime, Middle, and 3 prime respectively)
AFFX-PheX-3_at 285.1 A
M24537B subtilis pheB, pheA genes corresponding to nucleotides 2017-3334 of M24537 (-5, -M, -3 represent transcript regions 5 prime, Middle, and 3 prime respectively)
AFFX-ThrX-5_at 98.1 A
X04603 B subtilis thrC, thrB genes corresponding to nucleotides 248-2229 of X04603 (-5, -M, -3 represent transcript regions 5 prime, Middle, and 3 prime respectively)
AFFX-ThrX-M_at 220.3 A
X04603 B subtilis thrC, thrB genes corresponding to nucleotides 248-2229 of X04603 (-5, -M, -3 represent transcript regions 5 prime, Middle, and 3 prime respectively)
AFFX-ThrX-3_at 108.1 A
X04603 B subtilis thrC, thrB genes corresponding to nucleotides 248-2229 of X04603 (-5, -M, -3 represent transcript regions 5 prime, Middle, and 3 prime respectively)
AFFX-TrpnX-5_at -19.2 A
K01391 B subtilis TrpE protein, TrpD protein, TrpC protein corresponding to nucleotides 1883-4400 of K01391 (-5, -M, -3 represent transcript regions 5 prime, Middle, and 3 prime respectively)
AFFX-TrpnX-M_at -22.7 A
K01391 B subtilis TrpE protein, TrpD protein, TrpC protein corresponding to nucleotides 1883-4400 of K01391 (-5, -M, -3 represent transcript regions 5 prime, Middle, and 3 prime respectively)
AFFX-TrpnX-3_at 30.6 A
K01391 B subtilis TrpE protein, TrpD protein, TrpC protein corresponding to nucleotides 1883-4400 of K01391 (-5, -M, -3 represent transcript regions 5 prime, Middle, and 3 prime respectively)
AFFX-YFL039C5_at 12324.0 P
Saccharomyces cerevisiae /REF=V01288 /DEF=SGD:YFL039C Yeast S. cerevisiae gene for actin /LEN=1118 (5, M, 3 represent transcript regions 5 prime, Middle, and 3 prime respectively)

AFFX-YFL039CM_at 10299.6 P

Saccharomyces cerevisiae /REF=V01288 /DEF=SGD:YFL039C Yeast S. cerevisiae gene for actin /LEN=1118 (5, M, 3 represent transcript regions 5 prime, Middle, and 3 prime respectively)

AFFX-YFL039C3_at 9754.5 P

Saccharomyces cerevisiae /REF=V01288 /DEF=SGD:YFL039C Yeast S. cerevisiae gene for actin /LEN=1118 (5, M, 3 represent transcript regions 5 prime, Middle, and 3 prime respectively)

AFFX-YER148w5_at 5950.3 P

Saccharomyces cerevisiae /REF=X16860 /DEF=SGD:YER148W Yeast S. cervisiae TATA-binding protein (tfIId) /LEN=723 (5, M, 3 represent transcript regions 5 prime, Middle, and 3 prime respectively)

AFFX-YER148wM_at 7368.0 P

Saccharomyces cerevisiae /REF=X16860 /DEF=SGD:YER148W Yeast S. cervisiae TATA-binding protein (tfIId) /LEN=723 (5, M, 3 represent transcript regions 5 prime, Middle, and 3 prime respectively)

AFFX-YER148w3_at 10381.4 P

Saccharomyces cerevisiae /REF=X16860 /DEF=SGD:YER148W Yeast S. cervisiae TATA-binding protein (tfIId) /LEN=723 (5, M, 3 represent transcript regions 5 prime, Middle, and 3 prime respectively)

AFFX-YER022w5_at 617.1 P

Saccharomyces cerevisiae /REF=L12026 /DEF=SGD:YER022W Yeast S. cerevisiae subunit of RNA polymerase II holoenzyme/mediator complex /LEN=2064 (5, M, 3 represent transcript regions 5 prime, Middle and 3 prime respectively)

AFFX-YER022wM_at 1337.9 P

Saccharomyces cerevisiae /REF=L12026 /DEF=SGD:YER022W Yeast S. cerevisiae subunit of RNA polymerase II holoenzyme/mediator complex /LEN=2064 (5, M, 3 represent transcript regions 5 prime, Middle and 3 prime respectively)

AFFX-YER022w3_at 1249.5 P

Saccharomyces cerevisiae /REF=L12026 /DEF=SGD:YER022W Yeast S. cerevisiae subunit of RNA polymerase II holoenzyme/mediator complex /LEN=2064 (5, M, 3 represent transcript regions 5 prime, Middle and 3 prime respectively)

AFFX-18srRnaa_at 3132.9 P

Saccharomyces cerevisiae /REF=Z75578 /DEF=SGD:YLR154C Yeast S. cerevisiae 18S ribosomal RNA corresponds to 1-1799 in Z75578 /LEN=1799 (regions a-e represent transcript regions 5 prime to 3 prime respectively)

AFFX-18srRnab_at 3877.0 P

Saccharomyces cerevisiae /REF=Z75578 /DEF=SGD:YLR154C Yeast S. cerevisiae 18S ribosomal RNA corresponds to 1-1799 in Z75578 /LEN=1799 (regions a-e represent transcript regions 5 prime to 3 prime respectively)

AFFX-18srRnac_at 1342.2 P

Saccharomyces cerevisiae /REF=Z75578 /DEF=SGD:YLR154C Yeast S. cerevisiae 18S ribosomal RNA corresponds to 1-1799 in Z75578 /LEN=1799 (regions a-e represent transcript regions 5 prime to 3 prime respectively)

AFFX-18srRnad_at 2512.8 P

Saccharomyces cerevisiae /REF=Z75578 /DEF=SGD:YLR154C Yeast S. cerevisiae 18S ribosomal RNA corresponds to 1-1799 in Z75578 /LEN=1799 (regions a-e represent transcript regions 5 prime to 3 prime respectively)

AFFX-18srRnae_at 1426.5 P

Saccharomyces cerevisiae /REF=Z75578 /DEF=SGD:YLR154C Yeast S. cerevisiae 18S ribosomal RNA corresponds to 1-1799 in Z75578 /LEN=1799 (regions a-e represent transcript regions 5 prime to 3 prime respectively)

AFFX-25srRnaa_at 5920.1 P

Saccharomyces cerevisiae /REF=J01355 /DEF=Z73326 SGD:YLR154C Yeast S.cerevisiae 25S ribosomal RNA corresponds to complement of 4212-7605 in Z73326 /LEN=3394 (regions a-e represent transcript regions 5 prime to 3 prime respectively)

AFFX-25srRnab_at 2273.4 P

Saccharomyces cerevisiae /REF=J01355 /DEF=Z73326 SGD:YLR154C Yeast S.cerevisiae 25S ribosomal RNA corresponds to complement of 4212-7605 in Z73326 /LEN=3394 (regions a-e represent transcript regions 5 prime to 3 prime respectively)

AFFX-25srRnac_at 751.4 P

Saccharomyces cerevisiae /REF=J01355 /DEF=Z73326 SGD:YLR154C Yeast S.cerevisiae 25S ribosomal RNA corresponds to complement of 4212-7605 in Z73326 /LEN=3394 (regions a-e represent transcript regions 5 prime to 3 prime respectively)
AFFX-25srRnad_at 1355.5 P
Saccharomyces cerevisiae /REF=J01355 /DEF=Z73326 SGD:YLR154C Yeast S.cerevisiae 25S ribosomal RNA corresponds to complement of 4212-7605 in Z73326 /LEN=3394 (regions a-e represent transcript regions 5 prime to 3 prime respectively)
AFFX-25srRnae_at 10901.3 P
Saccharomyces cerevisiae /REF=J01355 /DEF=Z73326 SGD:YLR154C Yeast S.cerevisiae 25S ribosomal RNA corresponds to complement of 4212-7605 in Z73326 /LEN=3394 (regions a-e represent transcript regions 5 prime to 3 prime respectively)
AFFX-YEL002c/WBP1_at 8874.2 P
X61388 SGD: YEL002C Yeast S.cerevisiae WBP1 Oligosaccharyltransferase beta subunit
AFFX-YEL018w/_at 2463.7 P
U18530 SGD:YEL018W Yeast S. cerevisiae Protein of unknown function
AFFX-YEL024w/RIP1_at 7323.6 P
M23316 SGD:YEL024C Yeast S.cerevisiae RIP1 Rieske iron-sulfur protein of the mitochondrial cytochrome bc1 complex .
AFFX-YEL021w/URA3_at 970.0 P
K02207 SGD:YEL021W Yeast S.cerevisiae URA3 gene coding for OMP decarboxylase
11378_at 1018.0 A
Aldehyde dehydrogenase 1, mitochondrial
11379_at 758.1 P
Suppressor of Sulfoxyde Ethionine resistance
11380_at 509.6 P
hypothetical protein
11381_at -33.0 A
putative pseudogene
11382_at 170.8 A
putative pseudogene
11383_at -17.7 A
putative pseudogene
11384_at -135.9 A
hypothetical protein
11385_s_at 930.3 A
putative Flo1p homolog
11386_at 374.5 A
NADP-linked glutamate dehydrogenase
11387_at 432.4 A
similarity to alcohol/sorbitol dehydrogenase
11388_at 4964.4 P
similarity to alcohol/sorbitol dehydrogenase
11389_at 3913.6 P
ExtraCellular Mutant
11390_at 1362.7 P
Calnexin and calreticulin homolog
11391_at 462.0 A
questionable ORF
11392_at 728.2 P
similarity to hypothetical protein YOR371c
11393_at 3144.2 P
hypothetical protein
11356_at 2116.7 P
inducible acetyl-coenzyme A synthetase
11357_at 6197.0 P
strong similarity to hypothetical proteins YOR365c,YGL139w,YPL221w

11358_at 1467.7 P
peroxisome proliferating transcription factor
11359_at 8563.2 P
weak similarity to Legionella small basic protein sbpA
11360_at 462.5 P
weak similarity to GTP-binding proteins
11361_at 424.9 P
Spc72p interacts with Stu2p in the two-hybrid assay\; Spc72p localizes to the spindle pole bodies. Molecular weight is 72 kD
11362_at 2124.7 P
hypothetical protein
11363_at 472.8 P
hypothetical protein
11364_at 9182.0 P
H-protein subunit of the glycine cleavage system
11365_at 2508.9 P
pre-tRNA processing
11366_at -134.4 A
questionable ORF
11367_at 10382.4 P
Function unknown now
11368_at 1938.4 P
Guanine nucleotide exchange factor (a.k.a. GDP-release factor) for cdc42
11369_at 4877.3 P
G(sub)1 cyclin
11370_at 8620.5 P
cytochrome c heme lyase (CCHL)
11371_at 7108.5 P
Pyruvate kinase
11372_at 312.2 P
strong similarity to GTP-binding proteins
11373_at 8923.4 P
Function unknown now
11374_at 10355.6 P
97 kDa protein
11375_at 82.0 A
questionable ORF
11376_at 446.1 P
hypothetical protein
11377_at 957.6 P
Function unknown now
11333_at 4064.8 P
An integral subunit of RNase P and apparent subunit of RNase MRP
11334_at 199.4 A
Function unknown now
11335_at 1240.5 A
FUN21
11336_at 3223.8 P
homolog of Snc2p, vesicle-associated membrane protein (synaptobrevin) homolog, forms a complex with Snc2p and Sec9p
11337_at 5992.7 P
homolog of Snc2p, vesicle-associated membrane protein (synaptobrevin) homolog, forms a complex with Snc2p and Sec9p
11338_at 4469.0 P
myosin
11339_at 146.5 A

similarity to hypothetical protein YOR324c
11340_at 675.6 P
hypothetical protein
11341_at 1362.1 P
Membrane-spanning Ca-ATPase (P-type),member of the cation transport (E1-E2) ATPases
11342_at 2565.5 P
putative nuclear protein
11343_at 763.1 P
putative GTP-exchange protein
11344_at 11107.1 P
dolichyl phosphate-D-mannose:protein O-D-mannosyltransferase
11345_at 4379.3 P
predicted membrane protein
11346_at 7023.9 P
95 kDa containg leucine rich tandem repeats
11347_at 2151.9 P
Protein with similarity to human RCC1 protein
11348_at 2195.0 P
Shows homology to SNF2 transcriptional regulator
11349_at 539.7 P 3
transmembrane domains
11350_at 1931.2 P
Serine\/threonine kinase
11351_at 8357.8 P
protein phosphatase 2A regulatory subunit A
11352_at 1006.9 P
DNA glycosylase
11353_at 2710.4 P
protein of unknown function
11354_at 4680.5 P
regulation of phospholipid metabolism
11355_at 9991.1 P
cystathionine gamma-lyase
11310_at 619.3 P
possible mitochondrial transit peptide
11311_at 633.3 P
Mitochondrial outer membrane protein involved in mitochondrial morphology and inheritance
11312_at 2574.5 P
sporulation protein
11313_at 2170.0 P
protein of unknown function
11314_at 6827.4 P
p24 protein involved in membrane trafficking
11315_i_at 5408.4 P
Heat shock protein of HSP70 family, cytoplasmic
11316_r_at 0.0 A
Heat shock protein of HSP70 family, cytoplasmic
11317_s_at 15729.1 P
Heat shock protein of HSP70 family, cytoplasmic
11318_at 476.9 P
strong similarity to A.klebsiana glutamate dehydrogenase
11319_at 9022.0 P
Translation elongation factor EF-1beta, GDP\/GTP exchange factor for Tef1p\/Tef2p
11320_at 8993.6 P
Translation elongation factor EF-1beta, GDP\/GTP exchange factor for Tef1p\/Tef2p
11321_at -498.9 A

Vps8p is a membrane-associated hydrophilic protein which contains a C-terminal cysteine-rich region that conforms to the H2 variant of the RING finger Zn2+ binding motif.
11322_at 2438.2 P
transcription factor tau (TFIIIC) subunit 138
11323_at 607.7 P
transcription factor tau (TFIIIC) subunit 138
11324_at 5267.9 P
protein of unknown function
11325_at 11304.9 P
p24 protein involved in membrane trafficking
11326_at 2957.3 P
beta transducin domain
11327_at 8318.0 P
69 kDa subunit of the heterotrimeric RPA (RF-A) single-stranded DNA binding protein, binds URS1 and CAR1
11328_at 2261.9 P
34kDa subunit of the tetrameric tRNA splicing endonuclease
11329_at 4656.9 P
maximal growth
11330_at 7136.7 P
phosphoribosyl amino imidazolesuccinocarbozamide synthetase
11331_at 587.8 P
protein kinase
11332_at 854.6 P
protein kinase domain
11287_f_at 564.2 P
strong similarity to members of the srp1p/Tip1p family
11288_at 299.7 P
membrane protein
11289_at 866.9 P
membrane protein
11290_at 2278.9 P
membrane protein
11291_at 172.1 P
membrane protein
11292_at -120.5 A
hypothetical protein
11293_at 880.7 P
membrane protein
11294_g_at 2366.7 P
membrane protein
11295_r_at 1276.4 P
membrane protein
11296_s_at 902.8 P
membrane protein
11297_at 2138.6 P
Outer carnitine acetyltransferase, mitochondrial
11298_at 2477.5 P
ankyrin repeat
11299_at 1583.8 P
Shows homology to the human oxysterol binding protein (OSBP)
11300_at -22.9 A
predicted nuclear targeting signal
11301_i_at -542.4 A
FLO1 putative cell wall glycoprotein
11302_at 364.5 P

predicted membrane protein
11303_s_at 359.7 P
strong similarity to hypothetical protein YHR212c
11304_at 385.2 A
putative pseudogene
11305_s_at 144.3 A
putative pseudogene
11306_at 554.7 P
Potential membrane protein
11307_s_at 2020.6 P
identical to YHR214w hypothetical protein, similarity to Sta1p
11308_s_at 240.6 A
Potential membrane protein
11309_at 54.5 A
Potential membrane protein
11261_at -1428.5 A
potential mitochondrial transit peptide
11262_s_at 14489.5 P
Acid phosphatase, secreted
11263_f_at 7054.5 P
strong similarity to IMP dehydrogenases
11264_f_at 8109.6 P
strong similarity to IMP dehydrogenases
11265_i_at 694.8 P
hypothetical protein
11266_f_at 3869.8 P
hypothetical protein
11267_at 148.6 P
identified by SAGE
11268_at -8.7 A
hypothetical protein
11269_at 144.3 A
non-annotated SAGE orf Found forward in NC_001133 between 101217 and 101354 with 100% identity. See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251
11270_at -12.4 A
non-annotated SAGE orf Found forward in NC_001133 between 23764 and 23898 with 100% identity. See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251
11271_at 138.3 A
non-annotated SAGE orf Found reverse in NC_001133 between 31215 and 31373 with 100% identity. See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251
11272_at 434.8 P
non-annotated SAGE orf Found reverse in NC_001133 between 222994 and 223152 with 100% identity. See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251
11273_at 432.0 P
non-annotated SAGE orf Found forward in NC_001133 between 73444 and 73614 with 100% identity. See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251
11274_at 715.7 P
non-annotated SAGE orf Found reverse in NC_001133 between 139298 and 139468 with 100% identity. See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251
11275_at 946.9 P
non-annotated SAGE orf Found reverse in NC_001133 between 166468 and 166617 with 100% identity. See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251
11276_at 167.3 A
non-annotated SAGE orf Found reverse in NC_001133 between 3170 and 3394 with 100% identity. See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251
11277_at -6.9 A

non-annotated SAGE orf Found forward in NC_001133 between 19729 and 19968 with 100% identity.
See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251
11278_f_at 1065.3 P
non-annotated SAGE orf Found reverse in NC_001133 between 19977 and 20123 with 100% identity.
See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251
11279_s_at 496.7 P
non-annotated SAGE orf Found reverse in NC_001133 between 22397 and 22687 with 100% identity.
See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251
11280_at 95.7 A
non-annotated SAGE orf Found reverse in NC_001133 between 29012 and 29179 with 100% identity.
See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251
11281_at 200.2 A
non-annotated SAGE orf Found forward in NC_001133 between 29954 and 30166 with 100% identity.
See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251
11282_i_at -46.1 A
non-annotated SAGE orf Found reverse in NC_001133 between 182850 and 183005 with 100% identity.
See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251
11283_r_at 241.1 P
non-annotated SAGE orf Found reverse in NC_001133 between 182850 and 183005 with 100% identity.
See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251
11284_f_at 6673.9 P
non-annotated SAGE orf Found reverse in NC_001133 between 182850 and 183005 with 100% identity.
See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251
11285_at -9.9 A
non-annotated SAGE orf Found forward in NC_001133 between 198205 and 198339 with 100% identity.
See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251
11286_at 33.0 A
non-annotated SAGE orf Found reverse in NC_001133 between 199737 and 199886 with 100% identity.
See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251
11238_at 76.9 A
non-annotated SAGE orf Found forward in NC_001133 between 200934 and 201074 with 100% identity.
See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251
11239_at -370.0 A
non-annotated SAGE orf Found reverse in NC_001133 between 203077 and 203223 with 100% identity.
See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251
11240_s_at 103.1 P
non-annotated SAGE orf Found reverse in NC_001133 between 219555 and 219719 with 100% identity.
See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251
11241_at 379.5 P
non-annotated SAGE orf Found reverse in NC_001133 between 138484 and 138627 with 100% identity.
See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251
11242_f_at 30.6 A
non-annotated SAGE orf Found forward in NC_001133 between 223093 and 223230 with 100% identity.
See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251
11243_s_at 432.9 P
non-annotated SAGE orf Found forward in NC_001133 between 223253 and 223423 with 100% identity.
See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251
11244_s_at 366.6 P
non-annotated SAGE orf Found forward in NC_001133 between 223333 and 223476 with 100% identity.
See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251
11245_i_at -223.0 A
Centromere
11246_r_at -51.3 A
Centromere
11247_s_at 9611.9 P
strong similarity to members of the Sir1p/Tip1p family

11248_s_at 990.0 P
strong similarity to members of the Sir1p/Tip1p family
11249_f_at 2921.1 P
strong similarity to members of the Srp1p/Tip1p family
11250_s_at 1160.5 P
strong similarity to Pep1p
11251_s_at 347.5 P
homology to maltase(alpha-D-glucosidase)
11252_s_at -178.9 A
questionable ORF
11253_s_at 18.7 A
High-affinity hexose transporter
11254_at 241.2 P
strong similarity to E.coli galactoside O-acetyltransferase
11255_at 168.2 A
hypothetical protein
11256_at -3.2 A
strong similarity to Mal62p
11257_at 36.2 A
hypothetical protein
11258_at 189.6 A
High-affinity hexose transporter
11259_at 1302.2 P
similarity to Methanobacterium aryldialkylphosphatase related protein
11260_at 3019.9 P
strong similarity to S.pombe isp4 protein
11215_at 123.3 M
questionable ORF
11216_at 5045.9 P
CH3HC4 zinc-binding integral peroxisomal membrane protein
11217_at 1270.8 P
Protein required for COB mRNA stability or 5 processing
11218_at 3031.3 P
mitochondrial nuclease
11219_at 1405.4 P
weak similarity to rat omega-conotoxin-sensitive calcium channel alpha-1 subunit rbB-I
11220_at 736.2 P
similarity to YIL130p and Put3p
11221_at 6475.4 P
involved in secretion of proteins that lack classical secretory signal sequences
11222_at 2105.2 P
weak similarity to Tor2p
11223_at 898.8 P
RNA splicing factor
11224_at 92.1 A
questionable ORF
11225_at 631.6 P
ExtraCellular Mutant
11226_at 9197.4 P
strong similarity to aconitate hydratase
11227_at 1451.2 P
hypothetical protein
11228_at 9629.3 P
strong similarity to Pho87p
11229_at 1335.1 P
ubiquitin carboxyl-terminal hydrolase

11230_at 12584.7 P
Elongation enzyme 1, required for the elongation of the saturated fatty acid tetradecanoic acid (14:0) to that of hexadecanoic acid (16:0)
11231_at -57.4 A
questionable ORF
11232_at 1416.2 P
Protein involved in initiation of DNA replication
11233_at 4504.4 P
similarity to Sly41p
11234_at 3782.6 P
hypothetical protein
11235_at 8195.7 P
Ribosomal protein S14B (rp59B)
11236_at 4157.1 P
Ribosomal protein S22A (S24A) (rp50) (YS22)
11237_at 11305.2 P
Ribosomal protein L39 (L46) (YL40)
11192_at 743.5 P
questionable ORF
11193_at 4465.7 P
protein kinase homolog
11194_at 1953.2 P
putative mannosyltransferase
11195_at 198.8 P
hypothetical protein
11196_at 3157.5 P
hypothetical protein
11197_at 6022.0 P
A new gene encoding a protein that is related to Mnn10p, and that is in a complex containing other MNN gene products.
11198_at -81.3 A
questionable ORF
11199_at 2078.4 P
similarity to hypothetical protein YJR030c
11200_at 1275.0 P
essential for assembly of a functional F1-ATPase
11201_at 1202.5 P
Putative homolog of subunit 1 of bovine prefoldin, a chaperone comprised of six subunits
11202_at 7402.7 P
hypothetical protein
11203_i_at 13956.6 P
Ribosomal protein L17B (L20B) (YL17)
11204_s_at 8606.3 P
Ribosomal protein L17B (L20B) (YL17)
11205_i_at 7567.7 P
Ribosomal protein L17B (L20B) (YL17)
11206_f_at 13440.4 P
Ribosomal protein L17B (L20B) (YL17)
11207_at 666.0 P
transcription factor
11208_at 505.4 A
questionable ORF
11209_at 8640.4 P
Cell wall beta-glucan assembly
11210_at 10067.0 P
subunit 3 of replication factor-A

11211_at 3712.5 P
carboxypeptidase yscS
11212_at 6605.3 P
similarity to YBR162c
11213_at -159.9 A
An a-specific gene that is induced to a higher expression level by alpha factor
11214_at 36.4 A
questionable ORF
11170_at 611.2 A
transcription factor containing a SET domain
11171_at 8816.8 P
Farnesyl diphosphate synthetase (FPP synthetase)
11172_at 7736.8 P
Ubiquinol cytochrome-c reductase subunit 8 (11 kDa protein)
11173_at 2980.4 P
Protein kinase homolog, mutant is salt and pH sensitive
11174_at 2642.7 P
putative catalytic subunit of cAMP-dependent protein kinase
11175_at 178.7 P
hypothetical protein
11176_at 492.0 A
weak similarity to dnaJ proteins
11177_at 193.0 A
hypothetical protein
11178_at 653.6 P
member of the Pir1p/Hsp150p/Pir3p family
11179_at 8421.6 P
Heat shock protein, secretory glycoprotein
11180_at 8426.0 P
Protein with homology to Hsp150p and Pir1p, Pir2p, and Pir3p
11181_at 9180.0 P
Factor arrest protein
11182_at 1384.2 P
sensitive to sulfonylurea herbicides on complex media (YPD)
11183_at 1248.5 P
Fructose-2,6-bisphosphatase
11184_at 1582.8 P
Protein involved in vacuolar sorting
11185_at 136.4 P
L-myo-inositol-1-phosphate synthase
11186_at 1654.4 P
questionable ORF
11187_at 9700.8 P
similarity to hypothetical protein YDL123w
11188_at 711.8 P
questionable ORF
11189_at 681.7 P
similarity to hypothetical protein YDR131c
11190_at 8587.2 P
RNA polymerase I subunit, not shared (A34.5)
11191_at 938.7 P
weak similarity to C.elegans hypothetical protein C43G2.4
11147_at 961.4 P
IME2-Dependent Signalling
11148_at 4753.2 P
weak similarity to T.pacificus retinal-binding protein

11149_at	143.8	A	hypothetical protein
11150_at	9976.8	P	16.5 kDa inner membrane protein required for import of mitochondrial precursor proteins
11151_at	851.5	P	questionable ORF
11152_g_at	1953.8	P	questionable ORF
11153_at	1108.9	P	Serine-threonine protein kinase
11154_at	2292.2	P	fourth-largest subunit of RNA polymerase II
11155_at	2186.0	P	Probable glycosyltransferase of KRE2\/KTR1\/YUR1 family\; located in the Golgi
11156_s_at	11174.4	P	translation initiation factor eIF4A
11157_at	592.2	P	self-glucosylating initiator of glycogen synthesis\; similar to mammalian glycogenin
11158_i_at	4486.5	A	Ribosomal protein S21B (S26B) (YS25)
11159_s_at	10412.7	P	Ribosomal protein S21B (S26B) (YS25)
11160_at	260.1	P	questionable ORF
11161_at	5351.8	P	putative plasma membrane transporter capable of transporting sphingoid long chain bases into cells
11162_at	1495.6	P	mitochondrial carrier protein
11163_at	200.2	P	weak similarity to human phospholipase D
11164_at	1481.5	P	weak similarity to nonepidermal Xenopus keratin, type I
11165_at	10577.0	P	carbamoyl-phophate synthetase, aspartate transcarbamylase, and glutamine amidotransferase
11166_at	2045.9	P	180 kDa high affinity potassium transporter
11167_at	2400.1	P	MAP kinase kinase (MEK), may act as a scaffolding protein for Sho1p, Ste11p, and Hog1p
11168_at	375.0	P	negative transcriptional regulator
11169_at	1348.2	P	Nit2 nitrilase
11124_at	4053.2	P	translational repressor of GCN4
11125_at	3124.8	P	Like Sm-B protein\; contains the Sm consensus motifs and most closely resembles Sm-B (Fromont-Racine et al, 1997 Nature Genetics 16:277-282)
11126_at	6857.7	P	weak similarity to D.melanogaster troponin T and human nucleolin
11127_at	7670.5	P	weak similarity to dog-fish transition protein S2
11128_at	11315.5	P	D-ribulose-5-Phosphate 3-epimerase
11129_at	305.3	P	questionable ORF
11130_at	-221.2	A	

questionable ORF
11131_at 4606.3 P
hypothetical protein
11132_at 8498.1 P
Putative inorganic phosphate transporter
11133_at 2575.5 P
With NCA2, regulates proper expression of subunits 6 (Atp6p) and 8 (Atp8p) of the Fo-F1 ATP synthase
11134_at 4169.3 P
Anti-silencing protein that causes depression of silent loci when overexpressed
11135_at 1708.9 P
similarity to Met30p and N.crassa sulfur controller-2
11136_at 4092.6 P
Component of Chaperonin Containing T-complex subunit seven
11137_at 1241.6 P
GATA zinc finger protein 3 homologous to Dal80 in structure and function
11138_at 6253.8 P
weak similarity to ATPase Drs2p
11139_at 4008.7 P
strong similarity to hypothetical S. pombe protein
11140_at 279.1 P
similarity to hypothetical S. pombe protein
11141_at 443.7 P
Serine\/Threonine protein kinase, positively regulated by IME1
11142_at 24.0 A
similarity to hypothetical protein YKR029c
11143_at 995.4 P
weak similarity to C.elegans hypothetical protein F45G2.c
11144_at 486.4 P
putative regulatory protein
11145_at 2652.2 P
mitochondrial elongation factor G-like protein
11146_at 2250.9 P
gamma-glutamylcysteine synthetase
11102_at 3572.6 P
similarity to hypothetical C. elegans protein C56A3.8
11103_at 1463.4 P
Involved in chitin biosynthesis and\/or its regulation
11104_at 3157.6 P
SIT4 associated protein, MW of 185 kDa
11105_at 9114.5 P
similarity to hypothetical C. elegans protein T15B7.2
11106_at 4832.7 P
ribosomal protein YmL49, mitochondrial
11107_at 1432.6 P
putative 163 kDa protein kinase
11108_at 1772.9 P
similarity to E.hirae NaH-antiporter NapA
11109_at 1135.7 P
outward-rectifier potassium channel
11110_at 1591.9 P
DNA helicase
11111_at 4896.0 P
weak similarity to human G protein-coupled receptor
11112_at 1426.6 P
Part of the DNA polymerase II complex, acts in a checkpoiint pathway during S-phase
11113_at 127.2 A

shows homology to DNA binding domain of Gal4p, has a leucine zipper motif and acidic region\; lexA-Sip4p activates transcription
11114_at 1341.1 P
Ornithine carbamoyltransferase
11115_at 1062.6 P
tRNA ligase
11116_at 17.4 A
questionable ORF
11117_at 246.5 P
70 kD component of the Exocyst complex\; required for exocytosis
11118_at 1374.9 P
similarity to hypothetical protein YKR021w
11119_at 1078.8 P
similarity to hypothetical protein YKR019c
11120_at 1857.4 P
strong similarity to hypothetical protein YKR018c
11121_at 3982.9 P
54.8 kDa actin-related protein
11122_at 9733.9 P
May be required during cell division for faithful partitioning of the ER-nuclear envelope membranes, involved in control of mitotic chromsome transmission
11123_at 6021.2 P
Similar to plant PR-1 class of pathogen related proteins
11079_at 5316.5 P
Similar to plant PR-1 class of pathogen related proteins
11080_at 183.9 A
hypothetical protein
11081_at 6542.7 P
Establishes Silent omatin\; homolog of TOF2
11082_at 307.3 P
questionable ORF
11083_at 2210.7 P
required for structural maintenance of chromosomes
11084_at 2220.4 P
DnaJ-like protein of the endoplasmic reticulum membrane
11085_at 1700.4 P
hypothetical protein
11086_at 1275.7 P
Acetylglutamate Synthase
11087_at 572.4 P
similarity to AMP deaminases
11088_at 4677.5 P
similarity to C.elegans hypothetical protein
11089_at 4324.8 P
strong similarity to human esterase D
11090_at 1018.3 A
questionable ORF
11091_at 994.5 P
hypothetical protein
11092_at 5400.9 P
weak similarity to DNA-directed DNA polymerase II chain C
11093_at 116.2 A
hypothetical protein
11094_at 6301.0 P
Mitochondrial ribosomal protein MRPL8 (YmL8) (E. coli L17)
11095_at 2831.4 P

similarity to S.pombe SPAC13G6.3 protein
11096_at 797.2 P
82-kDa protein, with putative coiled-coil domain, has carboxy-terminal domain, containing heptad repeats, that binds Nsp1p\; nucleoporin
11097_at 2939.7 P
similarity to kynurenine aminotransferase and glutamine-phenylpyruvate transaminase
11098_at 612.6 P
Homolog of human CLN3
11099_at 220.5 A
strong similarity to hypothetical protein YBR270c
11100_at 192.5 P
probable serine\/threonine kinase
11101_at 1026.4 P
Metalloregulatory protein involved in zinc-responsive transcriptional regulation
11057_at 10050.6 P
similarity to R.fascians hypothetical protein 6
11058_at 3942.1 P
Translocase for the insertion of proteins into the mitochondrial inner membrane.
11059_at 1634.8 P
Vacuolar protein similar to mouse gene H<beta>58
11060_at 5961.0 P
Glyceraldehyde-3-phosphate dehydrogenase 1
11061_g_at 7194.3 P
Glyceraldehyde-3-phosphate dehydrogenase 1
11062_at 928.9 P
hypothetical protein
11063_at 4809.0 P
DEAD-box family helicase required for mRNA export from nucleus
11064_at 877.9 P
hypothetical protein
11065_at 3661.6 P
similarity to hypothetical protein YBR273c
11066_at 593.3 P
Regulator of Ty1 Transposition
11067_at 693.1 P
similarity to E.coli lipoate-protein ligase A
11068_at 171.5 A
strong similarity to succinate dehydrogenase flavoprotein
11069_at 699.2 P
GTPase-activating protein for Ypt6
11070_at -2683.9 A
similarity to hypothetical protein YKR015c
11071_at 7106.8 P
Putative microtubule-associated protein (MAP)
11072_at 7437.0 P
Nucleoskeletal protein found in nuclear pores and spindle pole body
11073_at 1676.3 P
similarity to human protein interacting with human nuclearpore protein Nup93
11074_at 7.4 A
strong similarity to hypothetical protein YJL037w
11075_at 1156.6 P
strong similarity to hypothetical protein YJL038c
11076_at 527.8 P
weak similarity to Mvp1p
11077_at 1758.0 P
weak similarity to P.gingivalis PgaA and B.japonicum nitrogen fixation protein

11078_at	10720.9	P	Homologue of mammalian BiP (GPR78) protein\; member of the HSP70 gene family
11034_at	5118.0	P	putative RNA helicase
11035_at	743.7	P	questionable ORF
11036_at	1219.7	P	Geranylgeranyltransferase Type II alpha subunit (PGGTase-II, alpha subunit)
11037_at	1522.8	P	spindle-assembly checkpoint protein
11038_at	2121.3	P	similarity to C.elegans hypothetical protein T05G5.8
11039_at	72.8	A	hypothetical protein
11040_at	1030.0	P	hypothetical protein
11041_at	10651.5	P	small subunit of ribonucleotide reductase
11042_at	795.9	P	member of yeast Pol I core factor (CF) also composed of Rrn11p, Rrn6p and TATA-binding protein
11043_at	893.0	P	similar to Aps1p and mammalian small subunit (sigma-2 adaptin) of plasma membrane-associated clathrin assembly complex (AP-2)
11044_at	320.4	P	Nuclear gene encoding mitochondrial protein
11045_at	-32.0	A	questionable ORF
11046_at	2469.4	P	weak similarity to S.pombe hypothetical protein SPAC23A1.16
11047_at	3960.1	P	similarity to P.falciparum glutamic acid-rich protein
11048_at	243.0	P	hypothetical protein
11049_g_at	628.6	P	hypothetical protein
11050_at	1982.4	P	questionable ORF
11051_at	802.2	P	hypothetical protein
11052_at	3285.9	P	weak similarity to hypothetical protein YNL278w and YLR187w
11053_at	173.2	P	questionable ORF
11054_at	6607.0	P	Cytoplasmic chaperonin subunit gamma
11055_at	809.0	P	Checkpoint protein required for cell cycle arrest in response to loss of microtubule function
11056_at	8931.3	P	weak similarity to regulatory protein PHO81
11010_at	5229.2	P	weak similarity to chicken hypothetical protein
11011_at	3166.6	P	weak similarity to C.elegans hypothetical protei ZK792.5
11012_at	1139.1	P	questionable ORF
11013_at	10980.1	P	

Component of Chaperonin Containing T-complex subunit eight
11014_at 68.2 A
hypothetical protein
11015_at 2919.4 P
cyclin-related subunit of the kinase complex that phosphorylates the RPO21 CTD (carboxy-terminal domain)\; also called CTDK-I beta subunit
11016_at 1665.8 P
adenylate cyclase
11017_at 2482.7 P
Multicopy suppressor of ypt6 null mutation
11018_at 1121.9 P
hypothetical protein
11019_at 12903.2 P
64-kDa, alpha subunit of oligosaccharyltransferase complex\; homologous to mammalian ribophorin I
11020_i_at 3252.4 P
Subunit of 20S proteasome
11021_f_at 4662.5 P
Subunit of 20S proteasome
11022_at 10417.2 P
Subunit of 20S proteasome
11023_at 8784.4 P
weak similarity to A.thaliana aminoacid permease AAP4
11024_at 4208.6 P
Protein component of the U3 small nucleolar ribonucleoprotein (snoRNP)
11025_at 1512.3 P
hypothetical protein
11026_at 10460.9 P
alpha-agglutinin
11027_at 1162.3 P
beta-adaptin, large subunit of the clathrin-associated protein complex
11028_at 1221.0 P
DNA-directed DNA polymerase delta, 55 KD subunit
11029_at 3836.3 P
Translation initiation factor eIF-2 alpha subunit
11030_at 206.1 A
similarity to S.pombe hypothetical protein
11031_s_at 14492.8 P
glyceraldehyde 3-phosphate dehydrogenase
11032_at 1303.2 P
ATP sulfurylase
11033_at 1689.4 P
Homologue of the SPC12 subunit of mammalian signal peptidase complex. Protein is important for efficient signal peptidase activity.
10988_at 350.6 P
hypothetical protein
10989_at 839.3 P
hypothetical protein
10990_at 2901.4 P
similarity to C.elegans B0491.1 protein
10991_at 5525.9 P
strong similarity to S.pombe hypothetical protein SPBC16C6.05
10992_at 2981.5 P
strong similarity to Sng1p
10993_at 11716.9 P
dihydroxyacid dehydratase
10994_at 10818.4 P

Peptidyl-prolyl cis\/trans isomerase (PPIase)
10995_at 1805.1 P
questionable ORF
10996_at 1946.0 P
peroxisomal acyl-CoA thioesterase
10997_at 193.8 P
questionable ORF
10998_at 230.4 P
meiotic recombination protein
10999_at 36.7 A
meiotic recombination protein
11000_at 737.3 P
Sm-like protein
11001_at 8.9 A
hypothetical protein
11002_at 6467.6 P
weak similarity to C.elegans Z49131_E ZC373.5 protein
11003_at 7758.9 P
3-hydroxyanthranilic acid dioxygenase
11004_at 730.6 A
similarity to hypothetical protein YJL181w
11005_at 2489.8 P
Component of a complex guanine nucleotide exchange activity for the ADP-ribosylation factor ARF
11006_at 1150.5 P a
cyclophilin related to the mammalian CyP-40\; physically interacts with RPD3 gene product
11007_at 977.9 P
similarity to Drosophila DmX gene
11008_at 1067.2 P
Required for assembly of active cytochrome c oxidase
11009_at 407.9 P
DNA-dependent ATPase, homologous to human Cockayne syndrome B gene ERCC6, that is a putative helicase
10965_at 703.7 P
similarity to human E6-associated protein
10966_at 132.4 A
questionable ORF
10967_at 328.6 A
questionable ORF
10968_at 547.1 P
hypothetical protein
10969_at 1232.0 P
putative transport protein involved in intracellular iron metabolism
10970_at 3979.0 P
hypothetical protein
10971_at 4610.1 P
Protein in nuclear pore complex\; may function in nuclear envelope integrity\; may also be involved in tRNA biogenesis
10972_at 82.6 A
third (55 kDa) subunit of DNA polymerase delta
10973_at 8792.3 P
weak similarity to putative transport protein YKR103w
10974_at 3820.0 P
Mitochondrial matrix protein involved in protein import\; subunit of SceI endonuclease
10975_at 2364.2 P
weak similarity to Xenopus vimentin 4
10976_at 3707.9 P

anaerobically expressed form of translation initiation factor eIF-5A
10977_at 12672.3 P
iso-1-cytochrome c
10978_at 1909.8 P
Associated with ferric reductase
10979_at 473.8 P
Interacts with Syf1p: Isy1p was identified through a two-hybrid screen with Syf1p as bait (SYF1 is synthetic lethal with PRP17 KO). A subsequent screen with Isy1p as bait isolated Syf1p, Prp39p and YPL213p (a homologue of U2A) suggesting an involvement in pre-mRNA splicing. Immunoprecipitation experiments demonstrated that Isy1p interacts with the spliceosome before step 1 of splicing, prior to the dissociation of Prp2p, and remains associated throughout both steps of splicing.
10980_at 1871.3 P
osmotic growth protein
10981_at 3613.0 P
Nucleotide excision repair protein involved in G(sub)2 repair of inactive genes
10982_at 329.5 P
hypothetical protein
10983_at 1760.3 P
similarity to hypothetical protein YML047c
10984_at 644.3 P
Protein required for growth at high temperature
10985_at 1260.0 P
hypothetical protein
10986_at 1947.9 P
thymidylate kinase
10987_at 5327.0 P
Clathrin-associated protein, small subunit
10943_at 2172.4 P
Putative serine\/threonine protein kinase that enhances spermine uptake
10944_at 99.6 M
basic helix-loop-helix protein
10945_at -84.9 A
similarity to Mnn4p
10946_at 1015.7 P
52-kDa amidase specific for N-terminal asparagine and glutamine
10947_at 6127.8 P
A12.2 subunit of RNA polymerase I
10948_at 11346.2 P
subunit of chaperonin subunit epsilon
10949_at 7310.4 P
actin-related gene
10950_at 1976.2 P
phosphatidylinositol kinase homolog
10951_at 1879.9 P
Essential protein of unknown function
10952_at 2467.9 P
Subunit 2 of Replication Factor C\; homologous to human RFC 37 kDa subunit
10953_at 4287.6 P
controls 6-N-hydroxylaminopurine sensitivity and mutagenesis
10954_at 12855.2 P
similarity to C.elegans hypothetical protein C14A4.1
10955_at -131.2 A
questionable ORF
10956_at 5636.6 P
strong similarity to C.elegans hypothetical protein and similarity to YLR243w
10957_at 8643.2 P

Methylene-fatty-acyl-phospholipid synthase (unsaturated phospholipid N-methyltransferase)
10958_at 5862.2 P
Protein interacts with Gsp1p
10959_at 2766.4 P
putative mannosyltransferase
10960_at 3869.0 P
Component of 10 nm filaments of mother-bud neck
10961_at 9150.0 P
Mir1p has been purified as a mitochondrial import receptor (p32) which can bind to signal sequence regions of mitochonidrial preproteins. In addition, it has been purified as PTP (PiC), a mitochondrial phosphate transport protein. Mir1p localizes between the inner and outer mitochondrial membranes
10962_at 1813.5 P
similarity to mammalian indoleamine 2,3-dioxygenase
10963_at 1975.1 P
questionable ORF
10964_at 4482.4 P
hypothetical protein
10920_at 115.7 P
questionable ORF
10921_at 432.8 P
hypothetical protein
10922_at 618.9 P
hypothetical protein
10923_at 1579.8 P
weak similarity to S.pombe hypothetical protein SPAC1B3.08
10924_at 12131.8 P
hypothetical protein
10925_at 1711.8 P
gamma subunit of G protein coupled to mating factor receptors
10926_at 1013.5 P
questionable ORF
10927_at 3076.5 P
weak similarity to S.pombe hypothetical protein SPBC14C8.18c
10928_at 978.9 P
hypothetical protein
10929_at 948.9 P F
box protein with several leucine rich repeats
10930_at 3536.9 P
Benomyl dependent tubulin mutant
10931_at 1441.8 P
Component of a pre-mRNA polyadenylation factor that interacts with poly(A) polymerase
10932_at 417.9 P
meiotic gene expression\; meiosis inducing protein
10933_at 6584.3 P
Ribosomal protein L43B
10934_at 237.0 P
protein related to mitochondrial carriers
10935_at 1415.2 P
similarity to Corynebacterium 2,5-diketo-D-gluconic acid reductase and aldehyde reductases
10936_at 647.5 P
weak similarity to Caj1p
10937_at 841.2 P
weak similarity to Bacillus licheniformis esterase
10938_at 543.1 P
ubiquitin hydrolase
10939_at 1914.1 P

weak similarity to Bud3p
10940_at 2881.1 P
weak similarity to superoxide dismutases
10941_at 1401.8 P
hypothetical protein
10942_at 5673.1 P
CTP synthase
10897_at 7099.0 P
Cu, Zn superoxide dismutase
10898_at 10511.2 P
strong similarity to human adenosine kinase
10899_at 379.3 A
ExtraCellular Mutant
10900_at 1215.3 P
weak similarity to acylglycerol lipase
10901_at 275.9 A
similarity to hypothetical protein YIL014c-a
10902_at 3047.6 P
carbamyl phosphate synthetase
10903_at 934.5 P
similarity to human myotubularin
10904_at 1756.9 P
weak similarity to E.coli colanic acid biosynthesis positive regulator RcsB
10905_at 1221.9 P
involved in nuclear function
10906_at 6658.9 P
similarity to bacterial, chloroplast and mitochondrial ribosomal protein S7
10907_at 1123.7 A
questionable ORF
10908_at 389.3 P
similarity to hypothetical protein YBL043w
10909_at 4873.3 P
similarity to hypothetical protein YPR114w
10910_at 6802.6 P
zinc metallo-protease that catalyzes the first step of N-terminal processing of the yeast a-factor precursor
10911_at 3363.5 P
weak similarity to Helicobacter pylori UreD protein
10912_at 249.5 P
similarity to human retinoblastoma binding protein 2
10913_at -380.8 A
hypothetical protein
10914_at 8456.5 P
F(1)F(0)-ATPase complex beta subunit, mitochondrial
10915_at 723.5 P
CCR4 associated factor
10916_at 10464.0 P
Ribosomal protein S5 (S2) (rp14) (YS8)
10917_at 2192.9 P
weak similarity to Staphylococcus multidrug resistance protein
10918_at 2468.3 P
similarity to human KIAA0171 protein
10919_at 2337.2 P
similarity to human prostate-specific membrane antigen and transferrin receptor protein
10875_at 2710.1 P
similarity to regulatory protein Ard1p
10876_at -159.8 A

questionable ORF
10877_at 1045.6 P
weak similarity to hypothetical protein YNL024c
10878_at 1970.2 P
similarity to O-succinylhomoserine (thiol)-lyase
10879_at 912.4 P
specific alpha-mannosidase
10880_at 1922.9 P
Putative Upf1p interacting protein
10881_at 10956.9 P
strong similarity to hypothetical protein YDR399w
10882_at 504.3 P
similarity to paramyosin, myosin
10883_at 51.7 P
Required for maintenance of chromosomes and minichromosomes
10884_at 1482.2 P
weak similarity to human 3 ,5 -cyclic-GMP phosphodiesterase
10885_at 5143.9 P
ExtraCellular Mutant
10886_at 854.3 P
similarity to C.elegans hypothetical protein T08A11.1
10887_at 11307.7 P
Homoserine dehydrogenase (L-homoserine:NADP oxidoreductase)
10888_at 1872.0 P
involved in cell-cycle regulation of histone transcription
10889_at 927.3 P
hypothetical protein
10890_at 1273.3 P
similarity to thiamin pyrophosphokinase
10891_at 8875.4 P
dolichyl phosphate-D-mannose:protein O-D-mannosyltransferase
10892_at 2875.0 P
involved in mitochondrial genome maintenance
10893_s_at 10939.4 P
Ribosomal protein S4A (YS6) (rp5) (S7A)
10894_at 826.4 P
questionable ORF
10895_at 3952.7 P
heat shock transcription factor homolog
10896_at 9471.8 P
Branched-Chain Amino Acid Transaminase
10851_at 1005.8 P
similarity to 2-nitropropane dioxygenase
10852_at -119.5 A
Protein induced during anaerobic growth
10853_at 1195.0 P
similarity to mucin proteins, YKL224c, Sta1p
10854_at 1439.4 P
allantoate permease
10855_at 333.7 P
Endo-polygalacturonase
10856_at 353.8 P
hypothetical protein
10857_at 1109.5 P
Hypothetical aryl-alcohol dehydrogenase (AAD)
10858_s_at 958.9 P

Thiamine biosynthetic enzyme
10859_at 62.6 A
hypothetical protein
10860_s_at 334.7 P
hexose transporter
10861_s_at 2265.8 P
sorbitol-induced sorbitol dehydrogenase
10862_s_at 66.5 A
strong similarity to Mal31p
10863_i_at 1029.2 P
identified by SAGE
10864_r_at 1584.3 A
identified by SAGE
10865_at 1387.0 P
C-terminal part of YJR030c
10866_at 2725.7 P
similarity to human DDP gene, hypothetical protein of S.pombe (YA94_SCHPO) and Mrs11p (YHR005c-a)
10867_s_at 2109.8 P
Co-assembles with Bud3p at bud sites
10868_at 6190.6 P
non-annotated SAGE orf Found reverse in NC_001142 between 159321 and 159545 with 100% identity. See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251
10869_at 3277.4 P
non-annotated SAGE orf Found reverse in NC_001142 between 181250 and 181408 with 100% identity. See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251
10870_i_at 95.0 P
non-annotated SAGE orf Found reverse in NC_001142 between 227571 and 227705 with 100% identity. See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251
10871_s_at 1346.3 P
non-annotated SAGE orf Found reverse in NC_001142 between 227571 and 227705 with 100% identity. See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251
10872_at 4589.4 P
non-annotated SAGE orf Found reverse in NC_001142 between 227590 and 227742 with 100% identity. See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251
10873_at 127.8 A
non-annotated SAGE orf Found reverse in NC_001142 between 471544 and 471738 with 100% identity. See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251
10874_at 6477.6 P
non-annotated SAGE orf Found forward in NC_001142 between 316419 and 316676 with 100% identity. See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251
10828_at 529.4 A
non-annotated SAGE orf Found forward in NC_001142 between 444820 and 444969 with 100% identity. See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251
10829_at 1080.8 P
non-annotated SAGE orf Found forward in NC_001142 between 445314 and 445592 with 100% identity. See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251
10830_at 265.9 A
non-annotated SAGE orf Found reverse in NC_001142 between 451797 and 451979 with 100% identity. See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251
10831_s_at 1162.0 P
non-annotated SAGE orf Found reverse in NC_001142 between 731735 and 731896 with 100% identity. See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251
10832_s_at 474.2 P
non-annotated SAGE orf Found reverse in NC_001142 between 740830 and 741003 with 100% identity. See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251

10833_at 1113.2 P
non-annotated SAGE orf Found forward in NC_001142 between 106232 and 106426 with 100% identity.
See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251
10834_at 152.3 P
non-annotated SAGE orf Found reverse in NC_001142 between 121504 and 121665 with 100% identity.
See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251
10835_at 1881.3 A
non-annotated SAGE orf Found reverse in NC_001142 between 187528 and 187671 with 100% identity.
See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251
10836_at 3913.5 P
non-annotated SAGE orf Found reverse in NC_001142 between 289382 and 289522 with 100% identity.
See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251
10837_at 242.6 P
non-annotated SAGE orf Found reverse in NC_001142 between 312518 and 312670 with 100% identity.
See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251
10838_at 12277.4 P
non-annotated SAGE orf Found reverse in NC_001142 between 410923 and 411120 with 100% identity.
See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251
10839_at 310.3 P
non-annotated SAGE orf Found reverse in NC_001142 between 518895 and 519053 with 100% identity.
See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251
10840_at -94.5 A
non-annotated SAGE orf Found forward in NC_001142 between 548093 and 548311 with 100% identity.
See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251
10841_at 1032.4 P
non-annotated SAGE orf Found forward in NC_001142 between 622714 and 622869 with 100% identity.
See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251
10842_at 4173.1 P
non-annotated SAGE orf Found forward in NC_001142 between 637618 and 637857 with 100% identity.
See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251
10843_at 24.5 A
non-annotated SAGE orf Found reverse in NC_001142 between 136546 and 136695 with 100% identity.
See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251
10844_at 170.5 P
non-annotated SAGE orf Found forward in NC_001142 between 90020 and 90184 with 100% identity.
See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251
10845_at 239.6 A
non-annotated SAGE orf Found reverse in NC_001142 between 116100 and 116291 with 100% identity.
See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251
10846_at 1035.6 M
non-annotated SAGE orf Found forward in NC_001142 between 142442 and 142669 with 100% identity.
See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251
10847_at 2906.5 P
non-annotated SAGE orf Found forward in NC_001142 between 180616 and 180768 with 100% identity.
See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251
10848_at 659.8 P
non-annotated SAGE orf Found forward in NC_001142 between 236437 and 236625 with 100% identity.
See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251
10849_at 547.8 A
non-annotated SAGE orf Found forward in NC_001142 between 337317 and 337583 with 100% identity.
See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251
10850_at 152.8 A
non-annotated SAGE orf Found reverse in NC_001142 between 416236 and 416439 with 100% identity.
See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251
10806_at -11.9 A
non-annotated SAGE orf Found reverse in NC_001142 between 424167 and 424301 with 100% identity.

See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251
10807_at 825.7 P
non-annotated SAGE orf Found reverse in NC_001142 between 448028 and 448162 with 100% identity.
See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251
10808_at 159.4 A
non-annotated SAGE orf Found forward in NC_001142 between 471954 and 472142 with 100% identity.
See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251
10809_g_at 216.8 P
non-annotated SAGE orf Found forward in NC_001142 between 471954 and 472142 with 100% identity.
See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251
10810_i_at 80.2 P
non-annotated SAGE orf Found forward in NC_001142 between 471988 and 472161 with 100% identity.
See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251
10811_at 308.0 A
non-annotated SAGE orf Found reverse in NC_001142 between 626834 and 627004 with 100% identity.
See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251
10812_s_at 254.6 P
non-annotated SAGE orf Found reverse in NC_001142 between 731905 and 732069 with 100% identity.
See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251
10813_s_at -60.2 A
non-annotated SAGE orf Found reverse in NC_001142 between 734995 and 735165 with 100% identity.
See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251
10814_s_at 2391.3 P
non-annotated SAGE orf Found forward in NC_001142 between 741740 and 741883 with 100% identity.
See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251
10815_at 3585.3 P
non-annotated SAGE orf Found reverse in NC_001142 between 104735 and 104932 with 100% identity.
See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251
10816_at 18.3 A
non-annotated SAGE orf Found reverse in NC_001142 between 172694 and 172930 with 100% identity.
See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251
10817_at 987.5 P
non-annotated SAGE orf Found forward in NC_001142 between 283262 and 283426 with 100% identity.
See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251
10818_at 900.9 P
non-annotated SAGE orf Found forward in NC_001142 between 322217 and 322453 with 100% identity.
See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251
10819_at 1088.9 P
non-annotated SAGE orf Found reverse in NC_001142 between 396887 and 397036 with 100% identity.
See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251
10820_at 2818.3 P
non-annotated SAGE orf Found forward in NC_001142 between 447886 and 448050 with 100% identity.
See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251
10821_g_at 28.9 P
non-annotated SAGE orf Found forward in NC_001142 between 447886 and 448050 with 100% identity.
See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251
10822_at 99.4 A
non-annotated SAGE orf Found forward in NC_001142 between 447920 and 448102 with 100% identity.
See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251
10823_at 796.7 P
non-annotated SAGE orf Found forward in NC_001142 between 549543 and 549719 with 100% identity.
See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251
10824_at 328.6 A
non-annotated SAGE orf Found forward in NC_001142 between 578016 and 578222 with 100% identity.
See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251
10825_at 472.4 P

non-annotated SAGE orf Found reverse in NC_001142 between 637602 and 637835 with 100% identity.
See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251
10826_at 19.1 A
non-annotated SAGE orf Found reverse in NC_001142 between 727961 and 728134 with 100% identity.
See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251
10827_s_at 552.2 P
non-annotated SAGE orf Found reverse in NC_001142 between 737313 and 737453 with 100% identity.
See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251
10782_at 5927.5 P
small nuclear RNA128
10783_at 179.2 A
small nuclear RNA190
10784_at 1778.0 P
small nuclear RNA37
10785_at 1629.3 P
snRNA
10786_i_at -72.1 A
Centromere
10787_at 2281.4 P
small nuclear RNA3
10788_at 39.0 A
ARS121 Found forward in NC_001142 between 683650 and 683699 with 100% identity.
10789_f_at 1171.0 P
strong similarity to members of the Srp1p/Tip1p family
10790_at 487.0 P
weak similarity to transcription factors, similarity to finger proteins YOR162c, YOR172w and YLR266c
10791_at -125.9 A
weak similarity to human X-linked PEST-containing transporter
10792_at 86.5 P
Ferric reductase, similar to Fre1p
10793_at 2738.6 P
Protein with similarity to subtelomerically-encoded proteins such as Cos5p, Ybr302p, Cos3p, Cos1p, Cos4p, Cos8p, Cos6p, Cos9p
10794_at 1262.1 P
threonine dehydratase
10795_at -116.6 A
carboxylic acid transporter protein homolog
10796_at 12092.4 P
dihydroorotate dehydrogenase
10797_at 3705.0 P
similarity to P. aeruginosa hyuA and hyuB
10798_at 5455.3 P
weak similarity to mouse transcriptional coactivator ALY
10799_at 4992.5 P
phospholipase A2-activating protein
10800_at 9341.6 P
integral membrane protein localizing to the ER and Golgi
10801_at 4467.1 P
anthranilate synthase Component II and indole-3-phosphate (multifunctional enzyme)
10802_at 8745.8 P
ubiquitin activating enzyme, similar to Uba2p
10803_at 245.4 P
ABC transporter, glycoprotein, component of a-factor secretory pathway
10804_at 1162.0 P
Subunit of complex involved in processing of the 3 end of cytochrome b pre-mRNA
10805_at 3782.2 P

hypothetical protein
10760_at 1486.8 P
hypothetical protein
10761_at 2608.9 P
nuclear protein LOS1
10762_at 5558.6 P
probable purine nucleotide-binding protein
10763_at 1808.6 P
phosphatidylinositol kinase homolg
10764_at 265.4 A
questionable ORF
10765_at 2846.6 P
member of the AAA-protein family
10766_at 8256.2 P
v-SNARE
10767_at 4207.9 P
similarity to rabbit histidine-rich calcium-binding protein
10768_at 1067.1 P
mitochondrial threonine-tRNA synthetase
10769_at 1607.0 P
Interacts with and may be a positive regulator of GLC7 which encodes type1 protein phosphatase
10770_at 9510.0 P
acyl carrier protein
10771_at 7921.4 P
diphthamide synthesis protein
10772_at 1191.9 P
Type 2B protein phosphatase\; regulatory B subunit of calcineurin
10773_at 3282.7 P
Type 2B protein phosphatase\; regulatory B subunit of calcineurin
10774_at 884.3 P
The homologue in Aspergillus nidulans, hymA, is involved in development, see Karos, M. and Fischer, R. (1996). hymA (hypha-like metulae), a new developmental mutant of Aspergillus nidulans. Microbiol. 142:3211-3218.
10775_at 259.3 P
peroxisomal ABC transporter 2
10776_at 396.4 P
strong similarity to hypothetical protein YLR413w
10777_at 2942.6 P
mRNA transport regulator
10778_at 1659.0 P
probable purine nucleotide-binding protein
10779_at 5192.8 P
Ornithine decarboxylase
10780_at 1613.3 P
hypothetical protein
10781_at 9190.5 P
pentafunctional enzyme consisting of the following domains : acetyl transferase, enoyl reductase, dehydratase and malonyl\/palmityl transferase
10737_at 12422.9 P
ribose-phosphate pyrophosphokinase
10738_i_at 226.9 A
Ribosomal protein L17A (L20A) (YL17)
10739_f_at 11203.0 P
Ribosomal protein L17A (L20A) (YL17)
10740_at 3945.4 P
kinesin-like protein

10741_at	8618.9	P	a factor recptor
10742_at	407.7	P	questionable ORF
10743_at	1938.4	P	hypothetical protein
10744_at	6553.9	P	weak similarity to E.coli hypothetical protein
10745_at	1422.7	P	probable transport protein
10746_at	2391.4	P	U5 snRNP-specific protein related to EF-2
10747_at	6852.6	P	Nucleolar protein
10748_at	650.9	P	probable serine\/threonine-specific protein kinase (EC 2.7.1.-)
10749_at	2389.8	P	mitochondrial ribosomal protein L14
10750_at	706.0	P	questionable ORF
10751_at	1218.7	P	probable serine\/threonine-specific protein kinase (EC 2.7.1.-)
10752_at	4648.9	P	16 kDa mitochondrial ribosomal large subunit protein
10753_at	1189.9	P	cAMP-dependent protein kinase catalytic subunit
10754_at	7543.9	P	Morphogenesis Checkpoint Dependent
10755_at	11374.6	P	Protein containing tandem internal repeats
10756_at	794.0	P	Protein containing tandem internal repeats
10757_at	235.9	P	hypothetical protein
10758_at	113.6	P	probable serine\/threonine-specific protein kinase (EC 2.7.1.-)
10759_at	9165.1	P	similarity to hypothetical S. pombe protein
10714_at	1251.4	P	hypothetical protein
10715_at	2344.9	P	hypothetical protein
10716_at	5626.8	P	aminopeptidase yscII
10717_at	11460.0	P	40S ribosomal protein S27A (rp61) (YS20)
10718_at	695.7	P	hypothetical protein
10719_at	1365.7	P	signal recognition particle receptor, beta chain
10720_at	182.8	P	questionable ORF
10721_at	10742.6	P	Phosphoglycerate mutase
10722_at	2365.2	P	similarity to C.elegans hypothetical protein R107.2

10723_at 3869.6 P
NADH-cytochrome b5 reductase
10724_at 900.0 P
debranching enzyme
10725_at 3428.4 P
flavoprotein subunit of succinate dehydrogenase
10726_at 563.0 P
questionable ORF
10727_at 9425.2 P
strong similarity to S.pombe hypothetical protein C3H1.09C
10728_at 11059.7 P
putative ATPase, 26S protease subunit component
10729_at 2317.2 P
Subunit of RNA polymerase III
10730_at 4758.1 P
low temperature viability protein
10731_at 5497.7 P
mitochondrial ribosomal protein
10732_at 8346.5 P
succinate dehydrogenase cytochrome b
10733_at 2245.4 P
triglyceride lipase-cholesterol esterase
10734_at 1399.0 P
alpha subunit of the kinase which phosphorylates the RNA polymerase largest subunit CTD (carboxyl-terminal domain)
10735_at 3337.4 P
15.5 kDa mitochondrial ribosomal protein YmL31
10736_at 1149.0 A
hypothetical protein
10692_at 928.0 P
questionable ORF
10693_at 2739.6 P
Beta-adaptin, large subunit of the clathrin-associated protein (AP-1) complex
10694_at 341.1 P
probable neutral zinc metalloproteinase
10695_at 293.1 P
probable purine nucleotide-binding protein
10696_at 1633.4 P
probable folyl-polyglutamate synthetase
10697_at 422.2 A
questionable ORF
10698_at 1615.2 P
Required for mother cell-specific HO expression
10699_at 804.1 P
myosin I
10700_at 7775.3 P
Phospo-mutase homolog
10701_at 5853.3 P
phosphoglucomutase, minor isoform
10702_at 3704.2 P
76.5 kDa Serine\/threonine protein kinase with similarity to protein kinase C, is 90\% identical to Ypk2p
10703_at 2800.8 P
DNA-independent RNA Polymerase I transcription factor
10704_at 262.2 A
suppressor of SHR3\; confers leflunomide resistance when overexpressed
10705_g_at -111.3 A

suppressor of SHR3\; confers leflunomide resistance when overexpressed
10706_at 920.8 P
questionable ORF
10707_at 6103.5 P
component of signal recognition particle
10708_at 1097.7 P
strong similarity to YMR102c
10709_at 11258.0 P
similarity to mitochondrial uncoupling proteins (MCF)
10710_at 1829.4 P
25.2 kDa protein involved in assembly of vacuolar H(+) ATPase
10711_at 170.8 P
questionable ORF
10712_at 9483.8 P
Hsp90 (Ninety) Associated Co-chaperone
10713_at 2710.4 P
probable serine\/threonine-specific protein kinase (EC 2.7.1.-)
10669_at 1631.6 M
questionable ORF
10670_at 3275.7 P
major apurinic\/apyrimidinic endonuclease\/3 -repair diesterase
10671_at 3364.1 P
42 kDa 5 to 3 exonuclease required for Okazaki fragment processing
10672_at 2720.5 P
transcriptional activator and ARS1 binding protein
10673_at 541.2 P
questionable ORF
10674_at 6963.2 P
Protein involved in resistance to K. lactis killer toxin
10675_at 4994.7 P
transcriptional activator protein of CYC1 (component of HAP2\/HAP3 heteromer)
10676_at -8.2 A
DNA replication and checkpoint protein 1
10677_at -52.7 A
weak similarity to S.antibioticus probable oxidoreductase
10678_at 3365.1 P
aspartate aminotransferase, mitochondrial
10679_at 1196.3 P
similarity to YMR086w
10680_at 7744.0 P
Glutamine_fructose-6-phosphate amidotransferase (glucoseamine-6-phosphate synthase)
10681_at 2391.9 P
vacuolar aminopeptidase ysc1
10682_at -483.4 A
hypothetical protein
10683_at 846.5 P
Putative protein kinase homologous to S. pombe cdr1\/nim1
10684_at 4206.2 P
similarity to C.elegans hypothetical protein
10685_at 945.3 P
similarity to C.elegans hypothetical proteins C18G6.06 and C16C10.2
10686_at 2416.4 P
hypothetical protein
10687_at 72.8 A
hypothetical protein
10688_at 8479.8 P

cell wall mannoprotein
10689_at 4983.1 P
cell wall mannoprotein
10690_at 489.1 P
similarity to C.elegans hypothetical proteins
10691_at 6016.5 P
weak similarity to E.coli hypothetical protein
10646_at 214.1 A
MBR1 protein precursor
10647_at 627.6 P
GTPase-activating protein (GAP) for Rsr1p\/Bud1p
10648_at 764.8 P
strong similarity to Sec14p
10649_at 608.2 P
hypothetical protein
10650_at 363.9 P
Centromere protein required for normal chromosome segregation and spindle integrity
10651_at 935.7 P
similarity to C.tropicalis hal3 protein, to C-term. of Sis2p and to hypothetical protein YOR054c
10652_at 2832.5 P
cytochrome c1 heme lyase
10653_at 514.2 P
hypothetical protein
10654_at 9342.6 P
mitochondrial malate dehydrogenase
10655_at 5313.5 P
strong similarity to S.pombe hypothetical protein SPAC29B12
10656_at 7186.3 P
weak similarity to C.elegans hypothetical protein
10657_at 233.0 P
questionable ORF
10658_at 8802.4 P
Translation elongation factor EF-1gamma
10659_at 12324.9 P
Translation elongation factor EF-1gamma
10660_at 8621.3 P
Vacuolar H-ATPas hydrophilic subunit C of V1 sector
10661_at 1245.2 P
kinesin heavy chain homolog, but is not believed to act as a kinesin, colocalizes with Myo2p
10662_at 2626.8 P
probable ATP-dependent RNA helicase
10663_at 7627.7 P
hypothetical protein
10664_at 534.9 P
questionable ORF
10665_g_at 1107.9 P
questionable ORF
10666_at 1151.4 P
hypothetical protein
10667_at 1779.4 P
involved in early pre-mRNA splicing
10668_at 1888.9 P
novel member of the Hsp70 family of molecular chaperones that localizes to the lumen of the endoplasmic reticulum:
10624_at 578.5 P
Binds Sin3p in two-hybrid assay

10625_at 223.4 A
weak similarity to A.parasiticus nor-1 protein
10626_at 112.9 P
similarity to B.subtilis transcriptional regulatory protein
10627_at 5033.5 P
strong similarity to hypothetical E.coli protein b1832
10628_at 4090.3 P
Nuclear pore complex protein homologous to Nup116p
10629_at 6359.9 P
Nucleoside diphosphate kinase
10630_at 4228.0 P
hypothetical protein
10631_at 7744.1 P
Yeast endoplasmic reticulum 25 kDa transmembrane protein
10632_at 2877.8 P
overexpression overcomes manganese toxicity
10633_at 2634.8 P
weak similarity to mammalian microtubule-associated protein MAP 1B
10634_at 3485.5 P
zinc finger protein
10635_at 526.5 P
hypothetical protein
10636_at 9023.0 P
aldolase
10637_at 2345.8 P
similarity to C.elegans hypothetical protein
10638_at 3971.6 P
Transcription factor IIA, small chain
10639_at 1539.3 P
100-kDa protein (predicted molecular weight is 120 kDa) with two leucine zipper motifs, coiled-coil region, and some homology to Nup133p
10640_at 10045.0 P
strong similarity to human IgE-dependent histamine-releasing factor
10641_at 191.9 P
probable acetoacetyl-CoA reductase
10642_at 10543.0 P
similarity to glutenin, high molecular weight chain proteins and Snf5p
10643_at 9929.5 P
similarity to C.elegans hypothetical protein T09A5.7 (12.5 kD)
10644_at 974.2 A
questionable ORF
10645_at 1472.5 P
hypothetical protein
10601_at 1465.7 P
hypothetical protein
10602_at 236.9 P
similarity to YMR031c
10603_at 833.7 P
high similarity to histone H3 and to human centromere protein CENP-A
10604_at 535.7 P
protein kinase
10605_at 1740.4 P
hypothetical protein
10606_at 6999.9 P
strong similarity to YMR238w
10607_at 1511.0 P

p58 polypeptide of DNA primase
10608_at 5086.3 P
hypothetical protein
10609_at 5879.0 P
putative transcription factor
10610_at 2008.4 P
component of the spindle pole body
10611_at 2111.7 P
endosomal Vps protein complex subunit
10612_at 2439.7 P
NifU-like protein B
10613_at 6372.0 P
Putative membrane protein
10614_at 2777.7 P
transcriptional repressor and activator
10615_at 1384.3 A
weak similarity to C.elegans ubc-2 protein
10616_at -61.3 A
questionable ORF
10617_at 11685.2 P
Uridinephosphoglucose pyrophosphorylase
10618_at 3010.1 P
weak similarity to YOL013c
10619_at 1218.5 P
hypothetical protein
10620_at 7791.3 P
intrastrand crosslink recognition protein
10621_at 786.7 A
hypothetical protein
10622_at 255.8 A
questionable ORF
10623_at 7639.8 P
mitochondrial malic enzyme
10579_at 4387.0 P
Large subunit of transcription factor tfIIE
10580_at 2797.7 P
similarity to E.coli molybdopterin-converting factor chlN
10581_at 1104.8 P
strong similarity to glutathione peroxidase
10582_at 3593.6 P
76-kDa subunit of Pab1p-dependent poly(A) ribonuclease (PAN)
10583_at 10142.8 P
uridine-monophosphate kinase (uridylate kinase)
10584_at 900.1 P
weak similarity to human cylicin II
10585_at 1146.4 P
putative metal-binding nucleic acid-binding protein, interacts with Cdc23p and Cdc27p to catalyze the conjugation of ubiquitin to cyclin B
10586_at 3915.6 P
contains four beta-transducin repeats
10587_at 1830.5 P
suppressor protein
10588_at 3249.7 P
CAAX farnesyltransferase alpha subunit
10589_at 2600.3 P
similarity to C.elegans hypothetical protein

10590_at 972.2 P
DNA helicase A
10591_at 5665.7 P
ATP synthase d subunit
10592_at 1261.6 P
zinc-finger transcription factor of the Zn(2)-Cys(6) binuclear cluster domain type
10593_at 3896.0 P
hypothetical protein
10594_at 4683.3 P
Arp Complex Subunit
10595_at 1292.9 P
Splicing component that associates with the yeast U1 small nuclear ribonucleoprotein particle
10596_at 1112.8 P
cruciform cutting endonuclease
10597_at 2906.6 P
Ubiquitin Fusion Degradation
10598_at 10332.4 P
mRNA turnover 4
10599_at 5755.9 P
strong similarity to Lag1p
10600_at 4398.7 P
alpha subunit of capping protein
10555_at 2200.2 P
required for transport of proteins between an early and a later golgi compartment. possible NSF attachment protein receptor (V-SNARE)
10556_i_at 18778.1 P
Ribosomal protein L14A
10557_f_at 10323.6 P
Ribosomal protein L14A
10558_s_at 11751.0 P
Ribosomal protein L14A
10559_at 2278.6 P
weak similarity to YKR029c and D.melanogaster transcription elongation factor DmS-II
10560_at 9488.2 P
aureobasidin-resistance protein
10561_at 4571.8 P
Mitochondrial ribosomal protein MRP17
10562_at 3014.5 P
similarity to hypothetical protein YKL041w
10563_at 3259.3 P
adenylylsulfate kinase
10564_at 3512.2 P
putative GTP-binding protein\; similar to mammalian Mx proteins
10565_at 2367.1 P
poly(A) polymerase
10566_at 2228.1 P
similarity to Kes1p, Hes1p and Osh1p
10567_at 1129.0 P
ExtraCellular Mutant
10568_at 613.2 P
hypothetical protein
10569_at 6771.9 P
mitochondrial ribosomal protein YmL13
10570_at 1955.5 P
weak similarity to Streptococcus protein M5 precursor
10571_at 1628.6 P

Member of RSC complex.
10572_at 711.7 P
peroxisomal multifunctional beta-oxidation protein
10573_at 231.1 A
topoisomerase I interacting factor 2
10574_at 1063.3 P
hypothetical protein
10575_at 1.8 A
questionable ORF
10576_at 14918.0 P
Similar to plant PR-1 class of pathogen related proteins
10577_at 2366.6 P
probable purine nucleotide-binding protein
10578_at -15.1 A
similarity to hypothetical protein YJL043w
10533_at 2357.9 P
weak similarity to mysoin heavy chain proteins
10534_at 87.7 A
similarity to human hypothetical KIAA0161 protein
10535_at 5422.3 P
strong similarity to hypothetical protein YJL082w
10536_at 297.2 P
Increased rDNA silencing
10537_at 131.5 A
hypothetical protein
10538_at 888.7 P
strong similarity to hypothetical protein YJL084c
10539_at 589.1 P
hypothetical protein
10540_at 296.3 P
similarity to S.pombe hypothetical protein SPAC23C4
10541_at 3849.2 P
putative RNA helicase
10542_at 1860.9 P
hypothetical protein
10543_at 6327.5 P
translation initiation factor eIF2B, 34 KD, alpha subunit\; negative regulator of GCD12, thereby serving indirectly as a positive regulator of GCN4
10544_at 1484.2 P
strong similarity to Chs6p
10545_at 3606.5 P
Type 2A-related protein phosphatase
10546_at 1094.3 P
similarity to YJL105w and Lentinula MFBA protein
10547_at 4541.4 P
weak similarity to NADH dehydrogenases
10548_at 2269.1 P
Phospholipase D
10549_at -94.7 A
hypothetical protein
10550_at 296.3 A
questionable ORF
10551_at -17.3 A
negative regulator of multiple nitrogen catabolic genes
10552_at 4145.7 P
RAD52 Inhibitor (Fifty Two Inhibitor)

10553_at 846.5 P
CCR4 associated factor
10554_at 1109.2 P
component of spindle pole
10510_at 3573.1 P
probable calcium-binding protein
10511_at 413.3 A
general amino acid permease
10512_at 1391.2 P
questionable ORF
10513_at 30.8 M
hypothetical protein
10514_at 10888.5 P
YOUTH, involved in determining yeast longevity
10515_at 8947.5 P
weak similarity to phosphoglycerate mutase
10516_at 1106.0 P
hypothetical protein
10517_at 883.6 P
hypothetical protein
10518_at 12850.8 P
hypothetical protein
10519_at 2415.5 P
questionable ORF
10520_at 10161.0 P
nucleosome assembly protein I
10521_at 2220.9 P
hypothetical protein
10522_at 1803.3 P
membrane protein\; low affinity potassium transport
10523_at 821.2 P
similarity to C.elegans hypothetical protein
10524_at 1261.1 P
mitochondrial carrier protein, highly homologous to Mrs3p
10525_at 654.7 P
DHS-1-P phosphatase
10526_at 2450.7 P
heavy chain of cytoplasmic dynein
10527_at 1323.2 P
ras homolog--GTP binding protein
10528_at 3244.3 P
endo-exonuclease yNucR
10529_i_at 1959.4 A
Ribosomal protein S21A (S26A) (YS25)
10530_at 182.5 P
self-glucosylating initiator of glycogen synthesis\; similar to mammalian glycogenin
10531_at 2691.3 P
hypothetical protein
10532_at 1374.4 P
putative mannosyltransferase\; type 2 membrane protein
10487_at 2104.7 P
Small subunit of TFIIE transcription factor
10488_at 1119.2 P
May regulate expression of genes involved in bud formation and morphogenesis
10489_at 908.3 P
weak similarity to transcription factors

10490_at	7034.0	P	hypothetical protein
10491_at	6564.4	P	Cytochrome-c peroxidase
10492_at	2817.5	P	strong similarity to Sct1p
10493_at	6986.1	P	Hydrophilic protein that acts in conjunction with SNARE proteins in targeting and fusion of ER to Golgi transport vesicles
10494_at	1817.3	P	siroheme synthase
10495_at	2049.7	P	strong similarity to S. pombe phosphatidyl synthase
10496_at	4806.8	P	weak similarity to C.elegans hypothetical protein
10497_at	4902.5	P	sit4 suppressor
10498_at	755.4	P	hypothetical protein
10499_at	4857.1	P	strong similarity to hypothetical S. pombe protein
10500_at	3323.3	P	weak similarity to negative regulator Reg1p
10501_at	895.4	P	ExtraCellular Mutant
10502_at	922.7	P	hypothetical protein
10503_at	390.5	P	similarity to Vps5p
10504_at	1758.3	P	similarity to S.pombe hypothetical protein SPAC1D4.10
10505_at	5712.2	P	NAD-dependent 5,10-methylenetetrahydrafolate dehydrogenase
10506_at	10159.0	P	hypothetical protein
10507_at	3712.1	P	Nuclear pore complex protein involved in poly(A)+ RNA transport, nuclear pore distribution, and possibly in the biogenesis of functional tRNA
10508_at	350.7	P	weak similarity to S.japonicum paramyosin
10509_at	3151.4	P	Protein related to translation elongation factor EF-1alpha and to Suf12p\/Sup2p\/Gst1p\/Sup35p
10464_at	3428.2	P	22.3 kDa mitochondrial ribosomal large subunit protein YmL20\; homologous to L17 of E. coli
10465_at	1176.1	P	putative ATP-binding protein
10466_at	2489.3	P	similarity to hypothetical Myxococcus xanthus protein
10467_at	4047.9	P	weak similarity to b.subtilis spore germination protein II
10468_at	1379.5	P	strong similarity to YOR081c
10469_at	1819.4	P	similarity to chicken Lim protein kinase and Islet proteins
10470_at	2292.9	P	Suppressor of rad53 lethality

10471_at 11675.5 P
nucleolar protein that is immunologically and structurally related to rat Nopp140, a nonribosomal protein of the nucleolus and coiled bodies.
10472_at 8800.0 P
Peptide transporter
10473_i_at 16378.0 P
Ribosomal protein L40B
10474_s_at 9099.5 P
Ribosomal protein L40B
10475_at 1656.2 P
myosin-like protein
10476_at 2720.4 P
similarity to mitochondrial aldehyde dehydrogenase Ald1p
10477_g_at 373.3 P
similarity to mitochondrial aldehyde dehydrogenase Ald1p
10478_at 420.8 P
phosphoenolpyruvate carboxylkinase
10479_at 999.6 P
Ubiquitin-specific protease
10480_at 764.0 P
Transcription factor regulating basal and induced activity of histidine and adenine biosynthesis genes
10481_at 2032.9 P
cause growth inhibition when overexpressed
10482_at 350.8 P
repressor of silent mating loci
10483_at 396.3 P
Protein with similarity to flocculation protein Flo1p
10484_at 315.1 P
similarity to multidrug resistance proteins
10485_at 173.1 P
similarity to multidrug resistance proteins
10486_s_at -46.3 A
strong similarity to Sge1p and hypothetical protein YCL069w
10442_s_at 523.9 P
regulates the mannosylphosphorylation
10443_at -7.4 A
hypothetical protein identified by SAGE
10444_at 835.2 P
hypothetical protein
10445_s_at 3225.9 P
regulates the mannosylphosphorylation
10446_s_at 1627.1 P
Protein of unknown function
10447_s_at 2444.5 P
probable serine\/threonine-specific protein kinase (EC 2.7.1.-)
10448_s_at 3360.2 P
strong similarity to holacid-halidohydrolase
10449_at -82.9 A
non-annotated SAGE orf Found forward in NC_001143 between 91618 and 91755 with 100% identity. See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251
10450_at 94.0 A
non-annotated SAGE orf Found forward in NC_001143 between 94073 and 94228 with 100% identity. See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251
10451_at 54.8 A
non-annotated SAGE orf Found forward in NC_001143 between 146588 and 146755 with 100% identity. See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251

10452_at 799.3 P
non-annotated SAGE orf Found reverse in NC_001143 between 403218 and 403517 with 100% identity.
See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251
10453_at 119.4 M
non-annotated SAGE orf Found forward in NC_001143 between 618527 and 618670 with 100% identity.
See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251
10454_at 128.9 A
non-annotated SAGE orf Found forward in NC_001143 between 618749 and 618886 with 100% identity.
See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251
10455_at 281.3 P
non-annotated SAGE orf Found reverse in NC_001143 between 16801 and 17055 with 100% identity.
See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251
10456_at 6403.9 P
non-annotated SAGE orf Found forward in NC_001143 between 98250 and 98414 with 100% identity.
See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251
10457_at 51.6 A
non-annotated SAGE orf Found forward in NC_001143 between 145707 and 145880 with 100% identity.
See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251
10458_at 460.6 P
non-annotated SAGE orf Found reverse in NC_001143 between 145751 and 145927 with 100% identity.
See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251
10459_at 1266.5 M
non-annotated SAGE orf Found reverse in NC_001143 between 164674 and 164820 with 100% identity.
See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251
10460_at 1089.7 P
non-annotated SAGE orf Found forward in NC_001143 between 178286 and 178429 with 100% identity.
See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251
10461_at 211.8 P
non-annotated SAGE orf Found reverse in NC_001143 between 195028 and 195171 with 100% identity.
See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251
10462_at 3686.3 P
non-annotated SAGE orf Found forward in NC_001143 between 233585 and 233836 with 100% identity.
See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251
10463_at 70.1 A
non-annotated SAGE orf Found reverse in NC_001143 between 261612 and 261797 with 100% identity.
See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251
10419_at 1482.4 P
non-annotated SAGE orf Found forward in NC_001143 between 320463 and 320651 with 100% identity.
See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251
10420_at 1715.5 P
non-annotated SAGE orf Found forward in NC_001143 between 612074 and 612223 with 100% identity.
See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251
10421_at 2120.4 P
non-annotated SAGE orf Found reverse in NC_001143 between 638531 and 638722 with 100% identity.
See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251
10422_at 736.7 P
non-annotated SAGE orf Found forward in NC_001143 between 219150 and 219308 with 100% identity.
See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251
10423_at 219.3 A
non-annotated SAGE orf Found forward in NC_001143 between 298846 and 299052 with 100% identity.
See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251
10424_at -377.0 A
non-annotated SAGE orf Found reverse in NC_001143 between 379033 and 379236 with 100% identity.
See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251
10425_at 3606.2 P
non-annotated SAGE orf Found reverse in NC_001143 between 464717 and 464851 with 100% identity.

See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251
10426_at 39.0 A
non-annotated SAGE orf Found reverse in NC_001143 between 18900 and 19061 with 100% identity.
See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251
10427_at 1462.9 P
non-annotated SAGE orf Found reverse in NC_001143 between 38930 and 39151 with 100% identity.
See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251
10428_at -64.7 A
non-annotated SAGE orf Found forward in NC_001143 between 46506 and 46670 with 100% identity.
See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251
10429_at 47.8 A
non-annotated SAGE orf Found reverse in NC_001143 between 93914 and 94054 with 100% identity.
See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251
10430_at 239.1 P
non-annotated SAGE orf Found reverse in NC_001143 between 98397 and 98609 with 100% identity.
See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251
10431_at -79.3 A
non-annotated SAGE orf Found reverse in NC_001143 between 108918 and 109193 with 100% identity.
See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251
10432_at 675.5 P
non-annotated SAGE orf Found reverse in NC_001143 between 136056 and 136247 with 100% identity.
See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251
10433_at 272.5 P
non-annotated SAGE orf Found reverse in NC_001143 between 136275 and 136457 with 100% identity.
See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251
10434_at 1118.4 P
non-annotated SAGE orf Found reverse in NC_001143 between 142825 and 142992 with 100% identity.
See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251
10435_at 1752.4 P
non-annotated SAGE orf Found reverse in NC_001143 between 184805 and 185014 with 100% identity.
See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251
10436_at -55.1 A
non-annotated SAGE orf Found reverse in NC_001143 between 219769 and 219951 with 100% identity.
See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251
10437_at 1477.5 P
non-annotated SAGE orf Found reverse in NC_001143 between 264148 and 264333 with 100% identity.
See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251
10438_at 148.2 A
non-annotated SAGE orf Found reverse in NC_001143 between 308237 and 308389 with 100% identity.
See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251
10439_at 1005.3 P
non-annotated SAGE orf Found forward in NC_001143 between 308848 and 309084 with 100% identity.
See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251
10440_at 363.9 P
non-annotated SAGE orf Found reverse in NC_001143 between 340484 and 340771 with 100% identity.
See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251
10441_at 61.7 A
non-annotated SAGE orf Found reverse in NC_001143 between 468524 and 468670 with 100% identity.
See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251
10396_at 120.3 A
non-annotated SAGE orf Found reverse in NC_001143 between 468759 and 468899 with 100% identity.
See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251
10397_at -213.1 A
non-annotated SAGE orf Found reverse in NC_001143 between 527004 and 527159 with 100% identity.
See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251
10398_at -236.0 A

non-annotated SAGE orf Found forward in NC_001143 between 533255 and 533518 with 100% identity.
See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251
10399_at 31.0 A
non-annotated SAGE orf Found reverse in NC_001143 between 137683 and 137847 with 100% identity.
See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251
10400_at 22.4 A
non-annotated SAGE orf Found forward in NC_001143 between 173981 and 174175 with 100% identity.
See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251
10401_at 317.7 P
non-annotated SAGE orf Found reverse in NC_001143 between 185056 and 185205 with 100% identity.
See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251
10402_at 727.8 P
non-annotated SAGE orf Found forward in NC_001143 between 219794 and 219961 with 100% identity.
See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251
10403_at -68.0 A
non-annotated SAGE orf Found reverse in NC_001143 between 442457 and 442639 with 100% identity.
See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251
10404_at 478.5 P
non-annotated SAGE orf Found reverse in NC_001143 between 447932 and 448156 with 100% identity.
See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251
10405_at 261.3 P
non-annotated SAGE orf Found forward in NC_001143 between 456740 and 456883 with 100% identity.
See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251
10406_at 2164.4 P
non-annotated SAGE orf Found forward in NC_001143 between 619142 and 619375 with 100% identity.
See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251
10407_at 207.6 P
snRNA
10408_at 1880.3 P
snRNA
10409_at 3242.1 P
snRNA
10410_at 661.5 A
snRNA
10411_f_at 381.5 P
Growth INhibitory protein
10412_f_at 1876.1 P
strong similarity to members of the Srp1/Tip1p family
10413_at 900.9 P
transacetylase
10414_at 270.6 P
weak similarity to M.leprae metH2 protein
10415_at 163.9 P
strong similarity to amino acid transport protein Gap1p
10416_at 865.1 P
Glutathione transferase
10417_at 3.2 A
hypothetical protein
10418_at 1481.7 P
similarity to N.crassa O-succinylhomoserine (thiol)-lyase
10373_at 38.7 A
similarity to E.coli dioxygenase
10374_at 852.7 P
weak similarity to Y.pseudotuberculosis CDP-3,6-dideoxy-D-glycero-L-glycero-4-hexulose-5-epimerase
10375_at 597.4 P
similarity to Dal5p

10376_at	1131.3	P
similarity to transcription factor Pip2p
10377_at	4155.1	P
similarity to water channel proteins
10378_at	2516.4	P
member of mip family transmembrane channels
10379_at	882.4	P
similar to FRE2
10380_at	12785.8	P
Cofilin, actin binding and severing protein
10381_at	525.8	P
hypothetical protein
10382_at	9820.3	P
yeast bile transporter, similar to mammalian bile transporter
10383_at	638.5	A
questionable ORF
10384_at	183.6	A
ribonucleoprotein 1
10385_i_at	19291.4	P
Ribosomal protein L8B (L4B) (rp6) (YL5)
10386_s_at	15009.8	P
Ribosomal protein L8B (L4B) (rp6) (YL5)
10387_at	458.7	P
questionable ORF
10388_at	3651.8	P
Suppressor of tps1\/fdp1 and member of the MIP family of transmembrane channels\; may be involved in glycerol efflux
10389_at	746.5	P
hypothetical protein
10390_at	4739.0	P
Succinate dehydrogenase (ubiquinone) iron-sulfur protein subunit
10391_at	3816.2	P
involved in regulating membrane traffic
10392_at	1557.9	P
ubiquitin
10393_at	701.3	P
weak similarity to YJR125c and YDL161w
10394_at	90.3	A
weak similarity to human platelet-activating factor receptor
10395_at	2367.9	P
RNA splicing factor
10351_at	719.5	P
hypothetical protein
10352_at	5734.8	P
similarity to mammalian valosin
10353_at	301.3	P
hypothetical protein
10354_at	771.8	P
hypothetical protein
10355_at	4446.7	P
similarity to hypothetical protein YJL062w
10356_at	-224.4	A
hypothetical protein
10357_at	2642.8	P
similarity to M.jannaschii X-Pro dipeptidase and S.pombe hypothetical protein
10358_at	9163.6	P

similarity to multidrug resistance proteins
10359_at 3131.6 P
similarity to H.influenzae and E.coli hypothetical proteins
10360_at 5179.5 P
heat shock protein 104
10361_f_at 37.2 A
strong similarity to members of the Srp1p/Tip1p family
10362_at 7817.3 P
member of 70 kDa heat shock protein family
10363_at 7368.4 P
similarity to hypothetical protein YLR064w
10364_at 4459.7 P
Hat1 Interacting Factor 1
10365_at 3173.3 P
spindle pole antigen
10366_i_at 5170.0 P
questionable ORF
10367_r_at 4453.8 P
questionable ORF
10368_s_at 2939.6 P
questionable ORF
10369_at 358.9 P
protein kinase homolog
10370_at 12578.8 P
Aspartyl-tRNA synthetase, cytosolic
10371_at 33.2 A
maybe part of SCD25
10372_at 169.7 P
homologous to cdc25
10328_at 1120.8 P
similarity to metal resistance proteins
10329_at 5504.1 P
hypothetical protein
10330_at 1875.8 P
similarity to Drosophila pumilio protein
10331_at 5681.1 P
similarity to triacylglycerol lipases
10332_at 6242.6 P
56 kDa nucleolar snRNP protein that shows homology to beta subunits of G-proteins and the splicing factor Prp4
10333_at 2849.2 P
strong similarity to hypothetical protein YLR019w
10334_at 3721.1 P
cysteine-rich cytoplasmic protein
10335_at 2986.2 P
putative ATP dependent RNA helicase
10336_at 275.8 P
hypothetical protein
10337_at 1753.8 P
mitochondrial outer membrane protein
10338_at 240.7 A
similarity to A.thaliana hyp1 protein
10339_at 1367.2 P
Third subunit of the origin recognition complex
10340_at 691.9 P
protein of unknown function

10341_at	1530.7	P	Killed in Mutagen, sensitive to diepoxybutane and\/or mitomycin C
10342_at	1626.5	P	Dynamin-related protein
10343_at	1135.6	P	hypothetical protein
10344_at	4464.0	P	similarity to hypothetical C. elegans protein
10345_at	3049.5	P	hypothetical protein
10346_at	608.2	P	similarity to allantoate transport protein
10347_at	5362.7	P	Component of RNA polymerase transcription factor TFIIH
10348_at	812.4	P	Two-component signal transducer that with Sln1p regulates osmosensing MAP kinase cascade(suppressor of sensor kinase)
10349_at	1180.5	P	hypothetical protein
10350_at	6179.1	P	similarity to hypothetical protein YNL328c
10305_at	7012.4	P	similarity to ribosomal protein L24.e.B
10306_at	629.2	A	weak similarity to Aquifex aeolicus adenylosuccinate synthetase
10307_at	1041.7	P	weak similarity to E.coli hypothetical 20.4 kDa protein
10308_at	-79.6	A	hypothetical protein
10309_at	-182.8	A	weak similarity to nitrogen regulatory proteins
10310_at	1018.6	P	zinc-finger transcription factor of the Zn(2)-Cys(6) binuclear cluster domain type
10311_at	582.0	P	weak similarity to S.pombe hypothetical protein SPBC13G1
10312_at	628.4	P	hypothetical protein
10313_at	5976.0	P	Protein that regulates ADH2 gene expression
10314_at	2260.2	P	hypothetical protein
10315_at	1668.6	P	strong similarity to YLL010c
10316_at	1687.5	P	similarity to triacylglycerol lipase
10317_at	1655.1	P	hypothetical protein
10318_at	1747.7	P	similarity to C.elegans and M.jannaschii hypothetical proteins
10319_at	6320.5	P	similarity to S.pombe hypothetical protein SPAC30D11.11
10320_at	1217.3	P	similarity to ubiquitin--protein ligase Ubr1p
10321_at	2697.9	P	involved in derepression of SUC2 in response to glucose limitation
10322_at	916.2	P	

Sed5p is a t-SNARE (soluble NSF attachment protein receptor) required in ER to Golgi transport.
10323_at 12250.3 P
aspartate aminotransferase, cytosolic
10324_at 6889.7 P
5-aminoimidazole-4-carboxamide ribonucleotide (AICAR) transformylase\/IMP cyclohydrolase
10325_at 12978.6 P
Ribosomal protein L15A (YL10) (rp15R) (L13A)
10326_g_at 12168.1 P
Ribosomal protein L15A (YL10) (rp15R) (L13A)
10327_at -259.6 A
hypothetical protein
10283_at 106.7 A
similarity to hypothetical protein YMR124w
10284_at 1421.9 P
putative ATPase\/DNA helicase
10285_at 991.1 P
hypothetical protein
10286_at 8068.9 P
strong similarity to SMF2 protein
10287_at 586.9 P
similarity to human mutL protein homolog
10288_at 2258.8 P
similarity to YIL089w
10289_f_at 2376.4 P
strong similarity to members of the Srp1p/Tip1p family
10290_at 10692.0 P
subunit VIb of cytochrome c oxidase
10291_at 1411.4 P
involved in transcription of ribosomal proteins and ribosomal RNA
10292_at 10252.4 P
weak similartity to hypothetical protein YIL011w
10293_at 190.1 P
questionable ORF
10294_at 1745.0 P
hypothetical protein
10295_at 9100.7 P
thioredoxin
10296_at 10523.4 P
pyruvate decarboxylase
10297_at 2087.3 P
May play a role in attachment, organization, and\/or dynamics of microtubule ends at the spindle pole body
10298_at 656.0 P
strong similarity to Rta1p and Rtm1p protein
10299_at 246.9 A
similarity to hypothetical protein YGL160w
10300_f_at 11914.5 P
Ribosomal protein S0B
10301_at 5881.8 A
Ribosomal protein S0B
10302_g_at 8312.2 P
Ribosomal protein S0B
10303_at 2440.4 P
hypothetical protein
10304_at 8050.8 P
weak similarity to human MAC30 C-terminus

10260_at 3271.0 P
similarity to human acidic 82 kDa protein
10261_at 1430.0 P
hypothetical protein
10262_at 51.8 A
hypothetical protein
10263_at 293.0 P
hypothetical protein
10264_at 3026.9 P
transcription factor, probable member of histone acetyltransferase SAGA complex
10265_at 10745.6 P
C-5 sterol desaturase
10266_at 1009.9 P
weak similarity to mouse alpha-mannosidase
10267_at 10168.5 P
serine hydroxymethyltransferase
10268_at 2683.8 P
suppressor of rna12/yme2
10269_at 9529.8 P
Phenylalanyl-tRNA synthetase, alpha subunit, cytoplasmic
10270_at 8316.3 P
Ribosomal protein L22A (L1c) (rp4) (YL31)
10271_at 584.4 P
questionable ORF
10272_at 1952.8 P
ser/thr protein kinase
10273_at 6319.4 P
weak similarity to Anopheles NADH-ubiquinone oxidoreductase, chain 4
10274_at 9265.3 P
hypothetical protein
10275_at 4736.1 P
signal peptidase subunit
10276_at 350.1 P
Involved in expression of mitochondrial COX1 by regulating translation of COX1 mRNA and by affecting transcription or stability of COX1 mRNAs
10277_at -109.9 P
hypothetical protein
10278_at 5318.4 P
mitochondrial elongation factor G-like protein
10279_at 711.0 P
strong similarity to sugar dehydrogenases
10280_at 4119.7 P
component of RNA polymerase II holoenzyme\/mediator complex, interacts with Sin4p, Gal11p, and a 50 kd polypeptide
10281_at 953.8 P
similarity to YFL042c, YFL043c, YDR326c and YHR080c
10282_at 1384.7 P
hypothetical protein
10238_at 6742.3 P
weak similarity to human zinc finger protein
10239_at 7523.7 P
Ribosomal protein L10\; Ubiquinol-cytochrome C reductase complex subunit VI requiring protein
10240_at 1439.8 P
questionable ORF
10241_at 1953.6 P
weak similarity to Xenopus RCC1 protein

10242_at 1716.6 P
necessary for vesicular transport from the ER to the Golgi complex
10243_at 1808.9 P
P40 inhibitor of Cdc28p-Clb5 protein kinase complex
10244_at 340.0 P
strong similarity to Emp47p
10245_at 149.9 A
galactose permease
10246_at 600.3 P
Suppressor of rad53 lethality
10247_at 11242.0 P
integral membrane protein\; p24a protein
10248_at 3809.3 P
weak similarity to S.pombe hypothetical protein SPAC6F6
10249_at 1962.2 P
Actin-related protein
10250_at 791.4 P
Smc4 protein, member of SMC family
10251_at 2508.5 P
hypothetical protein
10252_at 2868.0 P
Possible component of GPI:protein transamidase
10253_at 11404.2 P
strong similarity to alanine transaminases
10254_at 2437.3 P
Homolog of E. coli DnaJ, closely related to Ydj1p
10255_at 131.9 A
hypothetical protein
10256_at 1132.5 P
high affinity sulfate permease
10257_at 1014.9 P
vacuolar v-SNARE
10258_at 730.7 P
hypothetical protein
10259_at 4070.2 P
hypothetical protein
10215_at 3721.3 P
Serine\/threonine protein kinase
10216_at 541.9 P
hypothetical protein
10217_at 548.8 P
DNA-binding transcriptional activator or CHA1
10218_at 3257.0 P
similarity to YDR125c
10219_at 10319.7 P
similarity to rat ovarian specific protein
10220_at 401.7 P
questionable ORF
10221_at 444.7 P
subunit of the anaphase promoting complex (APC)
10222_at 1422.7 P
omosomal DNA replication initiation protein
10223_at 2463.6 P
hypothetical protein
10224_at 2993.8 P
tRNA splicing endonuclease subunit

10225_at	2921.3	P	similarity to Kaposi s sarcoma-associated herpes-like virus ORF73 homolog gene
10226_at	1077.0	P	similarity to Pan troglodytes prot GOR
10227_at	620.9	P	strong similarity to YDR132c
10228_at	11465.5	P	similarity to C.boidinii peroxisomal membrane protein 20K A
10229_at	727.2	A	strong similarity to Flo1p
10230_at	-272.0	A	hypothetical protein
10231_at	3887.4	P	hypothetical protein
10232_at	8944.9	P	mitogen-activated protein kinase (MAP kinase)
10233_at	1932.6	P	similarity to C.elegans hypothetical protein and YOR054c
10234_at	1184.5	P	Component of cleavage factor II (CF II)\; 105-kDa protein associated with polyadenylation factor 1 (PF I)
10235_at	2230.9	P	Branchpoint bridging protein -- component of the splicing commitment complex
10236_at	680.7	P	SYnthetic lethal with cdc40 (Forty)
10237_at	5050.1	P	similarity to several esterases
10192_at	438.5	P	suppressor of rna1-1 mutation
10193_at	6559.4	P	GPI-anchored aspartic protease
10194_at	5311.2	P	GPI-anchored aspartic protease
10195_at	20.3	A	hypothetical protein
10196_g_at	343.3	P	hypothetical protein
10197_at	289.5	P	questionable ORF
10198_at	432.0	P	hypothetical protein
10199_at	-80.3	A	hypothetical protein
10200_at	114.4	A	weak similarity to P.aeruginosa anthranilate synthase component II
10201_at	289.0	P	subunit of the anaphase promoting complex (APC)
10202_at	717.6	P	similarity to S.pombe hypothetical protein SPBC24E9
10203_at	5765.9	P	DOM34 Interacting Protein
10204_at	6469.9	P	Low-affinity zinc transport protein
10205_at	1767.3	P	zinc finger transcription factor
10206_at	646.4	P	hypothetical protein

10207_at	2586.1	P	choline kinase
10208_at	4901.4	P	pyruvate decarboxylase
10209_at	437.3	A	hypothetical protein
10210_at	177.3	A	zinc finger containing homolog of mammalian TIS11, glucose repressible gene
10211_at	1057.1	P	hypothetical protein
10212_at	1663.6	P	Putative Na+\/H+ antiporter
10213_at	435.1	P	73 kDa mitochondrial integral membrane protein
10214_at	99.0	A	questionable ORF
10170_g_at	5261.7	P	questionable ORF
10171_at	1268.9	P	transcription factor, member of UAF (upstream activation factor) along with Rrn9p and Rrn10p
10172_at	186.8	M	proline oxidase
10173_at	1477.8	P	weak similarity to Pyrococcus horikoshii hypothetical protein PHBJ017
10174_at	2749.0	P	Identified as an activity necessary for actin polymerization in permeabilized cells
10175_at	404.6	P	hypothetical protein
10176_at	1930.8	P	Spermine Synthase
10177_at	2286.5	P	encodes a core snRNP protein
10178_at	551.7	A	vacuolar membrane protein
10179_at	97.7	A	hypothetical protein
10180_at	12716.4	P	specific affinity for guanine-rich quadruplex nucleic acids
10181_at	515.8	P	weak similarity to A.thaliana hypothetical protein ATU78721
10182_at	1111.6	P	similarity to YOR3165w and YNL095c
10183_at	8445.3	P	acetyl-coenzyme A synthetase
10184_at	5095.3	P	hypothetical protein
10185_s_at	7989.7	P	nitrogen catabolite-regulated cell-wall L-asparaginase II
10186_s_at	101.8	A	identical to hypothetical proteins YLR161w and YLR159w
10187_at	4855.3	P	hypothetical protein
10188_at	3408.4	P	mitochondrial processing protease subunit
10189_at	647.0	A	strong similarity to Sdh4p

10190_at	526.7	P	weak similarity to H.influenzae hypothetical protein HI0176
10191_at	2078.8	P	100 kD component of the Exocyst complex\; required for exocytosis. The Exocyst complex contains the gene products encoded by SEC3, SEC5, SEC6, SEC8, SEC10, SEC15 and EXO70.
10147_at	11508.1	P	Ribosomal protein S31 (S37) (YS24)
10148_at	1949.9	P	probably involved in intramitochondrial protein sorting
10149_at	674.1	A	questionable ORF
10150_at	2498.6	P	clathrin-associated protein complex, small subunit
10151_at	498.9	P	questionable ORF
10152_at	7710.5	P	S-adenosylmethionine (AdoMet)-dependent methyltransferase of diphthamide biosynthesis
10153_at	160.7	A	hypothetical protein
10154_at	-2261.7	A	Cytosolic form of NADP-dependent isocitrate dehydrogenase
10155_at	10383.6	P	major low affinity 55 kDa Centromere\/microtubule binding protein
10156_at	1001.7	P	DNA binding protein, homologous to a family of mammalian RFX1-4 proteins which have a novel highly conserved DNA binding domain
10157_at	3094.4	P	similarity to suppressor protein Psp5p
10158_at	1906.2	P	suppressor of cdc25
10159_at	13002.3	P	similarity to Tfs1p
10160_at	8925.1	P	S-adenosylmethionine synthetase
10161_g_at	4723.3	A	S-adenosylmethionine synthetase
10162_at	947.9	P	hypothetical protein
10163_at	1449.6	P	regulatory protein
10164_at	1201.9	P	similarity to YDR501w
10165_at	667.3	P	weak similarity to ribulose-bisphosphate carboxylase
10166_at	597.2	A	60S ribosomal protein L37A (L43) (YL35)
10167_at	7853.4	P	strong similarity to S.pombe hypothetical protein C18G6.07C
10168_at	955.2	P	similarity to hypothetical protein YNL278w
10169_at	7425.4	P	ATP-binding cassette (ABC) transporter family member
10124_at	2478.3	P	similarity to P.aeruginosa rhamnosyltransferase 1 chain B
10125_at	2870.6	P	hypothetical protein

10126_at	665.8	P	Peroxisomal membrane protein that contains Src homology 3 (SH3) domain
10127_at	11179.0	P	weak similarity to fruit fly transcription factor 5 large chain
10128_at	1707.1	P	similarity to G.gallus px19 and Msf1p
10129_at	5440.2	P	hypothetical protein
10130_at	4687.7	P	N-myristoyl transferase
10131_at	9302.6	P	Protein with periodic trytophan residues that resembles members of beta-transducin superfamily because of presence of WD-40 repeats
10132_at	8719.8	P	homology to microtubule binding proteins and to X90565_5.cds
10133_at	1374.1	P	questionable ORF
10134_at	2589.5	P	hypothetical protein
10135_at	2959.0	P	Polypeptide 6 of a Yeast Non-native Actin Binding Complex, homolog of a component of the bovine NABC complex
10136_at	2750.9	P	similarity to hypothetical S. pombe protein
10137_at	625.9	P	questionable ORF
10138_g_at	731.0	P	questionable ORF
10139_i_at	14027.0	P	questionable ORF
10140_r_at	7265.5	P	questionable ORF
10141_at	6713.6	P	Protein involved in maturation of COX1 and COB mRNA
10142_at	3805.1	P	protein of unknown function
10143_at	5149.0	P	hypothetical protein
10144_at	4247.8	P	similarity to human tricohyalin and protein KIAA0171
10145_at	770.7	P	HMG-CoA Reductase Degradation
10146_at	10580.7	P	cytoplasmic protein involved in release of transport vesicles from the ER
10101_at	3744.2	P	strong similarity to purine-nucleoside phosphorylases
10102_at	1190.4	P	G(sub)2-specific B-type cyclin
10103_at	691.4	P	hypothetical protein
10104_at	1733.3	P	gamma tubulin-like protein, interacts with Spc98p and Spc97p, the Tub4p-Spc98p-Spc97p complex may be part of the microtubule attachment site at the spindle pole body
10105_at	580.8	P	similarity to UTR2 protein
10106_at	9017.8	P	

Ferric (and cupric) reductase
10107_at 1413.1 P
strong similarity to rat cell cycle progression related D123 protein
10108_at 11742.2 P a
cyclophilin related to the mammalian CyP-40\; physically interacts with RPD3 gene product
10109_at 311.1 A
questionable ORF
10110_at 1013.4 P
hypothetical protein
10111_at 1792.6 P
hypothetical protein
10112_at 1547.8 P
Possible transmembrane Ca2+ transporter
10113_at 4360.5 P
hypothetical protein
10114_at 4124.5 P
similarity to Dip2p
10115_at 2400.4 P
has a weak RNA-dependent ATPase activity which is not specific for rRNA
10116_at 1439.6 P
hypothetical protein
10117_at 3519.9 P
strong similarity to YDR222w
10118_at 2160.1 P
hypothetical protein
10119_at -26.6 A
hypothetical protein
10120_at 2437.8 P
strong similarity to YDR213w, weak similarity to Lys14p
10121_at 13786.1 P
member of the Rho subfamily of Ras-like proteins
10122_at 213.7 P
questionable ORF
10123_at 1917.2 P
strong similarity to rat kynureninase
10079_at 156.6 A
questionable ORF
10080_at 319.0 A
Telomere elongation protein (ever shorter telomeres)
10081_at 266.7 P
DNA Topoisomerase III
10082_at 432.3 P
questionable ORF
10083_g_at 171.2 A
questionable ORF
10084_at 1056.7 A
hypothetical protein
10085_at 3619.4 P
thiamine transporter
10086_at 1166.5 P
similarity to YDR200c
10087_at 1329.0 P
weak similarity to H.influenzae lipoate biosynthesis protein B
10088_at 3230.3 P
phosphatidylinositol 3-kinase
10089_at 1618.5 P

similarity to hypothetical S.pombe protein SPAC2G11.09
10090_at 462.6 P
weak similarity to C.elegans R05H5.5 protein and Nup120p
10091_at 5980.6 P
strong similarity to YOR262w
10092_at 3393.1 P
methionine aminopeptidase
10093_at 1376.4 P
strong similarity to B.subtilis cytidine deaminase
10094_at 1714.5 P
similarity to human DHHC-domain-containing cysteine-rich protein
10095_at 1654.9 P
similarity to S.pombe rad8 protein and Rdh54p
10096_at 7384.2 P
Serine\/threonine protein kinase
10097_at 9481.8 P
EF-3 (translational elongation factor 3)
10098_at 2923.8 P
secretory protein
10099_at -78.0 P
similarity to peroxisomal rat membrane protein PMP22
10100_at 411.8 P
questionable ORF
10055_at 1293.1 P
weak similarity to bacterial aminoglycoside acetyltransferase regulators
10056_at 893.8 P
hypothetical protein
10057_at 374.5 P
hypothetical protein
10058_at 1690.2 P
zinc-finger transcription factor of the Zn(2)-Cys(6) binuclear cluster domain type
10059_at 3665.5 P
hypothetical protein
10060_at 1031.1 P
Glycogen synthase (UDP-gluocse--starch glucosyltransferase)
10061_at 8613.9 P
heat shock protein 60\; chaperonin protein
10062_at 2222.0 P
sphingoid long chain base (LCB) kinase
10063_i_at 610.9 P
questionable ORF
10064_s_at 1762.5 P
questionable ORF
10065_at 465.9 P
highly homologous to the human GTPase, Rab6
10066_s_at 2638.2 P
strong similarity to F49C12.11 (Z68227_K) from C. elegans
10067_at 308.5 A
Meiosis-specific protein involved in homologous chromosome synapsis and chiasmata formation\; localizes to chromosome cores independently of Mei4p and Spo11p\; mRNA is induced in meiosis
10068_i_at 14084.3 P
Ribosomal protein S28B (S33B) (YS27)
10069_f_at 7334.8 P
Ribosomal protein S28B (S33B) (YS27)
10070_at 86.1 P
hypothetical protein

10071_at 517.6 P
weak similarity to transcription factors
10072_at -6.4 A
Bypass of PAM1
10073_at 3138.8 P
Synaptobrevin (v-SNARE) homolog present on ER to Golgi vesicles
10074_at -35.1 A
questionable ORF
10075_at 2479.5 P
strong similarity to YOR173w
10076_at 365.0 P
hypothetical protein
10077_at 1100.4 P
similarity to human hypothetical ORF
10078_at 252.0 A
Protein similar to Gac1p, a putative type 1 protein phosphatase targeting subunit
10032_at 451.4 P
Member of complex that acts at ARS s to initiate replication
10033_at 1102.0 P
U1 snRNP protein of the Sm class
10034_at 6466.5 P
DEAD-Box Protein 9
10035_at 2518.6 P
subunit of Polyadenylation factor I (PF I)
10036_at 813.5 P
weak similarity to regulatory proteins
10037_at 1577.8 A
questionable ORF
10038_i_at 1521.2 P
questionable ORF
10039_s_at 168.8 A
questionable ORF
10040_at 186.1 A
similarity to polypeptide chain release factors
10041_at 544.8 A
questionable ORF
10042_at 278.8 P
weak similarity to Smc2p
10043_at 202.4 A
Peroxisomal enoyl-CoA hydratase
10044_at 4576.1 P
hypothetical protein
10045_at 17355.1 P
Endochitinase
10046_at 580.4 P
weak similarity to S.pombe hypothetical protein SPAC22E12
10047_f_at 10483.9 P
Ribosomal protein S30A
10048_at 861.5 P
involved in checkpoint control and DNA repair
10049_at 613.5 P
GTPase
10050_at 2397.7 P
hypothetical protein
10051_at 8346.1 P
translation initiation factor eIF2b, 43 kDa subunit\; negative regulator of GCN4 expression

10052_at	5341.8	P	protein involved in membrane protein insertion into the ER
10053_at	12640.3	P	GTP-binding protein
10054_at	8000.7	P	questionable ORF
10010_at	6232.9	P	ATP synthase subunit h
10011_at	200.7	P	hypothetical protein
10012_at	1065.3	P	weak similarity to Vibrio vulnificus VvpC protein
10013_at	387.0	P	U1 snRNP protein required for pre-mRNA splicing
10014_at	2243.3	P	gamma-glutamyltransferase homolog
10015_at	10205.2	P	Exo-1,3-beta-glucanase
10016_at	7849.0	P	hypothetical protein
10017_at	-191.1	A	questionable ORF
10018_at	11843.3	P	O-Acetylhomoserine-O-Acetylserine Sulfhydralase
10019_at	11256.1	P	Aconitase, mitochondrial
10020_at	3944.9	P	encodes a phosphatidylinositol-4-kinase, homologous to VPC34
10021_at	767.2	P	Ubiquitin-conjugating enzyme
10022_at	-154.3	A	Chitin Deacetylase
10023_at	-305.0	A	Chitin Deacetylase
10024_at	4205.1	P	similarity to human centromere protein E
10025_at	701.3	P	regulatory protein of adenylate cyclase
10026_at	-302.4	A	weak similarity to S.tarentolae cryptogene protein G4
10027_at	33.2	A	hypothetical protein
10028_at	662.1	A	homologous to Spa2p, localizes to sites of polarized growth
10029_at	1068.3	P	Component of 10 nm filaments of mother-bud neck
10030_at	229.0	A	weak similarity to rat apolipoprotein A-IV
10031_at	3193.5	P	weak similarity to H.influenzae hypothetical protein HI0906
9986_at	1106.6	P	questionable ORF
9987_at	197.4	P	103 kD basic protein, catalytic subunit of telomerase
9988_at	1263.8	P	Actin Interacting Protein

9989_at 805.4 P

hypothetical protein

9990_at 2793.9 P

homolog of Snf5p, member of the chromatin remodeling complex, RSC

9991_at 253.9 A

questionable ORF

9992_at 933.7 P

weak similarity to N.crassa uvs2 protein

9993_at 197.9 A

strong similarity to YGR004w

9994_at 9949.3 P

Ribosomal protein L38

9995_at 1679.0 P

hypothetical protein

9996_at 323.2 P

strong similarity to Stf2p

9997_at 5052.6 P

strong similarity to YGR010w

9998_at -85.3 A

23 kDa protein containing a putative leucine zipper\; meiosis specific recombination protein\; mRNA is induced early in sporulation

9999_at 3915.7 P

Involved in chitin synthase III activity, also required for homozygosis in the first stages of mating

10000_at -2.1 A

questionable ORF

10001_at 4381.4 P

Protein required for mating

10002_i_at 14668.7 P

Ribosomal protein S25B (S31B) (rp45) (YS23)

10003_f_at 12572.5 P

Ribosomal protein S25B (S31B) (rp45) (YS23)

10004_at 55.0 A

questionable ORF

10005_at 4210.9 P

nuclear pore complex protein with central repetitive domain similar to that of NSP1 and NUP1

10006_at 2812.5 P

Suppressor of Glycerol Defect

10007_at 4176.2 P

Proline-rich protein verprolin

10008_at -203.4 A

questionable ORF

10009_at 42.9 A

questionable ORF

9964_at 3471.8 A

60S ribosomal protein P0 (A0) (L10E)

9965_at 27.6 A

hypothetical protein

9966_at 9738.3 P

1,3-beta-D-glucan synthase

9967_at 394.9 P

strong similarity to Gas1p and C.albicans pH responsive protein

9968_s_at 6109.9 P

Ribosomal protein L26A (L33A) (YL33)

9969_at 1488.4 P

similarity to Pfk26p and other 6-phosphofructo-2-kinases

9970_at 817.4 P

```
weak similarity to YGR035c
9971_at     2882.6      P
95 kDa structural and functional homolog of vertebrate karyopherin beta (importin 90)
9972_at     9313.5      P
mitochondrial dicarboxylate transport protein
9973_at     979.1       P
questionable ORF
9974_at     10573.5     P
strong similarity to YGR038w
9975_at     10262.2     P
Nit3 nitrilase
9976_at     1326.4      P
hypothetical protein
9977_at     2645.3      P
budding protein
9978_at     10750.0     P
Transaldolase, enzyme in the pentose phosphate pathway
9979_at     11836.2     P
acetohydroxyacid reductoisomerase
9980_at     1217.6      P
similarity to SCM4 protein
9981_at     664.4       P
questionable ORF
9982_at     2754.3      P
Member of RSC complex.
9983_at     8419.3      P
Adenylosuccinate Lyase
9984_at     225.6       P
protein involved in vacuolar sorting
9985_at     1847.3      P
similarity to YOR3329c
9941_at     1380.5      P
Ser\/Thr protein kinase\; MEKK homolog
9942_at     449.0       P
putative Upf1p-interacting protein
9943_at     1606.9      P
hypothetical protein
9944_at     112.5       P
weak similarity to Udf2p
9945_at     -41.5       A
hypothetical protein
9946_at     8693.6      P
Ribosomal protein S22B (S24B) (rp50) (YS22)
9947_i_at   19105.2     P
Ribosomal protein S22B (S24B) (rp50) (YS22)
9948_f_at   11468.5     P
Ribosomal protein S22B (S24B) (rp50) (YS22)
9949_at     1811.2      P
hypothetical protein
9950_at     940.7       P
Hsp70 protein
9951_at     3215.7      P
Arp2\/3 Complex Subunit
9952_at     2145.9      P
GDP-GTP Exchange Protein (GEP) for the Rho1p Small GTP-binding Protein\; high copy suppressor of
cik1 and kar3 deletion mutants.
```

9953_at 11893.4 P
required for conversion of 24-carbon fatty acids to 26-carbon species
9954_at 3732.1 P
similarity to hypothetical protein YGR071c
9955_at 306.0 A
questionable ORF
9956_at 4319.3 P
Involved in pre-tRNA splicing and in uptake of branched-chain amino acids
9957_at 753.8 P
hypothetical protein
9958_at 186.5 A
fructose-1,6-bisphosphatase
9959_at 11903.6 P
membrane component of ER protein translocation apparatus
9960_at -118.9 A
questionable ORF
9961_at 5218.0 P
weak similarity to SEC14 protein
9962_at 545.2 P
hypothetical protein
9963_at 2161.8 P
mitochondrial leucyl tRNA synthetase
9918_at 1576.6 P
Protein involved in recombination repair, homologous to S. pombe rad18
9919_at 6495.3 P
confers sensitivity to killer toxin
9920_at 173.9 P
hypothetical protein
9921_at 1779.8 P
similarity to hypothetical S. pombe protein
9922_at 4467.4 P
similarity to YBR267w
9923_f_at 8583.9 P
Ribosomal protein S29A (S36A) (YS29)
9924_at 1870.6 P
protease involved in a-factor processing
9925_at 2963.1 P
ExtraCellular Mutant
9926_at 10210.1 P
Secretory Stress Response protein 1
9927_at 318.0 P
hypothetical protein
9928_at 710.9 P
essential for assembly of a functional mitochondrial ATPase complex
9929_at 534.1 P
weak similarity to chicken RING zinc finger protein
9930_at 8859.0 P
Cytochrome-c oxidase chain VIII
9931_at 1215.2 P
Vacuolar sorting protein essential for vacuolar morphogenesis and function
9932_at 4581.7 P
homology to the CDC48 gene product
9933_at 4245.1 P
antiviral protein, putative helicase
9934_at 2743.8 P
Bdf1p contains two bromodomains, localizes to the nucleus and to chomosomes in spread meiotic nuclei

but is excluded from the nucleolus
9935_at 260.6 P
hypothetical protein
9936_at 2788.4 P
similarity to A.brasilense nifR3 protein
9937_at 1633.8 P
hypothetical protein
9938_at 1010.3 P
split zinc finger protein
9939_at 986.0 A
hypothetical protein
9940_at 2077.5 P
similarity to A.brasilense nifR3 protein
9895_i_at 8892.5 P
Ribosomal protein L31B (L34B) (YL28)
9896_f_at 9294.9 P
Ribosomal protein L31B (L34B) (YL28)
9897_f_at 18676.6 P
Ribosomal protein L31B (L34B) (YL28)
9898_at 1346.8 P
hypothetical protein
9899_at 713.6 P
hypothetical protein
9900_at 5495.1 P
strong similarity to S. pombe beta-transducin
9901_at 5137.4 P
Homologous to S. pombe asp1+
9902_at 8904.6 P
Copper Transporter
9903_at 2229.7 P
weak similarity to Candida maltosa cytochrome P450
9904_at 5193.5 P
strong similarity to YKL187c
9905_at 9007.4 P
weak similarity to YLR413w
9906_at -323.0 A
questionable ORF
9907_at 174.7 P
hypothetical protein
9908_at 451.9 P
defective in vacuolar protein sorting
9909_at 6130.3 P
Accessory factor associated with RNA polymerase II by affinity chromatography
9910_at 2682.2 P
similarity to helicases
9911_at 11297.8 P
dihydrooratase
9912_at 8924.1 P
weak similarity to human 42K membrane glycoprotein
9913_at 3498.7 P
similarity to human DOCK180 protein
9914_at 325.3 P
hypothetical protein
9915_at 164.8 P
weak similarity to Stu1p
9916_at 1086.2 P

hypothetical protein
9917_at 4631.8 P
weak similarity to 3-oxoacyl-[acyl-carrier-protein] reductase from E. coli
9873_at 596.8 P
weak similarity to 3-oxoacyl-[acyl-carrier-protein] reductase from E. coli
9874_at 3342.6 P
weak similarity to human transcription regulator Staf-5
9875_at 1048.0 P
questionable ORF
9876_at 4558.2 P
has homology to the Dictyostelium and human actin-binding protein coronin
9877_at 2146.6 P
component of a nuclear-localized tRNA splicing complex
9878_at 179.0 P
weak similarity to rabbit trichohyalin
9879_f_at 10618.3 P
strong similarity to IMP dehydrogenases, Pur5p and YML056c
9880_at 4419.7 P
Calcineurin subunit A\; type 2B protein serine\/threonine phosphatase catalytic subunit A1\; cytoplasmic
9881_at 3233.3 P
questionable ORF
9882_at 2277.5 P
hypothetical protein
9883_at 1926.4 P
ExtraCellular Mutant
9884_at 2408.7 P
hypothetical protein
9885_at 5790.5 P
ornithine aminotransferase
9886_at 6137.4 P
Putative snRNP protein containing Sm-like domain\; coprecipitates with U4, U5 and U6 snRNAs
9887_at 3815.6 P
Mitochondrial 60S ribosomal protein L4
9888_at 1793.4 P
hypothetical protein
9889_i_at 10567.6 P
Ribosomal protein S1A (rp10A)
9890_s_at 8257.0 P
Ribosomal protein S1A (rp10A)
9891_at 1674.5 P
regulator of silent mating loci
9892_at 1823.0 P
ExtraCellular Mutant
9893_at 204.0 P
questionable ORF
9894_at 14.5 A
hypothetical protein
9850_at 154.2 A
weak similarity to hexokinases
9851_at 8960.6 P
36 kDa subunit (D subunit of VO sector) of the vacuolar H(+) ATPase\; required for assembly
9852_at 10166.4 P
60S ribosomal subunit protein L6B (L17B) (rp18) (YL16)
9853_at 7401.9 P
60 kDa nuclear FK506 binding protein
9854_at 4826.4 P

3-hydroxy-3-methylglutaryl-coenzyme A (HMG-CoA) reductase isozyme
9855_at 742.8 P
zinc-finger transcription factor of the Zn(2)-Cys(6) binuclear cluster domain type
9856_at 6039.9 P
Protein involved in desensitization to alpha-factor pheromone
9857_at 237.6 P
Nuclear protein
9858_at 2705.3 P
similarity to YPR117w
9859_at 2022.2 P
weak similarity to human G/T mismatch binding protein
9860_at 733.4 P
strong similarity to YPR172w
9861_at 377.2 P
Nap1p-binding protein
9862_at -68.9 A
questionable ORF
9863_at 3894.0 P
cell division control protein
9864_at 257.2 A
similarity to C.carbonum toxD protein
9865_f_at 1437.1 P
member of the seripauperin protein\/gene family (see Gene_class PAU)
9866_i_at 483.7 M
questionable ORF
9867_s_at 431.2 P
questionable ORF
9868_at 1516.3 P
hypothetical protein identified by SAGE
9869_at 4700.0 P
identified by SAGE
9870_s_at 1867.8 P
Mitochondrial ribosomal protein MRPL15 (YmL15)
9871_at 1140.7 P
non-annotated SAGE orf Found forward in NC_001144 between 230974 and 231108 with 100% identity. See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251
9872_at 967.7 A
non-annotated SAGE orf Found forward in NC_001144 between 320496 and 320642 with 100% identity. See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251
9826_at 1237.4 P
non-annotated SAGE orf Found forward in NC_001144 between 341326 and 341589 with 100% identity. See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251
9827_at 2358.7 P
non-annotated SAGE orf Found forward in NC_001144 between 433871 and 434059 with 100% identity. See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251
9828_at 1690.5 P
non-annotated SAGE orf Found forward in NC_001144 between 449727 and 449897 with 100% identity. See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251
9829_at 1590.3 P
non-annotated SAGE orf Found forward in NC_001144 between 449825 and 449998 with 100% identity. See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251
9830_at 352.1 P
non-annotated SAGE orf Found forward in NC_001144 between 449919 and 450077 with 100% identity. See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251
9831_at 181.1 P
non-annotated SAGE orf Found forward in NC_001144 between 603628 and 603825 with 100% identity.

See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251
9832_at -200.4 A
non-annotated SAGE orf Found reverse in NC_001144 between 789953 and 790117 with 100% identity.
See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251
9833_at 25.1 A
non-annotated SAGE orf Found reverse in NC_001144 between 867146 and 867343 with 100% identity.
See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251
9834_at 419.9 A
non-annotated SAGE orf Found forward in NC_001144 between 92566 and 92730 with 100% identity.
See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251
9835_at 5931.4 P
non-annotated SAGE orf Found forward in NC_001144 between 198937 and 199176 with 100% identity.
See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251
9836_at 12439.0 P
non-annotated SAGE orf Found forward in NC_001144 between 199191 and 199331 with 100% identity.
See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251
9837_s_at 6091.0 P
non-annotated SAGE orf Found forward in NC_001144 between 451607 and 451783 with 100% identity.
See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251
9838_s_at 9194.8 P
non-annotated SAGE orf Found forward in NC_001144 between 453992 and 454132 with 100% identity.
See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251
9839_s_at 6861.8 P
non-annotated SAGE orf Found forward in NC_001144 between 455884 and 456024 with 100% identity.
See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251
9840_f_at -69.3 A
non-annotated SAGE orf Found reverse in NC_001144 between 596345 and 596530 with 100% identity.
See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251
9841_at 193.8 P
non-annotated SAGE orf Found forward in NC_001144 between 687338 and 687550 with 100% identity.
See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251
9842_at 2969.7 P
non-annotated SAGE orf Found reverse in NC_001144 between 849381 and 849677 with 100% identity.
See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251
9843_at 55.2 A
non-annotated SAGE orf Found reverse in NC_001144 between 906354 and 906650 with 100% identity.
See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251
9844_at 8193.4 P
non-annotated SAGE orf Found reverse in NC_001144 between 52940 and 53083 with 100% identity.
See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251
9845_at 3483.2 P
non-annotated SAGE orf Found reverse in NC_001144 between 121784 and 121936 with 100% identity.
See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251
9846_at 62.4 A
non-annotated SAGE orf Found reverse in NC_001144 between 228693 and 228839 with 100% identity.
See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251
9847_at 2667.6 P
non-annotated SAGE orf Found forward in NC_001144 between 371240 and 371515 with 100% identity.
See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251
9848_at 289.7 P
non-annotated SAGE orf Found forward in NC_001144 between 373195 and 373335 with 100% identity.
See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251
9849_at 1672.5 P
non-annotated SAGE orf Found forward in NC_001144 between 390278 and 390421 with 100% identity.
See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251
9804_at 941.7 P

non-annotated SAGE orf Found forward in NC_001144 between 441497 and 441667 with 100% identity. See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251
9805_at 660.5 P
non-annotated SAGE orf Found reverse in NC_001144 between 576670 and 576804 with 100% identity. See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251
9806_at 9634.2 P
non-annotated SAGE orf Found reverse in NC_001144 between 578108 and 578263 with 100% identity. See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251
9807_at 861.8 A
non-annotated SAGE orf Found reverse in NC_001144 between 669739 and 669894 with 100% identity. See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251
9808_at 77.7 P
non-annotated SAGE orf Found reverse in NC_001144 between 708168 and 708338 with 100% identity. See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251
9809_at -31.3 A
non-annotated SAGE orf Found forward in NC_001144 between 787418 and 787570 with 100% identity. See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251
9810_at 530.0 A
non-annotated SAGE orf Found forward in NC_001144 between 789869 and 790012 with 100% identity. See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251
9811_at 476.3 P
non-annotated SAGE orf Found reverse in NC_001144 between 315877 and 316053 with 100% identity. See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251
9812_at 299.4 P
non-annotated SAGE orf Found reverse in NC_001144 between 13652 and 13819 with 100% identity. See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251
9813_at 575.4 P
non-annotated SAGE orf Found reverse in NC_001144 between 223615 and 223821 with 100% identity. See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251
9814_at 134.3 P
non-annotated SAGE orf Found forward in NC_001144 between 293858 and 294037 with 100% identity. See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251
9815_at 295.9 P
non-annotated SAGE orf Found reverse in NC_001144 between 368522 and 368710 with 100% identity. See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251
9816_s_at 1647.5 P
non-annotated SAGE orf Found forward in NC_001144 between 458168 and 458302 with 100% identity. See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251
9817_at 575.1 P
non-annotated SAGE orf Found reverse in NC_001144 between 460511 and 460774 with 100% identity. See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251
9818_at -43.6 A
non-annotated SAGE orf Found forward in NC_001144 between 677930 and 678073 with 100% identity. See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251
9819_at 172.0 M
non-annotated SAGE orf Found reverse in NC_001144 between 884820 and 884975 with 100% identity. See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251
9820_s_at 2236.9 P
non-annotated SAGE orf Found forward in NC_001144 between 288 and 461 with 100% identity. See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251
9821_at -98.3 A
non-annotated SAGE orf Found reverse in NC_001144 between 156565 and 156759 with 100% identity. See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251
9822_at 227.6 A
non-annotated SAGE orf Found forward in NC_001144 between 171853 and 172017 with 100% identity. See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251

9823_at	7524.3	P

non-annotated SAGE orf Found reverse in NC_001144 between 185211 and 185492 with 100% identity. See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251

9824_at	3775.1	P

non-annotated SAGE orf Found reverse in NC_001144 between 388262 and 388474 with 100% identity. See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251

9825_s_at	844.7	P

non-annotated SAGE orf Found reverse in NC_001144 between 468959 and 469195 with 100% identity. See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251

9779_at	456.4	A

non-annotated SAGE orf Found forward in NC_001144 between 514745 and 514888 with 100% identity. See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251

9780_at	763.3	P

non-annotated SAGE orf Found forward in NC_001144 between 573921 and 574148 with 100% identity. See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251

9781_at	41.7	A

non-annotated SAGE orf Found reverse in NC_001144 between 658663 and 658803 with 100% identity. See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251

9782_at	-145.2	A

non-annotated SAGE orf Found forward in NC_001144 between 672894 and 673055 with 100% identity. See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251

9783_at	1316.4	P

non-annotated SAGE orf Found forward in NC_001144 between 710795 and 710935 with 100% identity. See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251

9784_at	723.1	P

non-annotated SAGE orf Found reverse in NC_001144 between 712124 and 712291 with 100% identity. See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251

9785_at	850.0	P

non-annotated SAGE orf Found forward in NC_001144 between 949308 and 949442 with 100% identity. See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251

9786_at	1276.5	P

non-annotated SAGE orf Found forward in NC_001144 between 949499 and 949633 with 100% identity. See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251

9787_at	5728.9	P

non-annotated SAGE orf Found forward in NC_001144 between 964875 and 965030 with 100% identity. See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251

9788_at	666.5	P

non-annotated SAGE orf Found forward in NC_001144 between 988140 and 988277 with 100% identity. See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251

9789_at	1298.8	P

non-annotated SAGE orf Found forward in NC_001144 between 1035773 and 1035940 with 100% identity. See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251

9790_i_at	-47.9	A

Centromere

9791_f_at	-18.8	A

Centromere

9792_s_at	1791.7	P

CEN12-associated

9793_at	351.7	P

snRNA

9794_at	4877.4	P

snRNA

9795_at	4980.7	P

snRNA

9796_at	1508.3	P

snRNA
9797_i_at 513.7 P
snRNA
9798_at 8372.3 P
snRNA
9799_at 1254.8 P
snRNA
9800_s_at 1745.4 A
hypothetical protein Y .2
9801_at 460.1 P
similarity to human leukotriene b4 12-hydroxydehydrogenase
9802_at 3080.0 P
required for protein disulfide bond formation in the ER
9803_at 3707.3 P
mitochondrial membrane protein
9757_at 724.4 P
C-terminal part starting with aa 262 cause growth inhibition when overexpressed
9758_at 7364.5 P
weak similarity to Los1p
9759_at 10747.1 P
Hydroxymethylglutaryl-CoA Synthase
9760_at 7363.1 P
strong similarity to cytochrome-b5- and nitrate reductases
9761_at 9041.2 P
alpha-tubulin
9762_at 11694.6 P
inorganic phosphate transporter, transmembrane protein
9763_at 47.3 A
hypothetical protein
9764_at 4619.8 P
Putative small GTPase
9765_at 3100.2 P
mitochondrial NADH ubiquinone 6 oxidoreductase
9766_at 614.2 P
hypothetical protein
9767_at 57.6 A
similarity to YMR285c
9768_at 1501.9 P
similarity to YPL184c
9769_g_at 2225.7 P
similarity to YPL184c
9770_at 2930.4 P
questionable ORF
9771_at 1614.2 P
predicted protein is very hydrophobic, has many membrane-spanning regions, several potential glycosylation sites, potential ATP-binding site
9772_at 3448.9 P
Vanadate resistance protein
9773_at 2395.0 P
hypothetical protein
9774_at 3551.0 P
datin, an oligo(dA).oligo(dT)-binding protein
9775_at 1018.2 P
CTD kinase-I gamma subunit
9776_at 1535.8 P
strong similarity to ubiquitination protein Bul1p

9777_at	11691.1	P	DBF2 Interacting Protein
9778_at	980.0	P	multicopy suppressor of a sin4 defect
9734_at	1159.7	P	hypothetical protein
9735_at	2739.8	P	hypothetical protein
9736_at	10481.5	P	Orotate phosphoribosyltransferase 1
9737_at	5033.9	P	signal recognition particle subunit, homologue of mammalian SRP19
9738_at	1043.7	P	Intermediate filament protein involved in organelle inheritance
9739_at	2217.0	P	Nucleoporin
9740_at	2726.6	P	p60 subunit of the yeast omatin Assembly Factor-I (CAF-I)
9741_at	-422.5	A	questionable ORF
9742_at	5166.2	P	weak similarity to YMR264w
9743_at	1832.5	P	123 kD regulatory subunit of trehalose-6-phosphate synthase\/phosphatase complex\; homologous to TPS3 gene product
9744_at	683.9	P	questionable ORF
9745_at	666.4	P	zinc-finger transcription factor of the Zn(2)-Cys(6) binuclear cluster domain type
9746_at	1807.8	P	TFIID subunit
9747_at	3839.0	P	required for Golgi to vacuole trafficking, shares similarity to mammalian ras inhibitors
9748_at	1346.7	P	similarity to asparagine synthases
9749_at	352.9	P	Endonuclease (with Rad1p) that degrades single-stranded DNA for repair
9750_at	79.0	A	questionable ORF
9751_at	5715.3	P	Putative homolog of subunit 5 of bovine prefoldin, a chaperone comprised of six subunits
9752_at	3306.5	P	similarity to P.falciparum liver stage antigen LSA-1
9753_at	12206.0	P	proteasome component Y7
9754_at	1577.3	P	subunit of mitochondrial RNase P
9755_at	37.1	A	hypothetical protein
9756_at	-21.0	A	questionable ORF
9711_at	1323.6	P	hypothetical protein
9712_at	28.8	A	strong similarity to YML125c, similarity to cytochrome-b5- and nitrate reductases
9713_at	8032.6	P	

D-arabinono-1,4-lactone oxidase
9714_at 12274.1 P
alpha-tubulin
9715_at -180.0 A
hypothetical protein
9716_at 7.7 A
hypothetical protein
9717_at 1683.5 P
similarity to N.crassa O-succinylhomoserine (thiol)-lyase
9718_at 2901.3 P
strong similarity to ZMS1 protein
9719_at 2618.6 P
similarity to A.brasilense nifR3 protein
9720_at 2073.8 P
weak similarity to Synechocystis sp. hypothetical protein sll1188
9721_at 11077.3 P
cyclophilin-3 (cyclosporin-sensitive proline rotamase-3)
9722_at 4909.6 P
Bet5p\/18kD component of TRAPP
9723_at 1529.8 P
weak similarity to transcription factor
9724_at 10062.1 P
3-hydroxy-3-methylglutaryl-coenzyme A (HMG-CoA) reductase isozyme
9725_at 9628.7 P
Prolyl cis-trans isomerase, also called proline rotamase or peptidylprolyl cis-trans isomerase (PPIase)
9726_at 12816.8 P
Ribosomal protein L6A (L17A) (rp18) (YL16)
9727_at 6997.5 P
similarity to YOR3141c and YNL087w
9728_at 3894.1 P
hypothetical protein
9729_at 5158.5 P
putative dihydroxyacetone kinase
9730_at 4705.0 P
Binds to catalytic subunit of DNA polymerase alpha (Pol1p)
9731_at 712.3 P
similarity to C.elegans hypothetical protein
9732_at 6367.7 P
weak similarity to YAL042w
9733_at 310.9 A
hypothetical protein
9689_at 1401.2 P
120-kDa (largest) subunit of origin recognition complex (ORC)\; shows homology to Cdc6p, Cdc18p, and Sir3p and to proteins from K. lactis, S. pombe, and humans
9690_at 1153.9 P
GTP-binding protein of the ras superfamily involved in termination of M-phase
9691_i_at 13228.1 P
Ribosomal protein S1B (rp10B)
9692_at 1090.3 P
Protein involved in mitochondrial import of fusion proteins
9693_at 1361.1 P 5
to 3 DNA helicase
9694_at 2975.9 P
43-kDa 8-oxo-guanine DNA glycosylase
9695_at 2475.2 P
similarity to C.elegans ZK370.4 protein

9696_at	8616.2	P	Suppressor of mec lethality
9697_at	123.1	A	questionable ORF
9698_at	2593.9	P	Catalytic A subunit of calcineurin, type 2B protein serine\/threonine phosphatase\; redundant with Cna1\; cytoplasmic
9699_at	10668.6	P	strong similarity to IMP dehydrogenases
9700_at	11828.4	P	strong similarity to IMP dehydrogenases
9701_at	5749.1	P	subunit of signal peptidase complex, homologous to mammalian protein SPC25
9702_at	367.0	P	Cytochrome b2 [L--lactate cytochrome-c oxidoreductase]
9703_at	3499.5	P	hypothetical protein
9704_at	7809.0	P	putative integral membrane protein
9705_at	5698.7	P	regulatory protein
9706_at	384.5	P	weak similarity to potato sucrose cleavage protein
9707_at	2064.3	P	RNA splicing and ER to Golgi transport
9708_at	6462.0	P	Glucose Signaling Factor
9709_at	684.4	P	questionable ORF
9710_at	427.7	P	strong similarity to YJR054w
9666_at	2578.4	P	RNA splicing factor associated with U1 snRNP
9667_at	369.8	P	Component of rDNA transcription factor CF, which also contains Rrn6p and Rrn7p, which is required for rDNA transcription by RNA polymerase I
9668_at	477.1	A	Carnitine O-acetyltransferase, peroxisomal and mitochondrial
9669_at	2891.1	P	hypothetical protein
9670_at	3269.7	P	hypothetical protein
9671_at	280.2	A	hypothetical protein
9672_at	1803.0	P	weak similarity to C.elegans hypothetical protein CELW03F8
9673_at	3678.6	P	putative alpha-mannosidase
9674_at	166.4	A	questionable ORF
9675_at	1085.4	P	similarity to YDR458c
9676_at	1293.5	P	similarity to YDR458c
9677_at	3408.9	P	Interacts with Rad51p by two hybrid analysis. mRNA is induced in meiosis during recombination

9678_at	693.2	A	questionable ORF
9679_at	4109.1	P	Nuclear envelope protein with multiple putative transmembrane domains
9680_at	4299.9	P	hypothetical protein
9681_at	1966.6	P	hypothetical protein
9682_at	9439.3	P	Thiol-specific antioxidant
9683_at	5708.1	P	Homeobox-domain containing protein
9684_s_at	13469.2	P	Ribosomal protein S18B
9685_at	1609.2	P	ribosomal protein, mitochondrial
9686_s_at	7001.1	P	Ribosomal protein S17A (rp51A)
9687_at	2865.0	P	weak similarity to Nmd2p
9688_at	8024.8	P	Adenine phosphoribosyltransferase
9643_at	2727.6	P	uracil DNA glycosylase
9644_at	1680.6	P	hypothetical protein
9645_at	6732.7	P	Putative new 37kDa subunit of N-oligosaccharyltransferase complex
9646_at	4022.8	P	similarity to YDR438w
9647_at	395.3	P	Polymerase suppressor 2\; Suppressors of group II intron-splicing defect.
9648_at	2214.1	P	serine-threonine phosphatase Z
9649_at	1678.2	P	TFIID subunit
9650_at	2318.8	P	similarity to C.elegans hypothetical protein C14B1.5
9651_at	1825.6	P	hypothetical protein
9652_at	-78.8	A	questionable ORF
9653_at	10860.8	P	Component of the COPII coat of certain ER-derived vesicles
9654_at	1994.0	P	hypothetical protein
9655_at	1668.8	P	transcription factor
9656_g_at	7039.2	P	transcription factor
9657_i_at	652.6	P	questionable ORF
9658_r_at	256.0	P	questionable ORF
9659_at	585.7	P	questionable ORF

9660_at	8327.0	P	Mitochondrial ribosomal protein MRPL39 (YmL39)
9661_at	11372.2	P	S-adenoslymethionine: delta 24-methyltransferase
9662_at	1423.9	P	jun-like transcription factor
9663_at	3060.2	P	hypothetical protein
9664_at	902.4	P	similarity to hypothetical S.pombe protein
9665_at	7870.3	P	lactoylglutathione lyase (glyoxalase I)
9620_at	181.9	P	hypothetical protein
9621_at	365.2	P	hypothetical protein
9622_at	8543.8	P	GTP-binding protein of the rab family\; required for homotypic fusion event in vacuole inheritance, for endosome-endosome fusion, and for fusion of endosomes to vacuoles when expressed from high copy plasmid
9623_at	2499.9	P	protein kinase which functions at the G(sub)2\/M boundary
9624_at	8825.4	P	similarity to hypothetical S.pombe and C.elegans proteins
9625_at	1908.5	P	hypothetical protein
9626_at	4051.4	P	Protein required for sorting proteins to the vacuole
9627_at	3837.5	P	Protein required for protein synthesis
9628_at	6710.5	P	strong similarity to Plb1p
9629_at	232.4	P	hypothetical protein
9630_at	9079.1	P	Phospholipase B (lypophospholipase)
9631_at	7755.1	P	weak similarity to P.aeruginosa regulatory protein mmsR
9632_at	2667.4	P	weak similarity to hypothetical protein YDR352w
9633_at	8610.3	P	high affinity hexose transporter-2
9634_at	7027.9	P	CLU1 is similar to the Dictyostelium cluA gene
9635_at	922.1	P	membrane protein required for core glycosylation
9636_at	2363.9	P	weak similarity to S.pombe hypothetical protein SPAC4F10
9637_at	8267.6	P	cytochrome P450 involved in C-22 denaturation of the ergosterol side-chain
9638_at	1731.2	P	displays homologies to several transcription factors
9639_at	34.1	A	DBF2 Interacting Protein\; SNAP 25 homolog
9640_at	153.7	A	similarity to tetratricopeptide-repeat protein PAS10

9641_at 935.2 P
Binds Sin3p in two-hybrid assay
9642_at 885.2 P
Multicopy suppressor of fenpropimorph resistance (fen2 mutant), shows similarity to Candida albicans corticosteroid-binding protein CBP1
9598_at 1529.4 P
metal-binding transcriptional activator
9599_at 7033.9 P
ubiquitin conjugating enzyme
9600_at 608.3 P
putative mitochondrial GTPase
9601_at 2932.4 P
Mitochondrial ribosomal protein MRPL3 (YmL3)
9602_at 662.0 A
hypothetical protein
9603_at 1163.1 P
C3HC4 zinc-binding integral peroxisomal membrane protein
9604_at 5655.4 P
High level expression reduced Ty3 Transposition
9605_at 425.5 P
42 kDa protein that pysically associates with the PP2A and SIT4 protein phosphatase catalytic subunits
9606_at 726.4 P
weak similarity to human nuclear autoantigen
9607_at 438.9 P
hypothetical protein
9608_at 1550.3 P
similarity to YKL050c and human restin
9609_at 358.6 A
questionable ORF
9610_at 1887.2 P
Cytokinesis
9611_at 4595.6 P
Actin-related protein
9612_at 213.5 A
weak similarity to YPR201w
9613_at 1232.6 P
Inner membrane protease (mitochondrial protein)
9614_at 1329.3 P
homolog of S. pombe cdc25
9615_at 3027.8 P
zinc finger protein
9616_at 8310.9 P
Homocitrate
9617_at 6546.8 P
suppressor of TFIIB mutations
9618_at 504.2 P
strong similarity to Yet1p
9619_at 806.6 P
weak similarity to Pseudomonas L-fucose dehydrogenase
9575_at 1740.6 P
Regulator of arginine-responsive genes with ARG81 and ARG82
9576_at 6658.0 P
putative transcriptional activator of alpha-specific genes
9577_at 4416.8 P
hypothetical protein
9578_at 4005.0 P

Nuclear pore complex protein that is member of GLFG repeat-containing family of nucleoporins and is highly homologous to Nup100p
9579_at 787.4 P
hypothetical protein
9580_at 8908.4 P
weak similarity to A.thaliana PRL1 protein
9581_at 192.9 P
Required for arrest in G1 in response to pheromone
9582_at 290.2 A
questionable ORF
9583_at 61.6 A
Binds Sin3p in two-hybrid assay and is part of large protein complex with Sin3p and Stb1p
9584_at 3767.3 P
vacuolar proton pumping ATPase, 110-kDa subunit\; not in vacuole membrane
9585_at 1993.0 P
Protein required for cell cycle arrest in response to loss of microtubule function
9586_at 1859.5 P
mitochondrial ADP\/ATP translocator
9587_at -47.4 A
hypothetical protein
9588_at 8561.9 P
multicopper oxidase
9589_at 1652.3 P
15kDa subunit of the tetrameric tRNA splicing endonuclease
9590_at 1120.8 P
mitochondrial import receptor, heterodimerizes with Tom70p, preferentially recognizes the mature regions of precursor proteins associated with ATP-dependent cytosolic chaperones
9591_at 653.9 P
component of the cleavage and polyadenylation factor CF I involved in pre-mRNA 3 -end processing
9592_at 1944.2 P
acetylornithine acetyltransferase
9593_at 255.7 A
Regulator of Rim1p, required for IME1 expression
9594_at 1076.2 P
basic, hydrophilic protein of 59 kDa
9595_at 843.8 P
appears to be required for the completion of nuclear membrane fusion and may play a role in the organization of the membrane fusion complex
9596_at 147.9 M
Synthesis Of Var
9597_at 1967.3 P
hypothetical protein
9553_at 279.7 P
weak similarity to mouse transcription factor NF-kappaB
9554_at 441.3 P
hypothetical protein
9555_at 843.3 P
2 Cys2-His2 zinc fingers at c-terminus, glutamine and asparagine rich
9556_at 7385.9 P
hypothetical protein
9557_at 8409.8 P
HMG-1 homolog, mitochondrial
9558_at 2634.9 P
weak similarity to C-terminal part of cytochrome b5 and b2
9559_at 2950.2 P
strong similarity to hypothetical S. pombe protein

9560_at 549.0 P
weak similarity to human Mi-2 protein
9561_at 128.3 A
questionable ORF
9562_at 2427.6 P
Precocious Dissociation of Sister chromatids
9563_at 992.4 P
similarity to SNF7 protein
9564_at 1969.3 P
chromosome transmission
9565_at 9634.2 P
phosphatidylinositol transfer protein
9566_at 3162.6 P
putative helicase
9567_at 467.2 A
May regulate NAM7 function, possibly at level of mRNA turnover
9568_at 311.9 A
hypothetical protein
9569_at 11918.9 P
alcohol dehydrogenase isoenzyme III
9570_at 299.5 A
putative pseudogene
9571_at -1.4 A
putative pseudogene
9572_at 2258.7 P
similarity to YKL105c
9573_at 379.5 A
questionable ORF
9574_at 458.5 P
hypothetical protein
9530_at 4094.5 P
similarity to multidrug resistance proteins
9531_at 3470.3 P
mitochondrial membrane ATPase of the CDC48\/PAS1\/SEC18 (AAA) family
9532_at 552.4 P
strong similarity to B. subtilis conserved hypothetical protein yhfK
9533_at 1631.3 P
nuclear protein localization factor
9534_at 3400.7 P
Protein localizes to actin cortical patches. Probable binding site on actin lies on front surface of subdomain 3 and 4.
9535_at 3996.9 P
weak similarity to Pwp2p
9536_at 125.7 P
58 kd component (Cbf3c) of the multisubunit Cbf3 kinetochore protein complex, which binds to the CDE III element of centromeres
9537_at 608.0 P
SNZ1 proximal ORF, stationary phase induced gene
9538_at 1187.0 P
encodes highly conserved 35 kDa protein that shows increased expression after entry into stationary phase
9539_at 813.0 P
weak similarity to M.genitalium hypothetical protein homolog MG442
9540_at 1085.5 P
hypothetical protein
9541_at 7387.6 P

similarity to P.ciliare possible apospory-associated protein
9542_at 1257.9 P
Homolog of samB gene of Aspergillus nidulans (deletion of samB results in mislocalization of septa
9543_at 465.8 P
similarity to YBR002c
9544_at 2950.7 P
strong similarity to YKL121w
9545_at 1199.5 P
hypothetical protein
9546_at 407.1 P
protein kinase
9547_at 1076.6 P
Phosphoglucomutase
9548_at 579.2 P
Ku80 homolog, exhibits DNA binding activity on its own, associates with Hdf1p to form major DNA end-binding complex
9549_at -24.0 A
hypothetical protein
9550_at 9205.1 P
acetolactate synthase
9551_at 4107.9 P
myosin I
9552_at 6689.2 P
similarity to aldehyde dehydrogenase
9507_at 445.3 P
weak similarity to MSN1 protein
9508_at 1733.8 P
hypothetical protein
9509_at 4319.5 P
similarity to folylpolyglutamate synthetases and strong similarity to YKL132c
9510_at 110.8 A
similarity to B. subtilis conserved hypothetical proteins yoqW and yoaM
9511_at 1533.1 P
similarity to YKL133c
9512_at 9325.3 P
WD repeat protein (G-beta like protein) that interacts with the translational machinery
9513_at 9224.5 P
WD repeat protein (G-beta like protein) that interacts with the translational machinery
9514_at 99.8 P
component of spindle pole
9515_at -8.4 A
strong similarity to succinate dehydrogenase
9516_at 1640.4 P
similarity to YNL008c
9517_g_at 3432.1 P
similarity to YNL008c
9518_at 1530.1 P
questionable ORF
9519_at 5316.6 P
5-aminoimidazole-4-carboxamide ribonucleotide (AICAR) transformylase\/IMP cyclohydrolase
9520_at 7231.8 P
Ribosomal protein L15B (YL10) (L13B) (rp15R)
9521_at 478.3 A
hypothetical protein
9522_at 10622.2 P
resistance against Pichia farinosa killer toxin (SMK toxin) when expressed by a multi copy plasmid

9523_at 648.9 P
weak similarity to YLR031w
9524_at 4180.9 P
transcriptional activator of glycolytic genes
9525_at 923.3 P
hypothetical protein
9526_at 638.6 P
Protein involved in silencing HMR, homologous to acetyltransferases
9527_at 4444.4 P
ExtraCellular Mutant
9528_at 4565.2 P
Nuclear pore membrane glycoprotein
9529_at 439.2 P
similarity to D.melanogaster Dreg-2 protein
9484_at 8272.0 P
similarity to human retinoblastoma-binding protein
9485_at 223.8 P
similarity to hypothetical S. pombe protein
9486_at -24.0 A
mRNA is induced early in sporulation
9487_at 2756.0 P
hypothetical protein
9488_at 619.0 P
hypothetical protein
9489_at 164.4 A
questionable ORF
9490_at 870.9 P
weak similarity to YIR013c and YLR013w
9491_at 361.9 A
interstrand crosslink repair protein
9492_at 945.6 A
GTP-binding protein
9493_at 3840.0 P
Serine\/threonine protein kinase, phosphorylates the mitotic activator IME1
9494_at 2480.7 P
hypothetical protein
9495_at 115.4 A
hypothetical protein
9496_at 15602.3 P
Ribosomal protein L13B
9497_i_at 2853.6 P
Ribosomal protein S16A (rp61R)
9498_f_at 10310.7 P
Ribosomal protein S16A (rp61R)
9499_at 292.2 P
weak similarity to Mlp1p
9500_at 8807.1 P
mitochondrial cytosolically directed NADH dehydrogenase
9501_at 9808.0 P
p39 subunit of translation initiation factor eIF3
9502_at 1767.4 P
hypothetical protein
9503_at 6142.5 P
hypothetical protein
9504_at 8365.8 P
oligosaccharyl transferase glycoprotein complex, delta subunit

9505_at 3946.9 P
Inner membrane protease (mitochondrial protein)
9506_at 118.3 A
hypothetical protein
9462_at 1233.9 P
mitochondrial inner membrane protease
9463_at 2858.6 P
similarity to Asm4p
9464_at -24.1 A
questionable ORF
9465_at 151.7 A
Involved in proteolytic processing of Rim1p
9466_at 680.1 P
weak similarity to E.coli hypothetical protein f402
9467_at 630.3 P
weak similarity to S.pombe hypothetical protein SPAC23C11
9468_at 3085.7 P
hypothetical protein
9469_at 1323.4 P
weak similarity to E.coli ribosomal S8 protein
9470_at -253.5 A
questionable ORF
9471_at -3.6 A
Protein homologous to human Sin3 complex component SAP18, possible coiled-coil protein
9472_at 1389.6 P
weak similarity to fruit fly ecdysone-inducible protein
9473_at 1084.8 P
Homologous to E coli dnaJ protein
9474_at 651.7 P
similarity to ATPases
9475_at 294.5 P
hypothetical protein
9476_at 1093.8 P
Predicted 758 amino acid polypeptide with poly-glutamine and poly-asparagine domains
9477_at 1782.3 P
involved in plasmid maintenance
9478_at 2487.8 P
similarity to members of the mitochondrial carrier protein family
9479_at 308.1 A
MutL homolog, forms a complex with Pms1p and Msh2p to repair mismatched DNA
9480_at 282.3 P
contains an N-terminal Zn2Cys6 type zinc finger domain, a C-terminal acidic domain and a putative coiled coil dimerization domain
9481_at 367.1 P
Aldehyde Dehydrogenase (NAD(P)+)
9482_g_at 2054.8 P
Aldehyde Dehydrogenase (NAD(P)+)
9483_at 627.3 P
aldehyde dehydrogenase, (NAD(P)+), likely cytosolic
9439_at 402.2 P
similarity to YKL124w
9440_at 418.0 P
similarity to MSN1 protein
9441_at -948.0 A
questionable ORF
9442_s_at 5906.3 P

flocculent specific protein\; contains >35 repeats of the amino acid sequence NNNDSYGS
9443_at 9152.8 P
questionable ORF
9444_at 1122.5 P
Cytoplasmic inhibitor of proteinase Pep4p
9445_at 20.3 A
protein of unknown function
9446_at 401.1 P
ExtraCellular Mutant
9447_at 1416.0 P
Protein involved in mitochondrial iron accumulation
9448_at 1849.2 P
similarity to C.elegans hypothetical protein
9449_at 494.5 P
non-specific DNA binding protein
9450_at 860.6 P
similarity to YPL228w
9451_at 523.0 P
similarity to YPL229w
9452_at 374.0 P
Putative transcriptional repressor with proline-rich zinc fingers
9453_at 3676.2 P
SSO1 and SSO2 encode syntaxin homologs\; act in late stages of secretion
9454_at 3331.3 P
hypothetical protein
9455_at 1487.5 P
hypothetical protein
9456_at 8932.6 P
constitutively expressed heat shock protein
9457_g_at 5548.9 P
constitutively expressed heat shock protein
9458_at 2895.9 P
hypothetical protein
9459_at 1875.0 P
weak similarity to bacterial ribosomal protein S17
9460_at 4742.1 P
Glycine decarboxylase complex (P-subunit), glycine synthase (P-subunit), Glycine cleavage system (P-subunit)
9461_at 759.2 P
has DNA helicase signature motifs
9416_at 2813.8 P
hypothetical protein
9417_at 158.1 M
similarity to mouse Tbc1 protein
9418_at 3714.3 P
Mitochondrial ribosomal protein MRPL24 (YmL24)
9419_at 494.7 P
questionable ORF
9420_i_at 3948.6 P
Ribosomal protein L36A (L39) (YL39)
9421_s_at 13408.4 P
Ribosomal protein L36A (L39) (YL39)
9422_at 4424.7 P
similarity to YPL250c
9423_at 704.0 P
hypothetical protein

9424_at 2430.5 P
Vti1p is a v-SNARE that interacts with two t-SNARES, Sed5p and Pep12p
9425_at 2154.4 P
spindle pole body associated protein
9426_at 3648.3 P
G(sub)1 cyclin
9427_at 5023.5 P
putative membrane protein
9428_at 592.7 P
human xeroderma pigmentosum group A DNA repair gene homolog
9429_at 14237.5 P
C-8 sterol isomerase
9430_at 11203.7 P
Mitochondrial outer membrane protein\; forms the outer membrane import channel
9431_at 706.0 P
weak similarity to D.melanogaster hypothetical protein DMC39E1
9432_at 11894.3 P
phosphofructokinase beta subunit
9433_at -288.7 A
weak similarity to hypothetical protein YNR014w
9434_at 645.2 P
Similar to acetyl-coenzyme A carboxylase
9435_at 5950.2 P
mevalonate kinase
9436_at 1694.8 P
hypothetical protein
9437_at 1713.0 P
similarity to P.glauca late embryogenesis abundant protein and YBR177c and YPL095c
9438_at 1271.5 P
weak similarity to beta tubulins
9394_at 2988.3 P
weak similarity to myosins
9395_at 420.5 P
S. cerevisiae homologue of S. pombe cdc5+
9396_at 5046.1 P
dnaJ homolog
9397_at 6991.2 P
similarity to GAS1 protein
9398_at 4785.3 P
Serine Protein Kinase
9399_at 11582.6 P
GMP synthase
9400_at 1471.4 P
hypothetical protein
9401_at 1520.1 P
Establishes Silent omatin
9402_at 11438.7 P
48 kDa Phosphomevalonate kinase
9403_at 8292.5 P
weak similarity to photosystem II protein D2
9404_at 5184.4 P
similarity to S.pombe dihydrofolate reductase
9405_at 1918.1 P
encodes putative deubiquitinating enzyme
9406_at 954.0 P
localizes to discrete sites in rad50s mutants. Mre11p, Rad50p, Mer2p and Xrs2p function in a complex by

immunoprecipitation and two-hybrid analyses\; mutations in these genes have similar phenotypes. mRNA is induced in meiosis
9407_at 2909.7 P
Mitochondrial ribosomal protein MRPL44 (YmL44)
9408_at 2477.8 P
Mitochondrial ribosomal protein MRPL44 (YmL44)
9409_at 10633.4 P
similarity to ketoreductases
9410_at 887.6 P
TFIID subunit
9411_at 1793.2 P
Mitochondrial RNA polymerase specificity factor
9412_at 9602.6 P
Protein required for processing of pre-rRNA
9413_f_at 281.0 P
Ribosomal protein S10B
9414_f_at 8240.3 P
Ribosomal protein S10B
9415_at 457.1 P
peripheral vaculor membrane protein\; putative Zn-finger protein
9371_at 453.7 P
involved in cell fusion during mating, also required for the alignment of parental nuclei before nuclear fusion
9372_at 2927.4 P
strong similarity to YOR295w
9373_at 421.8 P
ribonuclease H
9374_at 6274.7 P
Protein involved in RNA processing and export from nucleus
9375_at 7431.3 P
TFIID subunit
9376_at 4555.7 P
similarity to CHS6 protein
9377_at 5665.7 P
Protein required for filamentous growth, cell polarity, and cellular elongation
9378_at 2586.7 P
Ribonuclease III
9379_at 613.7 P
U2 snRNP protein
9380_at 9211.6 P
DNA-binding protein, mtDNA stabilizing protein, mitochondrial inner membrane protein with low homology to RIM2
9381_s_at 13869.8 P
Ribosomal protein L20A (L18A)
9382_at 10324.9 P
Zinc- and cadmium-resistance protein
9383_at 182.3 P
similarity to Uth1p, Nca3p, YIL123w and Sun4p
9384_at 3359.7 P
questionable ORF
9385_at 1280.9 P
weak similarity to mouse thyrotropin-releasing hormone receptor
9386_at 7933.7 P
long-chain fatty acid--CoA ligase and synthetase 4
9387_at 5423.7 P
hypothetical protein

9388_at 596.3 P
similarity to glutamate decarboxylases
9389_at 173.0 P
strong similarity to YKR076w and YGR154c
9390_at 7499.2 P
hyperosmolarity-responsive gene
9391_at 1035.8 P
hypothetical protein
9392_at 679.0 P
strong similarity to YPL264c
9393_at 126.6 M
hypothetical protein
9349_at 946.4 P
hypothetical protein
9350_at 10834.7 P
subunit VII of cytochrome c oxidase
9351_at 673.4 P
translational activator of cytochrome c oxidase subunit II
9352_at 1051.9 P
hypothetical protein
9353_at 2165.3 P
hypothetical protein
9354_at 9002.6 P
Translation initiation factor eIF1A
9355_at 4021.9 P
115 kD regulatory subunit of trehalose-6-phosphate synthase\/phosphatase complex
9356_at 731.8 P
similarity to S.pombe scn1 protein
9357_at 906.9 P
subunit of the histone deacetylase B complex
9358_at 4181.9 P
Cue1p assembles with Ubc7p. Cue1p recruits Ubc7p to the cytosolic surface of the endoplasmic reticulum. Assembly with Cue1p is a prerequisite for the function of Ubc7p
9359_at 855.1 P
hypothetical protein
9360_at 8793.6 P
similarity to A.thaliana hyp1 protein
9361_at 1857.4 P
mitochondrial inorganic pyrophosphatase
9362_at 515.1 P
U4\/U6 snRNA-associated splicing factor
9363_at 2072.5 P
weak similarity to C.elegans hypothetical protein CELT23B3
9364_at 1341.3 P
Upstream activation factor subunit
9365_at 433.1 P
Orotate phosphoribosyltransferase 2
9366_at 7866.2 P
desaturase\/hydroxylase enzyme
9367_at 2447.0 P
Negative regulator of cell polarity
9368_at 1321.5 P
Protease involved in ras and a-factor terminal proteolysis
9369_at 1913.9 P
Involved in the ubiquination pathway, possibly by functioning with Rsp5
9370_at 10599.4 P

ubiquitin-like protein
9326_at 1733.7 P
TFIIF interacting Component of CTD Phosphatase
9327_at 1323.2 P
similarity to phosphomannomutases
9328_at 412.2 A
strong similarity to aminotriazole resistance protein
9329_at 4.6 A
Zinc-cluster protein involved in activating gluconeogenic genes\; related to Gal4p
9330_at 1775.5 P
hypothetical protein
9331_at 1032.5 P
basic, hydrophilic 67.5 kDa protein
9332_at 910.8 P
Initiator methionine tRNA 2 -O-ribosyl phosphate transferase
9333_at 817.1 P
DNA binding protein
9334_at 1247.1 P
similarity to Ccr4p
9335_at 5177.0 P
Mitochondrial ribosomal protein MRPL33 (YmL33) (E. coli L30)
9336_at 845.1 P
Protein essential for mitochondrial biogenesis
9337_at 1130.7 P
strong similarity to hypothetical S.pombe and C.elegans proteins
9338_at 1579.6 P
hypothetical protein
9339_at 6425.3 P
Putative RNA-dependent helicase
9340_at 41.9 A
questionable ORF
9341_at 974.1 P
similarity to ser/thr protein kinase
9342_at 8719.5 P
strong similarity to C.elegans hypothetical protein
9343_at 836.4 P
similarity to amidases
9344_at 280.5 P
Coiled-coil domain protein required for proper nuclear migration during mitosis (but not during conjugation)
9345_at 567.2 A
questionable ORF
9346_at 12843.1 P
similarity to YGR273c
9347_at 7703.5 P
Probable component of serine palmitoyltransferase, which catalyzes the first step in biosynthesis of long-chain sphingolipids
9348_at 11066.3 P
carboxypeptidase Y (proteinase C)
9304_at 9772.2 P
hypothetical protein
9305_at 347.6 P
weak similarity to hypothetical protein YJL062w
9306_at 1337.6 P
phosphoribosylpyrophosphate amidotransferase
9307_at 2125.8 P

mitochondrial ABC transporter protein
9308_at 2056.8 P
Integral membrane mitochondrial protein
9309_at 1304.7 P
alcohol dehydrogenase II
9310_at 1028.7 P
encodes putative deubiquitinating enzyme
9311_at 443.6 P
questionable ORF
9312_at 13047.5 P
member of the glucanase gene family
9313_at 66.6 P
Protein with similarity to Gls1p and Gls2p (GB:Z49212)
9314_at 213.0 A
questionable ORF
9315_at 9414.3 P
cell surface glycoprotein 115-120 kDa
9316_at 12853.7 P
Karyopherin
9317_at 6823.4 P
~100 kDa cytoplasmic protein
9318_at 4497.3 P
similarity to YGR283c
9319_at 1631.1 P
Regulates activity of protein phosphatase 1, Glc7p, which is involved in proper chromosome segregation
9320_at 4983.9 P
hypothetical protein
9321_at 915.9 P
similarity to YKR089c and YOR081c
9322_at 11341.0 P
alpha-type of subunit of 20S proteasome
9323_at 9309.8 P
similarity to hypothetical S. pombe protein
9324_at 2851.3 P
similarity to YOR385w and YNL165w
9325_at 752.5 A
questionable ORF
9281_at 1230.1 P
questionable ORF
9282_at -41.0 A
similarity to mucins, glucan 1,4-alpha-glucosidase and exo-alpha-sialidase
9283_at 8483.8 P
strong similarity to alcohol-dehydrogenase
9284_at 2193.0 P
Low-affinity Fe(II) transport protein
9285_at 552.8 P
hypothetical protein
9286_s_at 7879.2 P
strong similarity to hypothetical proteins YPL273w and YLL062c
9287_s_at 38.1 M
strong similarity to YPL280w, YOR391c and YDR533c
9288_s_at 508.6 P
strong similarity to phosphopyruvate hydratases
9289_at 108.8 P
strong similarity to YBL108w, YCR103c and YKL223w
9290_f_at 1265.4 P

strong similarity to members of the Srp1p/Tip1p family
9291_at 11487.2 P
protein associated to the ATP synthase
9292_at 148.1 P
hypothetical protein identified by SAGE
9293_at 802.0 P
identified by SAGE
9294_at 8083.4 P
hypothetical protein
9295_g_at 4923.6 A
hypothetical protein
9296_at 155.8 P
non-annotated SAGE orf Found reverse in NC_001145 between 159029 and 159169 with 100% identity. See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251
9297_at 498.3 P
non-annotated SAGE orf Found reverse in NC_001145 between 390825 and 390965 with 100% identity. See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251
9298_at 468.4 P
non-annotated SAGE orf Found forward in NC_001145 between 31875 and 32045 with 100% identity. See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251
9299_at 309.3 A
non-annotated SAGE orf Found reverse in NC_001145 between 122312 and 122605 with 100% identity. See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251
9300_at 58.1 P
non-annotated SAGE orf Found reverse in NC_001145 between 503463 and 503660 with 100% identity. See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251
9301_at 45.2 A
non-annotated SAGE orf Found reverse in NC_001145 between 503665 and 503799 with 100% identity. See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251
9302_at -0.8 A
non-annotated SAGE orf Found reverse in NC_001145 between 768049 and 768219 with 100% identity. See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251
9303_at 425.3 A
non-annotated SAGE orf Found forward in NC_001145 between 769282 and 769425 with 100% identity. See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251
9258_at -79.0 A
non-annotated SAGE orf Found forward in NC_001145 between 46024 and 46185 with 100% identity. See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251
9259_at 228.4 P
non-annotated SAGE orf Found forward in NC_001145 between 171311 and 171469 with 100% identity. See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251
9260_at 406.9 A
non-annotated SAGE orf Found reverse in NC_001145 between 347179 and 347406 with 100% identity. See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251
9261_at -60.8 A
non-annotated SAGE orf Found forward in NC_001145 between 363103 and 363273 with 100% identity. See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251
9262_at 334.4 P
non-annotated SAGE orf Found forward in NC_001145 between 390814 and 390981 with 100% identity. See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251
9263_at 599.0 P
non-annotated SAGE orf Found reverse in NC_001145 between 492187 and 492357 with 100% identity. See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251
9264_at 467.2 A
non-annotated SAGE orf Found forward in NC_001145 between 632094 and 632234 with 100% identity. See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251

9265_at 462.4 P
non-annotated SAGE orf Found forward in NC_001145 between 752987 and 753121 with 100% identity. See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251
9266_at 933.1 P
non-annotated SAGE orf Found forward in NC_001145 between 762231 and 762389 with 100% identity. See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251
9267_at 11107.5 P
non-annotated SAGE orf Found reverse in NC_001145 between 849877 and 850053 with 100% identity. See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251
9268_at 1339.2 P
non-annotated SAGE orf Found forward in NC_001145 between 863528 and 863674 with 100% identity. See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251
9269_at 4604.5 A
non-annotated SAGE orf Found reverse in NC_001145 between 910809 and 910946 with 100% identity. See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251
9270_at -99.9 A
non-annotated SAGE orf Found forward in NC_001145 between 272960 and 273100 with 100% identity. See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251
9271_at 6250.5 P
non-annotated SAGE orf Found reverse in NC_001145 between 426343 and 426489 with 100% identity. See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251
9272_at 74.0 A
non-annotated SAGE orf Found forward in NC_001145 between 486399 and 486548 with 100% identity. See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251
9273_at -228.4 A
non-annotated SAGE orf Found reverse in NC_001145 between 501944 and 502096 with 100% identity. See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251
9274_at 96.3 A
non-annotated SAGE orf Found reverse in NC_001145 between 29913 and 30104 with 100% identity. See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251
9275_g_at -64.5 A
non-annotated SAGE orf Found reverse in NC_001145 between 29913 and 30104 with 100% identity. See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251
9276_at 70.8 A
non-annotated SAGE orf Found reverse in NC_001145 between 30023 and 30229 with 100% identity. See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251
9277_at 80.2 P
non-annotated SAGE orf Found forward in NC_001145 between 115459 and 115659 with 100% identity. See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251
9278_at -62.9 A
non-annotated SAGE orf Found forward in NC_001145 between 286805 and 287002 with 100% identity. See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251
9279_at 290.1 P
non-annotated SAGE orf Found reverse in NC_001145 between 297849 and 297983 with 100% identity. See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251
9280_at 294.0 P
non-annotated SAGE orf Found reverse in NC_001145 between 433097 and 433231 with 100% identity. See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251
9234_at 66.9 A
non-annotated SAGE orf Found reverse in NC_001145 between 433419 and 433640 with 100% identity. See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251
9235_at 892.4 P
non-annotated SAGE orf Found forward in NC_001145 between 433828 and 434049 with 100% identity. See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251
9236_at 741.4 A
non-annotated SAGE orf Found forward in NC_001145 between 434355 and 434564 with 100% identity.

See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251
9237_at 806.6 P
non-annotated SAGE orf Found forward in NC_001145 between 465271 and 465411 with 100% identity.
See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251
9238_at 297.9 P
non-annotated SAGE orf Found reverse in NC_001145 between 465281 and 465418 with 100% identity.
See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251
9239_at 16.3 A
non-annotated SAGE orf Found forward in NC_001145 between 478063 and 478257 with 100% identity.
See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251
9240_at 44.8 A
non-annotated SAGE orf Found forward in NC_001145 between 480651 and 480791 with 100% identity.
See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251
9241_at 914.7 P
non-annotated SAGE orf Found forward in NC_001145 between 480923 and 481186 with 100% identity.
See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251
9242_i_at -10.9 A
non-annotated SAGE orf Found forward in NC_001145 between 481528 and 481713 with 100% identity.
See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251
9243_at 237.9 A
non-annotated SAGE orf Found forward in NC_001145 between 481925 and 482149 with 100% identity.
See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251
9244_at 205.5 A
non-annotated SAGE orf Found forward in NC_001145 between 482056 and 482289 with 100% identity.
See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251
9245_at 30.2 P
non-annotated SAGE orf Found reverse in NC_001145 between 511289 and 511522 with 100% identity.
See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251
9246_at 591.2 A
non-annotated SAGE orf Found reverse in NC_001145 between 556676 and 556891 with 100% identity.
See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251
9247_g_at 761.9 A
non-annotated SAGE orf Found reverse in NC_001145 between 556676 and 556891 with 100% identity.
See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251
9248_at 216.2 A
non-annotated SAGE orf Found reverse in NC_001145 between 556746 and 556970 with 100% identity.
See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251
9249_i_at 50.7 A
non-annotated SAGE orf Found forward in NC_001145 between 625379 and 625540 with 100% identity.
See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251
9250_f_at -33.8 A
non-annotated SAGE orf Found forward in NC_001145 between 625379 and 625540 with 100% identity.
See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251
9251_at 349.0 P
non-annotated SAGE orf Found reverse in NC_001145 between 646818 and 647009 with 100% identity.
See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251
9252_at 10604.1 P
non-annotated SAGE orf Found reverse in NC_001145 between 762446 and 762586 with 100% identity.
See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251
9253_at 9998.8 P
non-annotated SAGE orf Found reverse in NC_001145 between 762597 and 762764 with 100% identity.
See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251
9254_at 579.8 A
non-annotated SAGE orf Found forward in NC_001145 between 837034 and 837171 with 100% identity.
See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251
9255_at -146.7 A

non-annotated SAGE orf Found reverse in NC_001145 between 915029 and 915199 with 100% identity.
See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251
9256_at	-106.6	A
non-annotated SAGE orf Found reverse in NC_001145 between 9829 and 10008 with 100% identity.
See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251
9257_at	-90.1	A
non-annotated SAGE orf Found reverse in NC_001145 between 13361 and 13621 with 100% identity.
See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251
9209_at	5110.4	P
non-annotated SAGE orf Found reverse in NC_001145 between 27916 and 28077 with 100% identity.
See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251
9210_at	1577.0	P
non-annotated SAGE orf Found forward in NC_001145 between 49819 and 49965 with 100% identity.
See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251
9211_at	5494.0	P
non-annotated SAGE orf Found reverse in NC_001145 between 62403 and 62543 with 100% identity.
See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251
9212_at	-3.2	A
non-annotated SAGE orf Found reverse in NC_001145 between 79732 and 79890 with 100% identity.
See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251
9213_at	42.9	A
non-annotated SAGE orf Found reverse in NC_001145 between 151565 and 151720 with 100% identity.
See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251
9214_at	-175.9	A
non-annotated SAGE orf Found reverse in NC_001145 between 234512 and 234685 with 100% identity.
See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251
9215_at	348.9	A
non-annotated SAGE orf Found forward in NC_001145 between 271996 and 272136 with 100% identity.
See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251
9216_at	127.9	P
non-annotated SAGE orf Found reverse in NC_001145 between 302614 and 302787 with 100% identity.
See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251
9217_at	622.3	P
non-annotated SAGE orf Found forward in NC_001145 between 337312 and 337602 with 100% identity.
See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251
9218_at	291.8	P
non-annotated SAGE orf Found forward in NC_001145 between 426559 and 426696 with 100% identity.
See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251
9219_i_at	97.3	P
non-annotated SAGE orf Found forward in NC_001145 between 483361 and 483495 with 100% identity.
See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251
9220_r_at	115.0	A
non-annotated SAGE orf Found forward in NC_001145 between 483361 and 483495 with 100% identity.
See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251
9221_f_at	-32.9	A
non-annotated SAGE orf Found forward in NC_001145 between 483361 and 483495 with 100% identity.
See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251
9222_at	132.5	A
non-annotated SAGE orf Found reverse in NC_001145 between 509507 and 509701 with 100% identity.
See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251
9223_at	40.5	A
non-annotated SAGE orf Found forward in NC_001145 between 611313 and 611507 with 100% identity.
See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251
9224_at	726.9	P
non-annotated SAGE orf Found reverse in NC_001145 between 623382 and 623516 with 100% identity.
See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251

9225_at	349.4	P
non-annotated SAGE orf Found forward in NC_001145 between 652852 and 653010 with 100% identity. See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251
9226_at	547.7	A
non-annotated SAGE orf Found forward in NC_001145 between 667253 and 667450 with 100% identity. See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251
9227_i_at	7705.8	P
non-annotated SAGE orf Found reverse in NC_001145 between 671528 and 671701 with 100% identity. See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251
9228_r_at	5399.8	P
non-annotated SAGE orf Found reverse in NC_001145 between 671528 and 671701 with 100% identity. See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251
9229_i_at	322.6	P
non-annotated SAGE orf Found forward in NC_001145 between 733267 and 733455 with 100% identity. See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251
9230_r_at	288.7	P
non-annotated SAGE orf Found forward in NC_001145 between 733267 and 733455 with 100% identity. See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251
9231_s_at	774.5	P
non-annotated SAGE orf Found forward in NC_001145 between 733267 and 733455 with 100% identity. See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251
9232_at	96.0	A
non-annotated SAGE orf Found forward in NC_001145 between 733313 and 733531 with 100% identity. See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251
9233_at	1856.1	P
non-annotated SAGE orf Found forward in NC_001145 between 774146 and 774280 with 100% identity. See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251
9186_at	3269.8	P
snRNA
9187_i_at	104.8	P
Centromere
9188_at	290.8	P
snRNA
9189_at	11701.2	P
snRNA
9190_at	547.0	P
snRNA
9191_at	2654.8	P
snRNA
9192_at	391.8	P
snRNA
9193_at	1785.8	P
snRNA
9194_at	2798.8	P
snRNA
9195_at	8469.0	P
snRNA
9196_s_at	374.6	A
similarity to M.verrucaria cyanamide hydratase, identical to hypothetical protein YFL061w
9197_s_at	2217.5	P
SNZ2 proximal ORF, stationary phase induced gene
9198_s_at	810.9	P
Snooze: stationary phase-induced gene family
9199_at	1964.7	P
Hypothetical aryl-alcohol dehydrogenase
9200_at	2363.0	P

histone deacetylase
9201_at 915.1 P
Member of the AAA-protein family that includes NSFp and PEX1p
9202_at 364.2 P
Protein of the mitochondrial inner membrane with similarity to E. coli DnaJ and other DnaJ-like proteins, function partially overlaps that of Mdj1p
9203_at 6246.8 P
Cell-cycle regulation protein, may be involved in the correct timing of cell separation after cytokinesis
9204_at 1348.7 P
similarity to YOL003c, YLR246w and C.elegans hypothetical protein ZK757.1
9205_at 768.4 P
FIG4 expression is induced by mating factor.
9206_at 123.0 A
hypothetical protein
9207_at 3308.4 P
strong similarity to YCR094w and YNR048w
9208_at 9916.3 P
Cell wall beta-glucan assembly
9163_at 3438.8 P
weak similarity to Vcx1p
9164_at 3369.5 P
strong similarity to S.pombe Bem46 protein
9165_at 348.7 A
questionable ORF
9166_at -53.0 A
hexose transport protein
9167_at 1177.4 P
similarity to A.thaliana PRL1/2 protein
9168_at 1457.4 P
prephenate dehydratase
9169_at 4899.3 P
essential for assembly of a functional F1-ATPase
9170_at 1263.2 P
positive regulator of allophanate inducible genes
9171_at 3306.0 P
similarity to C.elegans hypothetical protein
9172_at 5731.9 P
subunit 2 of replication factor RF-A\; 29\% identical to the human p34 subunit of RF-A
9173_at 488.7 P
hypothetical protein
9174_at 3545.1 P
similarity to S.pombe hypothetical protein SPAC24H6.02c
9175_at 378.9 A
Binds Sin3p in two-hybrid assay and is present in a large protein complex with Sin3p and Stb2p
9176_at 7874.0 P
similarity to S.pombe and C.elegans hypothetical proteins
9177_at 9130.5 P
43.1 kDa Serine\/threonine\/tyrosine protein kinase
9178_at 2729.8 P
ribosomal protein of the small subunit, mitochondrial
9179_at 6082.5 P
similarity to C-term. of A.nidulans regulatory protein (qutR)
9180_at 669.9 P
similarity to Ypt1p and rab GTP-binding proteins
9181_at 1293.2 P
hypothetical protein

9182_s_at	8924.7	P	Ribosomal protein S19B (rp55B) (S16aB) (YS16B)
9183_s_at	7333.6	P	Ribosomal protein L18B (rp28B)
9184_at	11466.0	P	Ribosomal protein L18B (rp28B)
9185_at	10307.0	P	hypothetical protein
9140_at	542.0	P	exhibits homology to Trf4p and Top1p
9141_at	2264.4	P	protein kinase, homologous to Ste20p, interacts with CDC42
9142_at	3183.9	P	similarity to S.pombe hypothetical protein SPAC23D3.13c
9143_at	222.5	P	questionable ORF
9144_at	491.9	P	hypothetical protein
9145_at	803.6	P	hypothetical protein
9146_at	663.1	P	Multicopy Suppressor of Bud Emergence
9147_at	3156.6	P	Pseudouridine synthase
9148_at	3125.0	P	N-glycosylated integral plasma membrane protein
9149_at	2313.6	P	Subunit 3 of Replication Factor C\; homologous to human RFC 36 kDa subunit
9150_at	1519.1	P	G(sub)1 cyclin that associates with PHO85
9151_at	3182.7	P	strong similarity to C.elegans hypothetical protein
9152_at	8753.6	P	non-clathrin coat protein involved in transport between ER and Golgi
9153_at	1019.9	P	Cold sensitive U2 snRNA Supressor
9154_at	426.7	P	hypothetical protein
9155_at	3053.4	P	Mitochondrial ribosomal protein MRPL10 (YmL10)
9156_at	3349.5	P	Putative integral membrane protein containing novel cysteine motif. Similarity to SLG1 (WSC1), WSC3 and WSC4
9157_at	1007.9	P	involved in processsing of tRNAs and rRNAs
9158_at	7863.3	P	strong similarity to YDR214w
9159_at	5973.5	P	sterol C-14 reductase
9160_at	976.5	P	hypothetical protein
9161_at	1506.6	P	similarity to YLR187w
9162_at	7.1	A	homoserine O-trans-acetylase
9118_at	462.6	M	questionable ORF

9119_at 1680.2 P
similarity to human band 3 anion transport protein
9120_at 1300.5 P
similarity to glycerate- and formate-dehydrogenases
9121_at 1720.8 P
topoisomerase I interacting factor 1
9122_at 935.6 P
Protein with coiled-coil domain essential for vesicular transport
9123_at 4008.7 P
contains formin homology domains\; homologous to BNR1 (BNI1 related protein)
9124_at 695.1 P
Protein highly homologous to permeases Can1p and Lyp1p for basic amino acids
9125_at 35.1 A
hypothetical protein
9126_at 9145.0 P
lysine permease
9127_at 1783.9 P
Phosphatidylinositol 4-kinase
9128_at 502.8 A
questionable ORF
9129_at 654.6 P
similarity to human protein KIAA0174
9130_at 2398.4 P
weak similarity to Sec14p
9131_at 4652.7 P
YIP1-Interacting Factor, shows similarity to NADH dehydrogenases
9132_at 2726.7 P
DNA polymerase II
9133_at 1655.2 P
Fifth largest subunit of origin recognition complex\; contains possible ATP-binding site
9134_at 575.0 P
hypothetical protein
9135_at 5158.8 P
Antioxidant protein and metal homeostasis factor, protects against oxygen toxicity
9136_at 1624.1 P
hypothetical protein
9137_at 1331.2 P
Interacts with SNF1 protein kinase
9138_at 2674.8 P
similarity to bacterial dihydropteroate synthase
9139_at 11974.0 P
strong similarity to nucleic acid-binding proteins
9095_at 268.4 P
hypothetical protein
9096_at 635.3 P
hypothetical protein
9097_at 3145.4 P
ribosomal protein of the large subunit (YmL30), mitochondrial
9098_at 1852.9 P
RNA recognition motif-containing protein that participates in sequence-specific regulation of nuclear pre-mRNA abundance
9099_at 654.9 P
protein contains a purine-binding domain, two heptad repeats and a hydrophobic tail, Rad50p interacts with Mre11p and Xrs2p in two-hybrid and immunoprecipitation analyses\; it co-localizes to spots with Mre11p and Xrs2p in a rad50s background
9100_at 360.4 P

similarity to YDR109c
9101_at 8470.1 P
49-kDa alpha subunit of RNA polymerase A
9102_at 6401.6 P
cysteinyl-tRNA synthetase
9103_at 4119.7 P
similarity to D.melanogaster SET protein
9104_at 878.8 P
hypothetical protein
9105_at 10242.0 P
translation initiation factor 3 (eIF3)
9106_at 7920.2 P
transmembrane protein
9107_at 968.4 P
similarity to human hypothetical protein KIAA0404
9108_at 9157.2 P
Glucose-6-phosphate dehydrogenase
9109_at 2429.5 P
strong similarity to K.marxianus LET1 protein
9110_at 4672.5 P
Ca2+-dependent serine protease
9111_at 190.6 P
Yeast putative Transmembrane Protein
9112_at 2815.6 P
component of RNA polymerase II holoenzyme\/mediator complex
9113_at 273.2 A
questionable ORF
9114_at 372.1 P
weak similarity to mouse hemoglobin zeta chain
9115_at 2110.5 P
Is required to link Chs3p and Chs4p to the septins
9116_at 3746.5 P
hypothetical protein
9117_at 3819.7 P
weak similarity to Sec14p
9073_at 1035.0 P
weak similarity to mammalian transcription elongation factor elongin A
9074_at 2223.9 P
transcriptional regulator, putative glutathione transferase
9075_at 565.0 P
similarity to dnaJ-like proteins
9076_at 2.5 A
questionable ORF
9077_at -226.9 A
questionable ORF
9078_at 888.1 P
chaotic nuclear migration\; predicted mass is 67kDa
9079_at 1143.0 P
hypothetical protein
9080_at 94.7 P
Aut2p interacts with Tub1p and Tub2p\; Aut2p forms a protein complex with Aut7p\; Aut2p mediates attachment of autophagosomes to microtubules
9081_at 2812.3 P
functionally related to TFIIB, affects start site selection in vivo
9082_at 3151.0 P
Component of nuclear RNase P and RNase MRP

9083_at 9841.3 P
adenylosuccinate synthetase
9084_at 5965.3 P
mannosyltransferase
9085_at 115.3 A
similarity to E.coli hypothetical protein in serS 5 region
9086_at 2360.8 P
weak similarity to E.coli bis(5 -nucleosyl)-tetraphosphatase
9087_at 1919.7 P
repressor activator protein
9088_at 473.3 P
similarity to hypothetical S. pombe protein
9089_at 426.7 P
23 kDa peroxisome associated protein, binds Pex14p
9090_at 1156.5 P
hypothetical protein
9091_at 3790.4 P
weak simlarity to C.cardunculus cypro4 protein
9092_at 1394.7 P
hypothetical protein
9093_at 54.0 P
encodes protein with RNA-binding motifs required for MRE2-dependent mRNA splicing
9094_s_at 10659.6 P
Heat shock protein of HSP70 family, homolog of SSB1
9050_at 11173.1 P
weak similarity to Colletotrichum gloeosporioides nitrogen starvation-induced glutamine rich protein
9051_at 5813.7 P
similarity to M.jannaschii hypothetical protein MJ1073
9052_at 1574.9 P
similarity to structure-specific recognition proteins
9053_at -120.2 A
questionable ORF
9054_g_at 90.6 P
questionable ORF
9055_at 316.5 P
sporulation-specific protein
9056_at -236.0 A
weak similarity to B.subtilis CDP-diacylglycerol--serine O-phosphatidyltransferase
9057_at 732.2 P
peroxisomal 2,4-dienoyl-CoA reductase
9058_at 1355.4 P
involved in regulation of carbon metabolism
9059_at 747.4 P
strong similarity to human TGR-CL10C
9060_at 802.2 P
Activates transcription of glycolytic genes\; homologous to GCR1\; may function in complex with Gcr2p
9061_at 187.3 A
questionable ORF
9062_at 1765.2 P
Protein involved in regulation of cell size
9063_at -250.7 A
sporulation-specific protein with a leucine zipper motif, regulated by the transcription factor Ume6 and expressed early in meiosis
9064_at 937.6 P
hypothetical protein
9065_at -83.9 A

strong similarity to YDL222c and similarity to Sur7p
9066_at 1441.6 P
hypothetical protein
9067_at 4316.0 P
chitin synthase 1
9068_at 1708.5 P
similarity to Synechocystis hypothetical protein
9069_at 12103.5 P
hypothetical protein
9070_at 5577.7 P
karyopherin alpha homolog of 60 kDa
9071_at 475.4 P
involved in spindle pole body duplication and karyogamy, interacts with Cdc31p, localizes to the spindle pole body
9072_at 611.2 P
hypothetical protein
9028_at 9884.4 P a
deubiquitinating enzyme
9029_at 1436.2 P
ribosomal protein of the large subunit, mitochondrial
9030_at 1007.2 P
questionable ORF
9031_at 1539.1 P
protein kinase homolog
9032_at 2213.8 P
weak similarity to S.pombe hypothetical protein
9033_at 3291.8 P
similarity to hypothetical S. pombe protein
9034_at 349.2 P
hypothetical protein
9035_at 10306.6 P
Ribosomal protein S3 (rp13) (YS3)
9036_at 1169.9 P
hypothetical protein
9037_at 2108.5 P
weak similarity to Hkr1p
9038_at 6567.5 P
similarity to S.pombe Rnp24p
9039_at 838.8 P
hypothetical protein
9040_at 940.3 P
multicopy suppressor of bem1 mutation, may be involved in G-protein mediated signal transduction
9041_at 2044.1 P
Component of the anaphase-promoting complex
9042_at 176.3 A
questionable ORF
9043_at 300.3 P
questionable ORF
9044_at 8848.5 P
Phosphatidylserine Decarboxylase 1
9045_at 3648.4 P
similarity to C.elegans ZK688.3 protein and E.coli hpcEp
9046_at 2538.0 P
CREB like repressor, bZIP protein that binds to CRE motifs, interacts with Mig1p
9047_at 1970.5 P
hypothetical protein

9048_at 1511.9 P
similarity to YOR385w and YMR316w
9049_at 2088.5 P
hypothetical protein
9005_at 3035.9 P
translation elongation factor eEF4
9006_s_at 10771.3 P
Ribosomal protein L42A (YL27) (L41A)
9007_at 1598.5 P
Protein kinase
9008_at 3403.4 P
YGP1 encodes gp37, a glycoprotein synthesized in response to nutrient limitation which is homologous to the sporulation-specific SPS100 gene
9009_at 954.6 P
hypothetical protein
9010_at 868.3 P
hypothetical protein
9011_at 4622.9 P
weak similarity to S.pombe hypothetical protein SPAC10F6
9012_at 7316.8 P
similarity to YHR133c
9013_at 1729.1 P
hypothetical protein
9014_at 3102.5 P
membrane-bound casein kinase I homolog
9015_at 6518.1 P
Putative homolog of subunit 4 of bovine prefoldin, a chaperone comprised of six subunits
9016_at 1462.7 P
hypothetical protein
9017_at 3829.3 P
31-kDa subunit of RNA polymerase III (C)\; HMG1 like protein
9018_at 1231.2 P
hypothetical protein
9019_at 4707.9 P
weak similarity to S.pombe hypothetical protein
9020_at 817.0 A
cofactor B
9021_at 1680.0 P
Sm-like protein
9022_at 266.3 P
hypothetical protein
9023_at 21.6 A
mating a-factor pheromone precursor
9024_at 101.3 A
similarity to YHR131c
9025_at 222.1 P
hypothetical protein
9026_at 461.3 P
Ammonia transport protein
9027_at 7655.2 P
Adenosine deaminase\/adenine aminohydrolase
8982_i_at 754.7 P
questionable ORF
8983_s_at 2056.6 P
questionable ORF
8984_at 11142.4 P

70-kDa adenylyl cyclase-associated protein

8985_at 5132.1 P

putative mitochondrial S4 ribosomal protein

8986_at 1240.9 P

similarity to neurofilament triplet M protein

8987_at 9563.8 P

peptidylprolyl cis-trans isomerase

8988_at 10300.9 P

similarity to C.carbonum toxD gene

8989_at 1029.8 P

hypothetical protein

8990_at 1926.1 P

similarity to A.ambisexualis antheridiol steroid receptor

8991_at 5298.2 P

Mitochondrial import receptor complex protein

8992_at 8690.2 P

sn-1,2-diacylglycerol cholinephosphotransferase

8993_at 1867.4 P

weak similarity to M.pneumoniae uridine kinase udk

8994_at 101.4 A

Similar to human tumor suppressor gene known as TEP1, MMAC1 and PTEN1. Contains sequence motifs characteristic of protein tyrosine phosphatases.

8995_at 1224.5 P

similarity to C.elegans hypothetical protein

8996_at 140.5 P

spindle pole body component, associates in a complex with Spc97p and Tub4p perhaps as part of the microtubule attachment site of the SBP

8997_at 5095.6 P

Protein with similarity to mammalian monocarboxylate transporters MCT1 and MCT2

8998_at 2659.5 P

similarity to hypothetical S. pombe protein

8999_at 6340.4 P

weak similarity to C.jejuni serine protease

9000_at 1071.0 P

hypothetical protein

9001_at 6756.6 P

70 kDa mitochondrial specialized import receptor of the outer membrane

9002_at 266.3 A

questionable ORF

9003_at 2278.5 P

weak similarity to M.jannaschii hypothetical protein MJ1257

9004_at 851.2 P

essential suppressor of the respiratory deficiency of a pet mutant

8959_at 342.1 A

carbon-catabolite sensitive malate synthase

8960_at 1374.1 P

weak similarity to RING zinc finger protein from Gallus gallus

8961_at 995.8 P

weak similarity to S.pombe hypothetical protein SPAC23C11

8962_at 1429.7 P

questionable ORF

8963_at 10645.5 P

subunit common to RNA polymerases I (A) and III (C)

8964_at 7574.7 P

ATP-dependent RNA helicase of DEAD box family

8965_at 9595.1 P

ATP-dependent RNA helicase of DEAD box family
8966_at 11345.3 P
cytochrome b5
8967_at 7285.5 P
weak similarity to fruit fly RNA-binding protein
8968_at 290.4 A
weak similarity to cytochrome-c oxidase
8969_at 4499.0 P
strong similarity to YOR110w
8970_at 1994.3 P
similarity to human AF-9 protein
8971_at 1331.5 P
inositol polyphosphate 5-phosphatase
8972_at 11.9 A
questionable ORF
8973_at 9450.1 P
alpha-isopropylmalate synthase (2-Isopropylmalate Synthase)
8974_at 1105.3 P
member of the leucine zipper family of transcriptional activators
8975_at 6375.8 P
DNA polymerase I alpha subunit, p180
8976_at 2789.7 P
similarity to YKL146w
8977_at 1859.2 P
hypothetical protein
8978_at 4847.1 P
similarity to YNL032w, YNL056w and YDR067c
8979_at 6767.9 P
Ras proto-oncogene homolog
8980_at 764.7 P
involved in transcriptional regulation of PHO5
8981_at 10098.3 P
Ribosomal protein S7B (rp30)
8936_at 14725.9 P
Ribosomal protein S7B (rp30)
8937_at 1261.6 P
strong similarity to YOR092w
8938_at 813.1 P
similarity to S.pombe hypothetical protein
8939_at 3.8 A
rab5-like GTPase involved in vacuolar protein sorting and endocytosis
8940_at -3.8 A
similarity to hypothetical C. elegans proteins Y48E1C.2 and Y48E1C.c
8941_at 3126.9 P
similarity to chicken h-caldesmon, Uso1p and YKL201c
8942_at 2892.3 P
GTP-binding protein of the rho subfamily of ras-like proteins
8943_at -185.4 A
questionable ORF
8944_at 2876.3 P
topoisomerase II, Top2p localizes to axial cores in meiosis
8945_at 4467.4 P
weak similarity to synaptogamines
8946_at 4254.2 P
hypothetical protein
8947_at 5437.7 P

Protein involved in propagation of M2 dsRNA satellite of L-A virus

8948_at 1257.8 P

Required for endocytosis and organization of the cytoskeleton

8949_at 1686.9 P

weak similarity to rabbit peroxisomal Ca-dependent solute carrier

8950_at 777.4 P

MutL homolog, similar to Mlh1p, associates with Mlh1p, possibly forming a heterodimer, Pms1p and Msh1p act in concert to bind to a Msh2p-heteroduplex complex containing a G-T mismatch

8951_at 1626.5 P

similarity to ribosomal protein S13

8952_at 3090.7 P

hypothetical protein

8953_at 10133.1 P

tropomyosin I

8954_at 5221.1 P

hypothetical protein

8955_at 382.7 P

similarity to dnaJ protein homolog YDJ1

8956_at 2113.2 P

negative regulator of Ras cAMP pathway, shares weak homology with Spt2p

8957_at 7386.1 P

similarity to YHR088w and C.elegans hypothetical protein F44G4.1

8958_at 1356.2 P

Protein of unknown function

8914_at 1707.1 P

mitochondrial lysine-tRNA synthetase

8915_at 2062.4 P

RNase H(35), a 35 kDa ribonuclease H

8916_at 6165.0 P

Dihydrolipoamide acetyltransferase component (E2) of pyruvate dehydrogenase complex

8917_at 8355.3 P

translocase of the outer mito. membrane

8918_at 13506.8 P

Ribosomal protein L16B (L21B) (rp23) (YL15)

8919_at 1472.1 P

Fork Head homolog two

8920_i_at 12328.4 P

Ribosomal protein L9B (L8B) (rp24) (YL11)

8921_s_at 10156.2 P

Ribosomal protein L9B (L8B) (rp24) (YL11)

8922_at 11842.6 P

Protein involved in the aging process

8923_at 3268.0 P

similarity to resistance proteins

8924_at 7795.2 P

yeast dnaJ homolog (nuclear envelope protein)\; heat shock protein

8925_at 1101.0 P

weak similarity to Mycoplasma protoporphyrinogen oxidase

8926_at 5128.0 P

RNA-binding (zeta) subunit of translation initiation factor 3 (eIF-3)

8927_at 9809.0 P

90-kDa protein, located in nucleolus, that is homologous to a human proliferation-associated nucleolar protein, p120

8928_at 1262.5 P

Actin-related protein

8929_at 4958.6 P

similarity to YIL117c
8930_at 229.1 P
questionable ORF
8931_at 3503.5 P
similarity to YNL032w and YNL099c
8932_at 13815.1 P
Outer mitochondrial membrane porin (voltage-dependent anion channel, or VDAC)
8933_at 1701.6 P
vacuolar protein
8934_at 940.0 P
Tyrosine protein phosphatase involved in adaptation response to pheromone
8935_at 9570.0 P
Cytochrome-c oxidase chain Va
8891_at 981.0 P
hypothetical protein
8892_at 754.2 P
hypothetical protein
8893_at 1821.2 P
putative zinc finger protein
8894_at 4026.0 P
Required for aspargine-linked glycosylation
8895_at 1400.1 P
similarity to probable transcription factor Ask10p and hypothetical protein YPR115w, and strong similarity to hypothetical protein YIL105c
8896_at 2773.5 P
hypothetical protein
8897_at 4236.0 P
strong similarity to human leukotriene-A4 hydrolase
8898_at 181.2 P
questionable ORF
8899_at 991.3 P
Bypass of PAM1
8900_at 1631.9 P
weak similarity to Mlp1
8901_at 1494.2 P
weak similarity to M.genitalium alanine--tRNA ligase
8902_at 2463.8 P
90 kd subunit of TFIIIB, also called TFIIIB90 or B or B 90 component
8903_at 1327.4 P
hypothetical protein
8904_at 4440.5 P
alpha-4-beta-4 subunit of mitochondrial isocitrate dehydrogenase 1
8905_at 3474.8 P
involved in secretion of proteins that lack classical secretory signal sequences
8906_at 1146.7 P
hypothetical protein
8907_s_at 67.0 A
nearly identical to YNL018c
8908_s_at 238.1 A
nearly identical to YNL019c
8909_at 2699.7 P
Tyrosine phosphatase
8910_at 10454.5 P
Histone H3 (HHT1 and HHT2 code for identical proteins)
8911_s_at 10171.7 P
Histone H4 (HHF1 and HHF2 code for identical proteins)

8912_at 2105.9 P
Putative mannosyltransferase of the KRE2 family
8913_at -191.2 A
questionable ORF
8868_at 1508.0 P
putative transcription factor
8869_at 2705.9 P
similarity to S.pombe hypothetical protein
8870_at 381.7 P
C-type cyclin associated with the Ssn3p cyclin-dependent kinase
8871_at 1049.7 P
weak similarity to YBR271w and YJR129c
8872_at 1248.3 P
Transcription factor homolog\; similarity to Drosophila melanogaster shuttle craft protein\; similarity to human NFX1 protein\; similarity to human DNA-binding protein tenascin
8873_at 2639.0 P
weak similarity to C.burnetii FMU protein
8874_at 2819.0 P
histone deacetylase, shares sequence similarity with Rpd3p, Hos1p, Hos2p, and Hos3p
8875_at 203.5 P
Predicted Ser\/thr kinase
8876_i_at 1069.5 P
hypothetical protein
8877_r_at 310.0 A
hypothetical protein
8878_s_at -127.2 A
hypothetical protein
8879_at 8993.6 P
poly(A)+ RNA-binding protein
8880_at 2521.4 P
Proteinase inhibitor I2B (PBI2), that inhibits protease Prb1p (yscB)
8881_at 203.4 A
translation elongation factor eEF3 homolog
8882_at 215.8 P
questionable ORF
8883_at 107.7 P
encodes a protein with high similarity to phospholipase B
8884_at 887.6 P
similarity to hypothetical A. thaliana protein T14G11.21
8885_at 8081.2 P
weak similarity to B.subtilis hypothetical protein ykrX
8886_at 318.6 P
peroxisomal NADP-dependent isocitrate dehydrogenase
8887_at 2947.8 P
similarity to YMR119w
8888_at 9918.4 P
sit4 suppressor, dnaJ homolog
8889_at 4142.5 P
Required for amino acid permease transport from the Golgi to the cell surface
8890_at 2365.0 P
Mitochondrial ribosomal protein MRP7 (YmL2) (E. coli L27)
8845_at 3909.3 P
hypothetical RNA-binding protein
8846_at 910.0 P
Member of family of mitochondrial carrier proteins
8847_at 7908.0 P

Significant sequence similarity to RPL7B, but neither can functionally replace the other. Does not correspond to any ribosomal component identified so far, based on its biochemical features

8848_at 2742.2 P

an ORF of unknown function located in a centromeric region duplicated between chromosomes III and XIV (DOM34 homologue on chromosome III is a pseudogene)

8849_at 10716.4 P

citrate synthase. Nuclear encoded mitochondrial protein.

8850_at 180.0 A

Putative transmembrane protein

8851_at 1632.6 P

34-kDa subunit of RNA polymerase III (C)

8852_at 80.2 P

weak similarity to bovine interferon gamma precursor

8853_at 6.6 A

questionable ORF

8854_at 2243.3 P

hydrophilic protein\; has cysteine rich putative zinc finger esential for function

8855_at 728.1 P

Protein involved in autophagocytosis during starvation

8856_at 3416.7 P

weak similarity to human phosphatidylcholine--sterol O-acyltransferase

8857_at 1404.8 P

hypothetical protein

8858_at 1112.7 P

Protein required for accurate mitotic chromosome segregation

8859_at 572.8 P

putative RNA-dependent ATPase

8860_at 1588.7 P

Uridine kinase

8861_at 6511.4 P

similarity to Pho87p and YJL198w

8862_at 232.8 P

weak similarity to hypothetical protein YMR206w

8863_at 2538.9 P

Suppressor of Mitochondrial Mutation in the tRNAasp gene

8864_at 12615.9 P

acetyl-CoA carboxylase

8865_at 7839.8 P

23 kDa mitochondrial inner membrane protein

8866_at 9139.2 P

hypothetical protein

8867_at 1717.3 P

Acyl-CoA cholesterol acyltransferase (sterol-ester synthetase)

8823_at 718.3 P

hypothetical protein

8824_at 5401.5 P

hypothetical protein

8825_at 1034.5 P

weak similarity to protein phosphatases

8826_at 1940.1 P

73 kDa subunit of the SWI\/SNF transcription activation complex, homolog of Rsc6p subunit of the RSC chromatin remodeling complex

8827_at 1829.5 P

weak similarity to Rpc31p

8828_at 1319.4 P

questionable ORF

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8829_at     2796.4     P
Guanine nucleotide exchange factor for Sar1p.
8830_at     3759.1     P
similarity to human pyridoxal kinase
8831_at     1848.2     P
Cyclophilin
8832_at     3986.7     P
similarity to P.denitrificans cobW protein
8833_at     4609.9     P
ExtraCellular Mutant
8834_at     2714.5     P                                                                A
MAP kinase kinase kinase\; activator of Pbs2p
8835_at     3501.5     P
Serine\/threonine protein phosphatase involved in glycogen accumulation
8836_at     1943.7     P
para-aminobenzoate synthase, PABA synthase
8837_at     947.3      P
shows similarity to glucose-6-phosphate dehydrogenase non-catalytic domains\; homologous to Sol2p
and Sol3p
8838_at     3499.6     P
Arp Complex Subunit
8839_at     5735.4     P
strong similarity to ribosomal protein S12
8840_at     2109.6     P
strong similarity to Mycoplasma ribosomal protein S19
8841_at     5319.3     P
putative RNA helicase
8842_at     1713.3     P
weak similarity to Anopheles mitochondrial NADH dehydrogenase subunit 2
8843_at     663.1      P
hypothetical protein
8844_at     2892.0     P
para hydroxybenzoate: polyprenyl transferase
8800_at     985.9      A
hypothetical protein
8801_at     13222.2    P
mevalonate pyrophosphate decarboxylase
8802_at     11408.8    P
anchorage subunit of a-agglutinin
8803_at     576.4      P
translational activator of cytochrome c oxidase
8804_at     6513.9     P
strong similarity to S.pombe hypothetical protein SPAC31A2.02
8805_at     598.3      P
similarity to ser/thr protein kinases
8806_at     625.5      P
strong similarity to YCR094w and YNL323w
8807_at     1582.9     P
small hydrophilic protein, enriched in microsomal membrane fraction, interacts with Sec1p
8808_at     7421.6     P
Saccharopine dehydrogenase (NADP+, L-glutamate forming) (saccharopine reductase) (EC 1.5.1.10)
8809_at     1649.2     P
weak similarity to chicken nucleolin
8810_at     5106.0     P
Putative transcription factor
8811_at     7002.4     P
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strong similarity to human breast tumor associated autoantigen
8812_at	5499.1	P
strong similarity to human breast tumor associated autoantigen
8813_at	2255.0	P
similarity to C.elegans hypothetical protein CEESL47F
8814_at	5901.3	P
Putative ion transporter similar to the major facilitator superfamily of transporters
8815_at	211.7	A
transmembrane regulator of KAPA\/DAPA transport
8816_at	1131.8	P
dethiobiotin synthetase
8817_at	592.4	P
7,8-diamino-pelargonic acid aminotransferase (DAPA) aminotransferase
8818_at	438.6	P
similarity to to alpha-1,3-mannosyltransferase
8819_at	450.3	P
similar to FRE2
8820_at	1315.2	P
weak similarity to hypothetical protein YDL218w
8821_at	167.0	P
weak similarity to H.influenzae L-lactate permease (lctP) homolog
8822_at	175.3	A
weak similarity to CYC1/CYP3 transcription activator
8776_at	-123.1	A
similarity to R.capsulatus 1-chloroalkane halidohydrolase
8777_at	4135.5	P
strong similarity to YJL222w, YIL173w and Pep1p
8778_at	851.9	P
strong similarity to Pep1p
8779_at	4113.4	P
similarity to beta-glucan-elicitor receptor - Glycine max
8780_at	413.3	P
similarity to Bul1p
8781_at	-39.0	A
similarity to central part of Bul1p
8782_at	92.1	A
strong similarity to Snq2p
8783_at	297.6	P
strong similarity to UDP-glucose 4-epimerase Gal10p
8784_s_at	342.6	A
strong similarity to E.coli D-mannonate oxidoreductase, identical to YEL070w
8785_at	2781.5	P
weak similarity to B.subtilis nitrite reductase (nirB)
8786_f_at	1939.7	P
member of the seripauperin protein\/gene family
8787_at	2018.1	P
hypothetical protein identified by SAGE
8788_at	641.8	P
hypothetical protein
8789_s_at	7137.3	P
Aminopeptidase of cysteine protease family
8790_s_at	5306.9	P
protein of unknown function
8791_at	226.9	A
non-annotated SAGE orf Found reverse in NC_001146 between 60023 and 60190 with 100% identity. See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251

8792_at -104.0 A
non-annotated SAGE orf Found reverse in NC_001146 between 60181 and 60321 with 100% identity.
See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251
8793_at 736.2 P
non-annotated SAGE orf Found reverse in NC_001146 between 118895 and 119086 with 100% identity.
See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251
8794_i_at -176.5 A
non-annotated SAGE orf Found forward in NC_001146 between 440983 and 441117 with 100% identity.
See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251
8795_r_at 290.4 A
non-annotated SAGE orf Found forward in NC_001146 between 440983 and 441117 with 100% identity.
See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251
8796_at 924.7 P
non-annotated SAGE orf Found forward in NC_001146 between 728144 and 728293 with 100% identity.
See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251
8797_f_at 244.6 P
non-annotated SAGE orf Found forward in NC_001146 between 101909 and 102082 with 100% identity.
See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251
8798_at -307.4 A
non-annotated SAGE orf Found reverse in NC_001146 between 301931 and 302119 with 100% identity.
See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251
8799_at 557.4 P
non-annotated SAGE orf Found forward in NC_001146 between 499414 and 499554 with 100% identity.
See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251
8752_f_at 233.3 P
non-annotated SAGE orf Found reverse in NC_001146 between 519600 and 519773 with 100% identity.
See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251
8753_at 505.0 A
non-annotated SAGE orf Found forward in NC_001146 between 547109 and 547366 with 100% identity.
See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251
8754_at 13.3 A
non-annotated SAGE orf Found forward in NC_001146 between 568130 and 568402 with 100% identity.
See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251
8755_at 2702.1 P
non-annotated SAGE orf Found forward in NC_001146 between 716393 and 716575 with 100% identity.
See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251
8756_i_at 14020.9 P
non-annotated SAGE orf Found forward in NC_001146 between 94941 and 95090 with 100% identity.
See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251
8757_at -355.9 A
non-annotated SAGE orf Found forward in NC_001146 between 281645 and 281881 with 100% identity.
See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251
8758_g_at 81.4 A
non-annotated SAGE orf Found forward in NC_001146 between 281645 and 281881 with 100% identity.
See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251
8759_at 19.0 A
non-annotated SAGE orf Found reverse in NC_001146 between 351383 and 351577 with 100% identity.
See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251
8760_at 12.1 A
non-annotated SAGE orf Found reverse in NC_001146 between 412222 and 412371 with 100% identity.
See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251
8761_at -2.4 A
non-annotated SAGE orf Found reverse in NC_001146 between 413306 and 413485 with 100% identity.
See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251
8762_at 3088.7 A
non-annotated SAGE orf Found reverse in NC_001146 between 478137 and 478292 with 100% identity.

See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251

8763_at 279.4 P

non-annotated SAGE orf Found reverse in NC_001146 between 478228 and 478365 with 100% identity.

See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251

8764_at 573.1 P

non-annotated SAGE orf Found forward in NC_001146 between 482996 and 483139 with 100% identity.

See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251

8765_at 1633.3 P

non-annotated SAGE orf Found forward in NC_001146 between 663707 and 663856 with 100% identity.

See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251

8766_at 2627.4 P

non-annotated SAGE orf Found reverse in NC_001146 between 17705 and 17908 with 100% identity.

See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251

8767_at 2178.5 P

non-annotated SAGE orf Found forward in NC_001146 between 140489 and 140683 with 100% identity.

See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251

8768_at 147.2 P

non-annotated SAGE orf Found reverse in NC_001146 between 254027 and 254161 with 100% identity.

See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251

8769_g_at -207.1 A

non-annotated SAGE orf Found reverse in NC_001146 between 254027 and 254161 with 100% identity.

See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251

8770_i_at 234.3 P

non-annotated SAGE orf Found reverse in NC_001146 between 254055 and 254201 with 100% identity.

See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251

8771_r_at 2.9 A

non-annotated SAGE orf Found reverse in NC_001146 between 254055 and 254201 with 100% identity.

See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251

8772_at 3528.0 P

non-annotated SAGE orf Found forward in NC_001146 between 283359 and 283541 with 100% identity.

See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251

8773_at 4669.5 P

non-annotated SAGE orf Found forward in NC_001146 between 465994 and 466167 with 100% identity.

See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251

8774_at 6062.9 P

non-annotated SAGE orf Found reverse in NC_001146 between 586598 and 586816 with 100% identity.

See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251

8775_at 1698.0 P

non-annotated SAGE orf Found forward in NC_001146 between 89019 and 89186 with 100% identity.

See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251

8729_at 2017.2 P

non-annotated SAGE orf Found forward in NC_001146 between 89212 and 89394 with 100% identity.

See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251

8730_g_at 9338.9 P

non-annotated SAGE orf Found forward in NC_001146 between 89212 and 89394 with 100% identity.

See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251

8731_at -30.5 A

non-annotated SAGE orf Found reverse in NC_001146 between 240147 and 240317 with 100% identity.

See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251

8732_at -62.6 A

non-annotated SAGE orf Found reverse in NC_001146 between 286092 and 286301 with 100% identity.

See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251

8733_at 880.8 P

non-annotated SAGE orf Found forward in NC_001146 between 330326 and 330544 with 100% identity.

See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251

8734_at 56.7 A

non-annotated SAGE orf Found reverse in NC_001146 between 335742 and 335897 with 100% identity.
See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251
8735_at 1176.4 P
non-annotated SAGE orf Found reverse in NC_001146 between 355301 and 355477 with 100% identity.
See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251
8736_at 166.8 P
non-annotated SAGE orf Found forward in NC_001146 between 366082 and 366222 with 100% identity.
See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251
8737_i_at 22.6 A
non-annotated SAGE orf Found reverse in NC_001146 between 546974 and 547210 with 100% identity.
See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251
8738_s_at -8.6 P
non-annotated SAGE orf Found reverse in NC_001146 between 546974 and 547210 with 100% identity.
See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251
8739_at 79.5 P
non-annotated SAGE orf Found forward in NC_001146 between 553015 and 553233 with 100% identity.
See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251
8740_f_at 59.3 A
non-annotated SAGE orf Found forward in NC_001146 between 563260 and 563397 with 100% identity.
See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251
8741_at 736.4 A
non-annotated SAGE orf Found forward in NC_001146 between 586648 and 586803 with 100% identity.
See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251
8742_at 303.2 A
non-annotated SAGE orf Found forward in NC_001146 between 591162 and 591341 with 100% identity.
See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251
8743_at 247.8 P
non-annotated SAGE orf Found reverse in NC_001146 between 604522 and 604659 with 100% identity.
See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251
8744_at 303.9 A
non-annotated SAGE orf Found reverse in NC_001146 between 661997 and 662158 with 100% identity.
See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251
8745_at 544.8 P
non-annotated SAGE orf Found reverse in NC_001146 between 663592 and 663789 with 100% identity.
See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251
8746_at 9.4 A
non-annotated SAGE orf Found reverse in NC_001146 between 779443 and 779604 with 100% identity.
See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251
8747_at 188.2 P
non-annotated SAGE orf Found forward in NC_001146 between 91546 and 91713 with 100% identity.
See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251
8748_at 279.8 A
non-annotated SAGE orf Found reverse in NC_001146 between 104727 and 104876 with 100% identity.
See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251
8749_at -24.1 A
non-annotated SAGE orf Found forward in NC_001146 between 116677 and 116865 with 100% identity.
See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251
8750_at -92.8 A
non-annotated SAGE orf Found forward in NC_001146 between 191051 and 191257 with 100% identity.
See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251
8751_at 1854.4 P
non-annotated SAGE orf Found reverse in NC_001146 between 267404 and 267571 with 100% identity.
See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251
8705_at 1006.6 P
non-annotated SAGE orf Found reverse in NC_001146 between 342215 and 342487 with 100% identity.
See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251

8706_at 167.4 P
non-annotated SAGE orf Found forward in NC_001146 between 394507 and 394662 with 100% identity.
See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251
8707_at 318.8 P
non-annotated SAGE orf Found forward in NC_001146 between 449543 and 449731 with 100% identity.
See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251
8708_at 208.5 A
non-annotated SAGE orf Found forward in NC_001146 between 452136 and 452276 with 100% identity.
See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251
8709_at 1637.0 P
non-annotated SAGE orf Found reverse in NC_001146 between 614367 and 614516 with 100% identity.
See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251
8710_at 763.2 P
non-annotated SAGE orf Found forward in NC_001146 between 623131 and 623265 with 100% identity.
See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251
8711_i_at -132.3 A
non-annotated SAGE orf Found reverse in NC_001146 between 651893 and 652045 with 100% identity.
See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251
8712_r_at 110.7 A
non-annotated SAGE orf Found reverse in NC_001146 between 651893 and 652045 with 100% identity.
See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251
8713_at 3995.3 P
snRNA
8714_at 165.9 P
snRNA
8715_at 67.7 A
hypothetical protein
8716_s_at 1088.4 P
Hypothetical aryl-alcohol dehydrogenase (AAD)
8717_at 370.9 P
similarity to Pseudomonas alkyl sulfatase
8718_at 160.3 A
similarity to P.putida phthalate transporter
8719_at 307.9 A
strong similarity to hypothetical protein YIL166c
8720_f_at -164.5 P
strong similarity to members of the Srp1p/Tip1p family
8721_at 7.5 A
hypothetical protein
8722_at 838.9 P
hypothetical protein
8723_at 3843.3 P
similarity to subtelomeric encoded proteins
8724_at 2714.2 P
similarity to glucan 1,4-alpha-glucosidase Sta1p and YAR066w
8725_g_at 3305.3 P
similarity to glucan 1,4-alpha-glucosidase Sta1p and YAR066w
8726_at 492.2 P
similarity to S.fumigata Asp FII
8727_at -9.7 A
strong similarity to Cps1p
8728_at 1277.5 P
similar to FRE2
8683_at 499.9 P
induced by osmotic stress\; similar to dihydroflavonol 4-reductase from plants
8684_at 105.9 A

questionable ORF
8685_at 1672.3 P
Decapping protein involved in mRNA degradation
8686_at 497.3 P
transcription factor, member of the histone acetyltransferase SAGA complex
8687_at 7218.5 P
Peroxisomal membrane protein
8688_at 2365.8 P
hypothetical protein
8689_at 513.7 P
CTR9 is required for normal CLN1 and CLN2 G1 cyclin expression
8690_at 1167.7 P
hypothetical protein
8691_at 10263.9 P
6,7-dimethyl-8-ribityllumazine synthase (DMRL synthase)
8692_at 8849.0 P
strong similarity to hypothetical S. pombe protein
8693_at 519.4 P
similarity to YDR435c and C.elegans hypothetical protein
8694_at 2107.6 P
Acetylornithine aminotransferase
8695_at 10220.0 P
mRNA cap binding protein eIF-4E
8696_at 1062.7 P
hypothetical protein
8697_at 1207.1 P
weak similarity to tetracycline resistance proteins
8698_at 1167.8 P
6-phosphofructo-2-kinase
8699_at 1491.8 P
Stoichiometric member of mediator complex
8700_at 14.8 A
questionable ORF
8701_at 4980.2 P
High level expression Reduces Ty3 Transposition
8702_at 937.6 P
similarity to glycophospholipid-anchored surface glycoprotein Gas1p
8703_at 64.2 A
hypothetical protein
8704_at 3024.3 P
ALuminium Resistance 1
8660_at 6167.7 P
similarity to hypothetical S. pombe protein
8661_at 1592.4 P
strong similarity to protein kinase Mck1p
8662_at 12176.1 P
Ribosomal protein L25 (rpl6L) (YL25)
8663_at 12427.1 P
cytosolic malate dehydrogenase
8664_at 2046.2 P
hypothetical protein
8665_at 4708.1 P
weak similarity to M.jannaschii hypothetical protein
8666_at 6319.0 P
Putative polyadenylated-RNA-binding protein located in nucleus\; similar to vertebrate hnRNP A\B protein family

8667_at 4279.4 P
has been localized to both the plasma membrane and the mitochondrial membrane
8668_at 13335.0 P
Ribosomal protein L18A (rp28A)
8669_at 3389.4 P
similarity to monocarboxylate transporter proteins
8670_at 137.1 P
hypothetical protein
8671_at 468.1 P
weak similarity to human sodium channel alpha chain HBA
8672_at 452.4 P
43 kDa protein, transcriptional activator
8673_at 1177.1 P
homologous to Trf5p and Top1p, associates with Smc1p and Smc2p
8674_at 316.2 P
similarity to human DS-1 protein
8675_at 537.6 P
Serine\/threonine protein kinase with similarity to Ste20p and Cla4p
8676_at 1322.9 P
Multicopy Suppressor of Bud Emergence
8677_at 6030.9 P
weak similarity to human ubiquitin-like protein GDX
8678_at 3191.6 P
Involved in RAS localization and palmitoylation
8679_at 10269.9 P
Overexpression yields resistance to Zeocin
8680_at 846.5 P
Transcription factor involved in activation of phospholipid synthetic genes
8681_at 391.1 P
weak similarity to human PL6 protein
8682_at 704.6 P
questionable ORF
8638_at 1136.5 P
Putative integral membrane protein containing novel cysteine motif. Similarity to SLG1 (WSC1), WSC2 and WSC4
8639_at 356.9 P
Involved in meiotic chromosome segregation\; may stabilize homologus DNA interactions at telomeres and is required for a telomere activity in distributive segregation\; is associated with telomeres
8640_at 5208.8 P
myo-inositol transporter
8641_at 2201.0 P
tRNA 2 -phosphotransferase
8642_at 1017.7 P
similarity to YOL002c and YDR492w
8643_at 176.2 P
Ser\/Thr protein kinase
8644_at 135.5 A
questionable ORF
8645_at 7137.0 P
similarity to hypothetical S.pombe protein
8646_at 10981.2 P
cytoplasmic tryptophanyl-tRNA synthetase
8647_at 1387.9 P
3,4-dihydroxy-5-hexaprenylbenzoate methyltransferase
8648_at 715.9 P
Helicase in MItochondria

8649_at 1357.6 P
Subunit 4 of Replication Factor C\; homologous to human RFC 40 kDa subunit
8650_at 1457.2 P
similarity to C.elegans hypothetical protein F25H8.1
8651_at 6608.4 P
strong similarity to YBR147w
8652_at 26.0 A
hypothetical protein
8653_at 1823.3 P
MutS homolog encoding major mismatch repair activity in mitosis and meiosis, functions with Pms1p and Pms2\/Mlh1p in a complex which interacts with either Pms3\/Msh6p to repair single-base and insertion-deletion mispairs, or Msh3p to repair only insertion-deletion mispairs
8654_at 1526.2 P
putative transcription factor\; contains a zinc finger
8655_at 1652.5 P
protein disulfide isomerase related protein
8656_at 880.0 P
similarity to S.pombe hypothetical protein
8657_at 7350.3 P
Alcohol dehydrogenase
8658_at 27.7 A
hypothetical protein
8659_at 272.4 P
similarity to A.thaliana hyp1 protein
8615_at 918.6 P
similarity to YOL082w
8616_at 1900.0 P
similarity to YOL083w
8617_at 1155.8 P
encodes a GTPase activating protein, highly homologous to Ira1p, homologue of neurofibromin
8618_at 2618.3 P
strong similarity to X.laevis XPMC2 protein
8619_at 224.1 A
similarity to NADH dehydrogenases
8620_at 600.7 P
hypothetical protein
8621_at 7265.8 P
strong similarity to C.elegans K12H4.3 protein
8622_at 1828.2 P
Dislikes Extra CIN8, (MDM) Mitochondrial distribution and morphology
8623_at 1293.3 P
similarity to A.gambiae ATP-binding-cassette protein
8624_at 2209.5 P
hypothetical protein
8625_at 2804.9 P
hypothetical protein
8626_at 1061.1 P
similarity to hypothetical S. pombe protein
8627_at 1293.3 P
hypothetical protein
8628_at 259.9 A
53-kDa coiled-coil protein
8629_at 4377.7 P
Homolog of SIR2
8630_at 284.5 P
Transcription factor (bHLH) involved in interorganelle communication between mitochondria,

peroxisomes, and nucleus
8631_at 2442.2 P
DRAP deaminase
8632_at 669.5 P
inositol polyphosphate 5-phosphatase
8633_at 5148.3 P 3
(2)5 -bisphosphate nucleotidase
8634_at 1005.8 P
hypothetical protein
8635_at 1870.0 P
Clathrin associated protein, medium subunit
8636_at 7931.1 P
Phosphoribosylpyrophosphate synthetase (ribose-phosphate pyrophosphokinase)
8637_at 2046.3 P
similarity to C.elegans hypothetical protein M02F4.4
8592_at 3225.8 P
Glycerol-3-phosphate dehydrogenase (NAD+)
8593_at 5305.9 P
arginosuccinate synthetase
8594_at 380.3 P
similarity to hypothetical C. elegans protein F02E9.6
8595_at 1535.4 P
phosphoglycerate mutase
8596_at 939.1 P
similarity to B. subtilis transcriptional activator tenA
8597_at 1305.1 P
weak similarity to transcription factors
8598_at 948.4 P
hypothetical protein
8599_at 2430.7 P
DNA Damage Responsive
8600_at 6779.9 P
S-adenosylmethionine decarboxylase
8601_at 2799.9 P
Component of the RNA polymerase II holoenzyme complex, positive and negative transcriptional regulator of genes involved in mating-type specialization
8602_at 168.3 P
questionable ORF
8603_at 4772.4 P
Glutathione Synthetase
8604_at 680.8 P
similarity to YAL018c and YOL047c
8605_at 207.7 A
weak similarity to hypothetical proteins YAL018c and YOL048c
8606_at -33.7 A
questionable ORF
8607_at 1723.5 P
similarity to ser/thr protein kinase
8608_at 1251.7 P
44 kDa phosphorylated integral peroxisomal membrane protein
8609_at 1570.2 P
Endonuclease III-like glycosylase 2
8610_at 1608.3 P
similarity to CCR4 protein
8611_at 1805.5 P
weak similarity to M.sativa nuM1, hnRNP protein from C. tentans and D. melanogaster, murine/bovine

poly(A) binding protein II, and Nsr1p
8612_at 10205.9 P
40S ribosomal protein S15 (S21) (rp52) (RIG protein)
8613_at 8825.6 P
60S acidic ribosomal protein P2A (L44) (A2) (YP2alpha)
8614_at 10161.9 P
alpha-type of subunit of 20S proteasome
8570_at 86.2 P
questionable ORF
8571_at 3061.4 P
weak similarity to YMR317w
8572_at 357.3 A
questionable ORF
8573_at 727.8 P
similarity to S.pombe rad18 and rpgL29 genes and other members of the SMC superfamily
8574_at 649.3 P
Mitochondrial glutamyl-tRNA synthetase
8575_at 477.8 P
hypothetical protein
8576_at 1581.4 P
weak similarity to Y.lipolytica Sls1 protein precursor
8577_at 6582.1 P
strong similarity to glycoprotein Gas1p
8578_at 1988.6 P
hypothetical protein
8579_at 1225.8 P
bZIP protein
8580_at 3489.3 P
similarity to YPR125w
8581_at 7124.9 P
hypothetical protein
8582_at 1799.4 P
Affects longevity
8583_at 362.5 A
hypothetical protein
8584_at 510.6 P
mitochondrial initiation factor 2
8585_at 3909.8 P
weak similarity to rat apoptosis protein RP-8
8586_at 3532.8 P
possible component of RCC1-Ran pathway
8587_at 3574.4 P
Tryptophan permease, high affinity
8588_at 6066.8 P
similarity to Rim9p and YFR012w
8589_at 687.9 P
tSNARE that affects a Late Golgi compartment
8590_at 189.8 P
similarity to YFR013w
8591_at 1913.6 P
Calmodulin-dependent protein kinase
8547_at -304.2 A
weak similarity to YKR015c
8548_at 1617.2 P
hypothetical protein
8549_at 870.4 P

Hmg-coa Reductase Degradation
8550_at 7555.5 P
An evolutionarily conserved member of the histone H2A F\/Z family of histone variants
8551_at 829.2 P
strong similarity to phospholipases
8552_at 2634.7 P
putative RNA 3 -terminal phosphate cyclase
8553_at 1722.1 P
Mdm12p is a mitochondrial outer membrane protein. An Mdm12p homolog exists in S. Pombe which confers a dominant negative phenotype when expressed in S. cerevisiae
8554_at 1270.5 P
hypothetical protein
8555_at 2092.3 P
Appears to be a structural component of the chitin synthase 3 complex
8556_at 2343.1 P
topoisomerase I
8557_at 5995.6 P
RNA polymerase II subunit, homologous to S. pombe Rpb11p subunit
8558_at 5406.6 P
DNA binding protein involved in transcriptional regulation
8559_at 1651.5 P
similarity to C.elegans hypothetical protein, YDR126w, YNL326c and YLR246w
8560_at 5448.7 P
strong similarity to YDR492w and S.pombe hypothetical protein
8561_at 1830.1 P
negative transcriptional regulator
8562_at 5150.8 P
Ribosomal RNA Processing
8563_at 4186.3 P
Required for glucosylation in the N-linked glycosylation pathway
8564_at 1566.8 P
subtilisin-like protease III
8565_at 8428.7 P
weak similarity to hypothetical protein YDR339c
8566_at 205.0 P
ATP dependent DNA ligase
8567_at 1697.1 P
similarity to M.jannaschii hypothetical protein MJ0708
8568_at 9008.0 P
small glutamine-rich tetratricopeptide repeat containing protein
8569_at 1908.2 P
Cell wall integrity and stress response component 1
8525_at -6.8 A
Killed In Mutagen, reduced growth in diepoxybutane and\/or mitomycin C
8526_at 2186.7 P
similarity to Tir1p and Tir2p
8527_at 6127.4 P
Cold-shock induced protein of the Srp1p\/Tip1p family of serine-alanine-rich proteins
8528_at 1333.5 P
strong similarity to ATP-dependent permeases
8529_at 498.1 P
similarity to YDR391c
8530_g_at 571.4 P
similarity to YDR391c
8531_at 1528.4 P
strong similarity to YDR391c

8532_at 2118.2 P
B-type regulatory subunit of protein phosphatase 2A (PP2A)
8533_at 3618.2 P
hypothetical protein
8534_at 2240.6 P
p24 protein involved in membrane trafficking
8535_at 2701.0 P
Mitochondrial membrane protein
8536_at 630.4 P
Resistance to o-dinitrobenzene, calcium, and zinc
8537_at 362.7 P
similarity to YDR474c
8538_at 11069.9 P
10 kDa mitochondrial heat shock protein
8539_at 7635.5 P
similarity to Pyrococcus horikoshii hypothetical protein PHBQ041
8540_at 731.6 P
weak similarity to D.melanogaster probable Ca2+ transporter rdgB
8541_at 2841.0 P
hypothetical protein
8542_at 382.3 P
hypothetical protein
8543_at 636.1 P
Homolog of SIR2
8544_at 2023.1 P
Protein required for cell cycle arrest in response to loss of microtubule function
8545_at 10589.3 P
Heat shock protein also induced by canavanine and entry into stationary phase
8546_at 973.3 P
bZIP protein, can activate transcription from a promoter containing a Yap recognition site
8502_at 217.0 A
hypothetical protein
8503_at 388.9 P
involved in invasive growth upon nitrogen starvation
8504_at 818.7 P
Metallothionein-like protein
8505_at 783.6 P
myc-family transcription factor homolog
8506_at 941.0 P
Protein that complements a drug-hypersensitive mutation
8507_at 768.8 P
Protein involved in constitutive endocytosis of Ste3p
8508_at 888.2 P
Required for mother cell-specific HO expression
8509_at 363.1 P
integral membrane protein\; c-terminal TMD\; located in endosome
8510_at 658.2 P
cytochrome c mitochondrial import factor
8511_at 3127.0 P
putative repressor protein\; contains nuclear targeting signal
8512_at 3675.5 P
Casein kinase II, beta subunit
8513_at 221.2 P
Mitochondrial glyoxylase-II
8514_at 278.1 P
questionable ORF

8515_at 1470.8 P
weak similarity to YDR273w
8516_at 1196.5 P
Protein involved in growth regulation
8517_at 2531.9 P
weak similarity to YDR275w
8518_at 11839.7 P
outer mitochondrial membrane protein, component of the mitochondiral protein translocation complex, associates with Isp42p
8519_at 11759.5 P
RNA helicase
8520_at 5652.2 P
homologous to MTH1\; interacts with the SNF1 protein kinase and TBP in two-hybrid and in in vitro binding studies
8521_at 1378.5 P
RNA trafficking protein\; transcription activator
8522_at -55.5 A
similarity to YER185w, Rta1p
8523_at 112.8 A
hypothetical protein
8524_at 4028.6 P
weak similarity to myosin heavy chain proteins
8480_at 3992.4 P
hypothetical protein
8481_at 1060.3 P
similarity to protamines
8482_at 1112.0 P
similarity to Sis2p protein and C.tropicalis hal3 protein
8483_at 41.3 A
questionable ORF
8484_at 4449.4 P
weak similarity to human phosphorylation regulatory protein HP-10
8485_at 1062.7 P
G2 allele of skp1 suppressor
8486_at 1257.0 P
encodes component of the spindle midzone
8487_at 2090.2 P
weak similarity to YGL144c
8488_at 667.0 P
hypothetical protein
8489_at 7219.9 P
alpha subunit of casein kinase II
8490_at 1626.3 P
strong similarity to YKR075c
8491_at 11718.0 P
Ribosomal protein L3 (rp1) (YL1)
8492_at 2119.6 P
weak similarity to human retinoblastoma binding protein 2
8493_at 5094.0 P
Cytochrome c1
8494_at 2104.0 P
hypothetical protein
8495_at 7256.3 P
glycosyl transferase
8496_at 116.6 A
hypothetical protein

8497_at 767.9 P
GTPase activating protein
8498_at 942.0 P
strong similarity to Thi10p
8499_at 497.4 A
hypothetical protein
8500_at 1003.5 P
hypothetical protein
8501_at 967.4 P
endoplasmic reticulum t-SNARE, coprecipitates with Sec20p, Tip1p. and Sec22p
8457_at 1364.9 P
similarity to Hbs1p, Sup2p and EF1-alpha
8458_at 166.9 P
similarity to mouse KIN17 protein
8459_at 3484.4 P
weak similarity to YMR172w
8460_at 3322.7 P
Multi-copy suppressor of SOD-linked defects
8461_at 1502.4 P
hypothetical protein
8462_at 5077.1 P
strong similarity to YKR089c
8463_at 992.9 P
questionable ORF
8464_at 803.4 P
weak similarity to YKR091w
8465_at 5378.8 P
hypothetical protein
8466_at 7568.2 P
34-kDa, gamma subunit of oligosaccharyl transferase glycoprotein complex
8467_at 3503.0 P
weak similarity to synaptogamines
8468_at 1516.0 P
hypothetical protein
8469_g_at 1848.0 P
hypothetical protein
8470_at 1766.3 P
weak similarity to human calcium influx channel
8471_at 4270.1 P
small GTP-binding protein\; geranylgeranylated\; geranylgeranylation required for membrane association\; also involved in endocytosis post vesicle internalization
8472_at 1518.8 P
similarity to ser/thr protein phosphatases
8473_at 994.2 P
similarity to hypothetical S.pombe protein D83992_G
8474_at 1588.0 P
ExtraCellular Mutant
8475_at 960.7 P
similarity to S.pombe hypothetical protein SPAC22F3.04
8476_at 2954.1 P
GTP-binding ADP-ribosylation factor
8477_at 6978.4 P
Ribose-5-phosphate ketol-isomerase
8478_at 13228.6 P
Ribosomal protein S7A (rp30)
8479_at 5585.8 P

Ribosomal protein S7A (rp30)
8434_at 829.5 P
hypothetical protein
8435_at 4297.6 P
nuclear pore complex protein
8436_at 6056.1 P
type 2 membrane protein\; probable secretory protein
8437_at 155.7 P
similarity to mitochondrial carrier proteins
8438_at 5787.3 P
ras proto-oncogene homolog
8439_at 13.5 A
questionable ORF
8440_at 1906.3 P
16-kDa, epsilon subunit of oligosaccharyltransferase complex\; 40\% identical to vertebrate DAD1 protein
8441_at 884.0 P
hypothetical protein
8442_g_at 907.1 P
hypothetical protein
8443_at 465.0 P
member of the syntaxin family of proteins\; predicted C-terminal TMD
8444_at 524.4 A
weak similarity to human G-0/G-1 switch regulatory protein 8
8445_at 6191.5 P
putative isoform of Leu4p
8446_at 2927.8 P
inositol polyphosphate 5-phosphatase
8447_at 2367.7 P
TFIIIC (transcription initiation factor) subunit, 55 kDa
8448_at 370.6 P
weak similarity to B.subtilis maf protein
8449_at 1571.9 P
similarity to C.elegans hypothetical protein
8450_at 270.1 P
probable transcription factor, asparagine-rich zinc-finger protein, suppressor of mutation in the nuclear gene for the core subunit of mitochondrial RNA polymerase
8451_at 305.6 P
hypothetical protein
8452_at 2316.7 P
involved in targeting and fusion of ER to golgi transport vesicles
8453_at 2802.7 P
RNA polymerase III large subunit
8454_at 7278.5 P
Probable 26S protease subunit and member of the CDC48\/PAS1\/SEC18 family of ATPases
8455_at 968.4 P
hypothetical protein
8456_at 1075.9 P
similarity to a C.elegans ZK632.3 protein
8412_at 1084.7 P
Similar to mammalian aldo\/keto reductases
8413_at 27.7 A
questionable ORF
8414_at 12338.0 P
profilin (actin-binding protein)
8415_at 4490.7 P
extremely hydrophilic protein

8416_at	3086.1	P	Ubiquitin-specific protease
8417_at	1034.0	P	may encode a protein involved in one or more monoxygenase or hydroxylase steps of ubiquinone biosynthesis
8418_at	1838.0	P	isoamyl acetate hydrolytic enzyme
8419_at	2083.7	P	rho type GTPase activating protein
8420_at	6613.2	P	phosphoribosylamino-imidazole-carboxylase
8421_at	1645.1	P	hypothetical protein
8422_at	749.3	P	mitochondrial integral membrane protein
8423_at	3161.7	P	weak similarity to E.coli hypothetical 27K protein
8424_at	3313.6	P	Peripheral membrane protein required for vacuolar protein sorting
8425_s_at	12114.7	P	translation elongation factor 2 (EF-2)
8426_at	-277.2	A	GTPase activating protein (GAP)
8427_at	-43.7	A	questionable ORF
8428_at	9721.7	P	NAD+-dependent isocitrate dehydrogenase
8429_at	707.3	P	similarity to YLR361c
8430_at	1837.1	P	hypothetical protein
8431_at	528.0	A	questionable ORF
8432_at	2992.3	P	Transcription factor
8433_at	1766.8	P	Actin-related protein
8389_at	7794.5	P	Succinate-CoA Ligase (ADP-Forming)
8390_at	769.6	P	Thiamin pyrophosphokinase
8391_at	1866.8	P	weak similarity to human DNA-binding protein PO-GA and to bacterial H+-transporting ATP synthases
8392_at	10141.9	P	strong similarity to hypothtical S. pombe protein and to hypothetical C. elegans protein
8393_at	115.6	M	questionable ORF
8394_at	175.9	P	similarity to YHR194w
8395_at	1854.1	P	required for final stages of splicesome maturation\; promotes step 1 of splicing
8396_at	587.8	P	Involved in plasmid maintenance
8397_at	2805.9	P	ribosomal protein of the large subunit, mitochondrial
8398_at	7561.9	P	

second largest subunit of RNA polymerase II
8399_at 189.5 P
hypothetical protein
8400_at 8528.0 P
multidrug resistance transporter
8401_at 1385.3 P
similarity to hypothetical A. thaliana proteins F19G10.15 and T19F06.21
8402_at 1210.8 P
similarity to 5 -flanking region of the Pichia MOX gene
8403_at 348.9 P
Interacts with C-terminus of CDC12
8404_at 10174.9 P
putative proteasome subunit
8405_at 2245.6 P
Mitochondrial ribosomal protein of small subunit
8406_at 1913.4 P
homologue of human E core protein
8407_at 2587.2 P
Protein involved in mRNA transport from nucleus to cytoplasm
8408_at 543.4 P
similarity to C.elegans cosmid F35C8
8409_at 936.6 P
transcription factor
8410_at 4086.8 P
strong similarity to S.pombe SPAC13G6.14 protein
8411_at 3418.1 P
hypothetical protein
8366_at 3072.0 P
similarity to E.histolytica surface lectin
8367_at 1434.2 P
hypothetical protein
8368_i_at 10482.6 P
Ribosomal protein S28A (S33A) (YS27)
8369_f_at 9029.5 P
Ribosomal protein S28A (S33A) (YS27)
8370_at 6053.8 P
glutaminyl-tRNA synthetase
8371_at 711.8 P
questionable ORF
8372_at 196.5 P
questionable ORF
8373_at 1072.1 P
sphingoid long chain base (LCB) kinase
8374_at 1652.0 P
similarity to finger protein YKL222c, YOR162c and YLR266c
8375_at 129.5 P
strong similarity to YLR270w
8376_at 2609.8 P
Stoichiometric member of mediator complex
8377_at 4714.8 P
similarity to human and murine C3f protein
8378_at 4027.9 P
ferrochelatase (protoheme ferrolyase)
8379_at 207.9 P
weak similarity to rat SCP1 protein
8380_at 41.0 A

Regulatory subunit for Glc7p
8381_at 1235.3 P
similarity to BRR5 protein
8382_at 160.8 P
Peroxisomal enoyl-CoA hydratase
8383_at 1781.2 P
Actin assembly factor
8384_f_at 10007.7 P
Ribosomal protein S30B
8385_at -66.6 A
hypothetical protein
8386_at 8916.3 P
phosphoserine transaminase
8387_at 1179.8 P
GTP binding protein, almost identical to Gsp1p
8388_at 425.9 A
hypothetical protein
8343_at 8173.4 P
Translation elongation factor Tu, mitochondrial
8344_at 1722.3 P
Protein that may play a role in polarity establishment and bud formation
8345_at 1656.1 P
weak similarity to chicken nonhistone chromosomal protein HMG-2
8346_at 56.5 A
sporulation-specific exo-1,3-beta-glucanase
8347_at 644.0 P
contains motifs that are present in a family of DNA-dependent ATPases, the SWI2\/SNF2-like proteins
8348_i_at 1261.0 P
strong similarity to Thi10p
8349_f_at 2027.6 P
strong similarity to Thi10p
8350_at 298.4 P
weak similarity to YPL112c
8351_at 2083.9 P
Transcription factor IIA, large chain
8352_at 734.1 P
possible leucine zipper
8353_at 2273.3 P
Involved in lipoic acid metabolism
8354_at 5997.7 P
hypothetical protein
8355_at 8394.1 P
Multicopy suppressor of BFA (Brefeldin A)-induced lethality\; implicated in secretion and nuclear segregation
8356_at -31.1 A
questionable ORF
8357_at 531.4 P
questionable ORF
8358_at 3908.6 P
Ribose methyltransferase for mitochondrial 21S rRNA
8359_at 4816.9 P
imidazoleglycerol-phosphate dehydratase
8360_at 1323.1 P
questionable ORF
8361_at 7644.7 P
ATP-dependent RNA helicase of DEAD box family\; suppressor of a pre-mRNA splicing mutation, prp8-1

8362_at 1546.0 P
hypothetical protein
8363_at 3075.4 P
similarity to Brettanomyces RAD4 and to S.pombe hypothetical protein
8364_at 8477.7 P
second-largest subunit of RNA polymerase III
8365_at 2384.9 P
protein tyrosine phosphatase
8320_at 7945.8 P
homology to bacterial nicotinate phosphoribosyl transferase
8321_at 9960.3 P
RNA polymerase II subunit
8322_at 829.9 P
encodes protein with GTP-binding domain related to dynamin
8323_at 6102.2 P
beta subunit of G protein coupled to mating factor receptor
8324_at 460.1 P
Involved in silencing at telomeres, HML and HMR
8325_at -160.0 A
hypothetical protein
8326_at 1498.8 P
similarity to M.xanthus hypothetical protein
8327_at 780.1 P
Relieves uso1-1 Transport Defect
8328_at 2964.0 P
Subunit 1 of Replication Factor C\; homologous to human RFC 140 kDa subunit
8329_at 1065.0 P
questionable ORF
8330_at 3109.4 P
dipeptidyl aminopeptidase
8331_at 3603.7 P
hypothetical protein
8332_at 1925.2 P
malonyl-CoA:ACP transferase
8333_at 18.5 A
malonyl-CoA:ACP transferase
8334_at 896.6 P
similarity to ADP/ATP carrier proteins
8335_at 1071.2 P
protein of unknown function
8336_at 12340.4 P
16-kDa RNA polymerase subunit (common to polymerases I, II and III)
8337_at 1552.2 P
questionable ORF
8338_at 9701.0 P
NifU-like protein A
8339_at 1641.6 P
similarity to microtubule-interacting protein Mhp1p
8340_at 3030.0 P
weak similarity to YNR013c
8341_at 4209.5 P
Transcriptional modulator
8342_at 11201.2 P
Transcriptional modulator
8297_at 1814.8 P
protein kinase involved in protein kinase C pathway

8298_at 3325.4 P
GrpE homolog, mitochondrial matrix protein
8299_at 4089.9 P
protein kinase
8300_f_at 9785.3 P
Ribosomal protein L33B (L37B) (rp47) (YL37)
8301_at -14.9 A
encodes snRNA U3, SNR17B also encodes snRNA U3
8302_at 2588.6 P
dihydrofolate reductase
8303_at -46.8 A
homology to human oxysterol binding protein
8304_at 2698.8 P
similarity to hypothetical S. pombe protein
8305_at 2066.0 P
hypothetical protein
8306_at 3945.5 P
similarity to C.elegans ZK1058.5 protein
8307_at 7083.5 P
tetrahydrofolylpolyglutamate synthase
8308_at 354.2 P
Sporulation Specific
8309_at 6522.9 P
similarity to M.jannaschii hypothetical protein MJ0588
8310_at 1892.7 P
Acetyltransferase in the SAS gene family
8311_at 2694.7 P
similarity to hypothetical C. elegans proteins
8312_at 5171.0 P
weak similarity to reductases
8313_at 11357.1 P
Suppressor of rad53 lethality
8314_g_at 11835.2 P
Suppressor of rad53 lethality
8315_i_at 8722.2 P
questionable ORF
8316_at 668.6 P
subunit of the anaphase promoting complex
8317_at 1399.6 P
CLeavage\/Polyadenylation factor IA subunit\; interacts with Pcf11p in the 2-hybrid system
8318_at 3821.4 P
similarity to thiosulfate sulfurtransferases
8319_at 1706.1 P
hypothetical protein
8274_at 2130.4 P
hypothetical protein
8275_at 2388.0 P
Protein involved in protein import into ER
8276_at -14.6 A
hypothetical protein
8277_at 1293.8 P
strong similarity to secretory protein Ssp134p
8278_at 3593.3 P
calcium-binding protein component of spindle pole bodies, localizes to half-bridges and interacts with KAR1
8279_at 772.5 P

hypothetical protein
8280_at 6430.9 P
ATPase\; component of the 26S proteasome cap subunit
8281_at 8962.5 P
translation initiation factor eIF2b gamma subunit\; negative regulator in the general control of amino acid biosynthesis
8282_at 4505.2 P
Subunit of the regulatory particle of the proteasome
8283_at 1597.6 P
similarity to YLR243w
8284_at 52.9 A
questionable ORF
8285_at 1585.0 P
hypothetical protein
8286_at 5509.4 P
Binds to beta-tubulin and may participate in microtubule morphogenesis
8287_at 409.7 P
Pentamidine resistance protein
8288_at 6820.8 P
similarity to ser/thr protein kinases
8289_at 203.7 P
hypothetical protein
8290_at 510.6 P
Required for viability in the absence of the kinesin-related Cin8p mitotic motor.
8291_at 9674.0 P
Vacuolar H-ATPase 100 kDa subunit of membrane (V0) sector, essential for vacuolar acidification and vacuolar H-ATPase activity
8292_at 11807.2 P
strong similarity to Rattus tricarboxylate carrier
8293_at 7435.6 P
microtubule-associated protein
8294_at 3221.2 P
similarity to resistance proteins
8295_at 935.0 P
transfer RNA isopentenyl transferase
8296_at 538.4 P
similarity to A.nidulans palA protein
8252_at 10234.7 P
Binds to eIF4E, the mRNA cap-binding protein, and represses cap-dependent translation initiation by interfering with the interaction of eIF4E and eIF4G
8253_at 184.4 A
questionable ORF
8254_at 1925.9 P
uroporphyrinogen III synthase
8255_at 131.3 M
hypothetical protein
8256_at 2820.5 P
similarity to S.pombe dihydrofolate reductase
8257_at 5554.2 P
weak similarity to phosducins
8258_at 209.0 A
questionable ORF
8259_at 2768.1 P
weak similarity to phosphoglycerate mutases
8260_at 928.1 P
weak similarity to M.jannaschii hypothetical protein MJ0694

8261_at	9271.0	P	similarity to D.melanogaster heat shock protein 67B2
8262_at	7942.7	P	similarity to D.melanogaster heat shock protein 67B2
8263_at	1256.3	P	weak similarity to PITSLRE protein kinase isoforms
8264_at	1610.0	P	Disulfide isomerase related protein
8265_at	404.1	P	similarity to C.elegans hypothetical protein
8266_at	4476.8	P	transcriptional regulator
8267_at	3178.3	P	similarity to cation translocating ATPases
8268_at	756.3	P	similarity to human and mouse glomerulosclerosis protein Mpv17
8269_f_at	8240.9	P	Ribosomal protein S10A
8270_f_at	16812.3	P	Ribosomal protein S10A
8271_at	4274.9	P	similarity to human hypothetical protein
8272_at	175.3	P	weak similarity to SWI/SNF complex 60 KDa subunit from man and mouse
8273_at	1103.0	P	similarity to hypothetical S. pombe protein
8229_at	4042.9	P	similarity to Sdh4p
8230_at	58.7	A	required for meiosis
8231_at	9031.7	P	multiprotein bridging factor
8232_at	2045.5	P	BUD site selection
8233_g_at	1713.4	P	BUD site selection
8234_at	175.6	A	questionable ORF
8235_at	3315.8	P	hypothetical protein
8236_at	3694.9	P	CPA1 leader peptide
8237_at	5671.2	P	Carbamoyl phosphate synthetase, arginine specific
8238_at	1281.5	P	has strong homology to Drosophila ISWI
8239_at	1888.7	P	AIP3 binding protein
8240_at	1491.1	P	hypothetical protein
8241_at	3931.8	P	similarity to human X-linked PEST-containing transporter
8242_at	3172.3	P	homolog of chloroplast phosphate transporter
8243_at	781.5	P	weak similarity to YIL149c

8244_i_at	12386.7	P	questionable ORF
8245_r_at	1329.1	P	questionable ORF
8246_s_at	8945.0	P	questionable ORF
8247_at	11383.9	P	57 kDa nucleolar protein
8248_at	8346.8	P	similarity to hypothetical S. pombe protein
8249_at	456.7	P	sporulation-specific protein
8250_at	239.7	A	hypothetical protein
8251_at	1847.8	P	hypothetical protein
8206_at	2398.8	P	Protein involved in cobalt accumulation\; dosage dependent suppressor of cobalt toxicity
8207_at	5318.0	P	long chain fatty acyl:CoA synthetase
8208_at	177.7	M	hypothetical protein
8209_at	488.5	P	homolog of mammalian splicing factor\/U2 snRNP protein
8210_at	1798.3	P	hypothetical protein
8211_at	1852.4	P	dolichyl phosphate-D-mannose:protein O-D-mannosyltransferase
8212_at	2418.6	P	similarity to hypothetical S.pombe protein SPAC1F12.05
8213_at	10536.3	P	gamma-glutamyl phosphate reductase
8214_at	788.6	P	similarity to YAL028w
8215_at	-33.8	A	questionable ORF
8216_at	3891.7	P	myosin-1
8217_at	9512.4	P	vesicle-associated membrane protein (synaptobrevin) homolog
8218_at	2388.4	P	Putative ABC transporter highly similar to Pdr5p
8219_at	1280.0	P	Multicopy suppressor of clathrin deficiency and of ts mutants of IPL1
8220_at	513.1	P	catalytic subunit of mitochondrial DNA polymerase
8221_at	420.7	P	questionable ORF
8222_at	8034.4	P	27-kDa subunit of the vacuolar ATPase\; E subunit of V1 sector
8223_at	190.8	P	questionable ORF
8224_at	994.7	P	splicing factor
8225_at	7079.9	P	Cytoplasmic alanyl-tRNA synthetase gene

8226_at 3223.4 P
Appears to function early in (1,6)-beta-D-glucan synthesis pathway
8227_at 2162.9 P
Mutants are defective in Ty1 Enhancer-mediated Activation
8228_at 1081.1 P
similarity to YAL034c
8183_at -87.6 A
strong similarity to E2 ubiquitin-conjugating enzymes
8184_at 4229.6 P
DNA-dependent RNA polymerase I subunit A43
8185_at 11424.2 P
RNA polymerase I subunit 190 (alpha)
8186_at 2533.1 P
weak similarity to YAl037w
8187_at 313.3 A
hypothetical protein
8188_at 2665.8 P
TYE7, a 33 kDa serine-rich protein, is a potential member of the basic region\/helix-loop-helix\/leucine-zipper protein family
8189_at 63.0 A
questionable ORF
8190_at 1214.1 P
deoxycytidyl transferase
8191_at 1795.7 P
Pyruvate kinase, glucose-repressed isoform
8192_at 360.0 P
putative proline-specific permease
8193_at 56.3 A
Protein involved in chromosome segregation, required for microtubule stability
8194_at 325.8 A
weak similarity to Esp1p and mitochondrial L.illustris cytochrome oxidase I
8195_at -66.8 A
mRNA is induced in meiosis, encodes a meiosis-specific serine\/threonine protein kinase which interacts with and is believed to phosphorylate Hop1p
8196_at 1013.3 P
hypothetical protein
8197_at 824.5 P
weak similarity to adenylate cyclases
8198_at 1969.8 P
hypothetical protein
8199_at 4318.8 P
nam9-1 suppressor
8200_at 5539.7 P
strong similarity to human electron transfer flavoprotein-ubiquinone oxidoreductase
8201_at 1730.7 P
Grd19p that is epitope tagged with the HA epitope at the C-terminus is functional, migrates at 28 kDa, fractionates predominantly in the cytosolic fraction (however a minor amount associates with membranes), and shows diffuse cytosolic labeling when immunolocalized in wild-type yeast\; however, in vps27 mutant cells (a class E vps mutant, which accumulates a prevaculoar compartment), Grd19p-HA co-localizes with the vacuolar H+-ATPase in the prevaculoar compartment\; Grd19p contains PX domain, which is found in proteins such as human SNX1 (Sorting Nexin-1) (Ponting, C.P. 1996. Protein Science 5:2353-2357)
8202_at 822.8 P
Component, along with Hap2p and Hap3p, of CCAAT-binding transcription factor
8203_at 4017.4 P
hypothetical protein

8204_at	1747.7	P	low-Km (high-affinity) cAMP phosphodiesterase
8205_at	9727.5	P	translation initiation factor eIF3 subunit
8161_at	7950.8	P	proteasome component YC1 (protease yscE subunit 1)
8162_at	677.2	P	Activator of peroxisome proliferation
8163_at	271.2	P	hypothetical protein
8164_at	49.3	A	strong similarity to YAL053w
8165_at	146.2	P	questionable ORF
8166_at	2276.8	P	Calponin homolog
8167_at	312.6	A	encodes a putative 3 ->5 exonuclease
8168_at	12863.5	P	40S ribosomal protein S12
8169_at	3133.5	P	protein of the TCD\/MRS6 family of GDP dissociation inhibitors (Rab escort protein)\; component of Rab geranylgeranyl transferase
8170_at	345.1	P	similarity to YAL056w
8171_at	2096.7	P	hypothetical protein
8172_at	1402.4	P	nuclesome assembly protein I
8173_at	4596.4	P	aldehyde dehydrogenase (E.C. 1.2.1.5) (sold by SIGMA under the catalogue number A5550, according to A. Blomberg)
8174_at	9857.0	P	NADP-specific glutamate dehydrogenase
8175_at	216.5	A	hypothetical protein
8176_at	654.3	P	Alcohol acetyltransferase
8177_at	59.1	A	strong similarity to aminotriazole resistance protein
8178_at	107.3	A	questionable ORF
8179_at	761.6	P	weak similarity to Pdr3p
8180_at	202.6	P	similar to FRE2
8181_at	1148.1	P	hypothetical protein
8182_at	7089.3	P	weak similarity to L.mexicana secreted acid phosphatase 2
8138_at	-36.1	A	similar to FRE2
8139_at	2052.8	P	strong similarity to hypothetical protein YMR316w
8140_at	240.7	P	photolyase

8141_at -20.7 A
strong similarity to YGL258w
8142_s_at -30.2 A
Protein with similarity to formate dehydrogenases
8143_at 793.7 P
strong similarity to putative pseudogenes YPL277c and YPL278c
8144_g_at 467.5 P
strong similarity to putative pseudogenes YPL277c and YPL278c
8145_s_at 2056.2 P
nearly identical to YPL279c
8146_at 86.1 P
hypothetical protein
8147_s_at 55.0 A
strong similarity to members of the Srp1p/Tip1p family
8148_at 138.7 P
hypothetical protein identified by SAGE
8149_at 1020.9 P
identified by SAGE
8150_s_at 955.3 P
Sorting nexin I homologue
8151_s_at 2282.8 P
Thymidylate synthase
8152_f_at 585.2 P
Thymidylate synthase
8153_at 2881.9 P
non-annotated SAGE orf Found forward in NC_001147 between 33183 and 33335 with 100% identity.
See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251
8154_at -78.3 A
non-annotated SAGE orf Found reverse in NC_001147 between 35996 and 36175 with 100% identity.
See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251
8155_at 361.0 A
non-annotated SAGE orf Found forward in NC_001147 between 242830 and 243045 with 100% identity.
See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251
8156_g_at -117.7 A
non-annotated SAGE orf Found forward in NC_001147 between 242830 and 243045 with 100% identity.
See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251
8157_at 284.6 P
non-annotated SAGE orf Found forward in NC_001147 between 571039 and 571224 with 100% identity.
See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251
8158_g_at 3298.6 P
non-annotated SAGE orf Found forward in NC_001147 between 571039 and 571224 with 100% identity.
See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251
8159_at 366.5 P
non-annotated SAGE orf Found forward in NC_001147 between 571131 and 571283 with 100% identity.
See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251
8160_at 339.5 A
non-annotated SAGE orf Found reverse in NC_001147 between 882274 and 882417 with 100% identity.
See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251
8112_at 787.6 P
non-annotated SAGE orf Found reverse in NC_001147 between 14772 and 15044 with 100% identity.
See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251
8113_at 446.0 P
non-annotated SAGE orf Found reverse in NC_001147 between 241012 and 241308 with 100% identity.
See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251
8114_i_at -116.9 A
non-annotated SAGE orf Found forward in NC_001147 between 464469 and 464630 with 100% identity.

See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251
8115_f_at 3559.4 P
non-annotated SAGE orf Found forward in NC_001147 between 464469 and 464630 with 100% identity.
See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251
8116_f_at 90.8 A
non-annotated SAGE orf Found reverse in NC_001147 between 599528 and 599743 with 100% identity.
See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251
8117_i_at 46.2 A
non-annotated SAGE orf Found forward in NC_001147 between 703721 and 703864 with 100% identity.
See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251
8118_i_at 239.7 A
non-annotated SAGE orf Found reverse in NC_001147 between 703986 and 704222 with 100% identity.
See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251
8119_f_at 385.4 P
non-annotated SAGE orf Found reverse in NC_001147 between 703986 and 704222 with 100% identity.
See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251
8120_at 1644.4 P
non-annotated SAGE orf Found forward in NC_001147 between 60049 and 60273 with 100% identity.
See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251
8121_at 268.8 P
non-annotated SAGE orf Found reverse in NC_001147 between 85271 and 85453 with 100% identity.
See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251
8122_at -36.3 A
non-annotated SAGE orf Found forward in NC_001147 between 106351 and 106605 with 100% identity.
See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251
8123_at 185.3 A
non-annotated SAGE orf Found reverse in NC_001147 between 136277 and 136426 with 100% identity.
See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251
8124_at 1562.7 P
non-annotated SAGE orf Found forward in NC_001147 between 185437 and 185643 with 100% identity.
See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251
8125_at 580.5 A
non-annotated SAGE orf Found forward in NC_001147 between 254904 and 255071 with 100% identity.
See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251
8126_at 3099.0 P
non-annotated SAGE orf Found reverse in NC_001147 between 290642 and 290797 with 100% identity.
See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251
8127_at -97.9 A
non-annotated SAGE orf Found reverse in NC_001147 between 316261 and 316395 with 100% identity.
See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251
8128_at 997.8 P
non-annotated SAGE orf Found reverse in NC_001147 between 372047 and 372184 with 100% identity.
See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251
8129_at 1217.8 P
non-annotated SAGE orf Found reverse in NC_001147 between 397425 and 397667 with 100% identity.
See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251
8130_at 97.0 A
non-annotated SAGE orf Found reverse in NC_001147 between 414243 and 414401 with 100% identity.
See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251
8131_at 300.9 P
non-annotated SAGE orf Found forward in NC_001147 between 423955 and 424104 with 100% identity.
See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251
8132_at 5176.0 P
non-annotated SAGE orf Found forward in NC_001147 between 646896 and 647093 with 100% identity.
See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251
8133_at 86.6 A

non-annotated SAGE orf Found forward in NC_001147 between 658442 and 658603 with 100% identity. See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251

8134_at -220.4 A
non-annotated SAGE orf Found reverse in NC_001147 between 671186 and 671422 with 100% identity. See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251

8135_at 190.0 A
non-annotated SAGE orf Found forward in NC_001147 between 680789 and 680935 with 100% identity. See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251

8136_at 4480.0 P
non-annotated SAGE orf Found reverse in NC_001147 between 715388 and 715549 with 100% identity. See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251

8137_at 9714.4 P
non-annotated SAGE orf Found forward in NC_001147 between 738543 and 738683 with 100% identity. See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251

8088_i_at -255.8 A
non-annotated SAGE orf Found forward in NC_001147 between 792336 and 792482 with 100% identity. See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251

8089_at 3559.4 P
non-annotated SAGE orf Found forward in NC_001147 between 850067 and 850213 with 100% identity. See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251

8090_at 163.9 P
non-annotated SAGE orf Found forward in NC_001147 between 918334 and 918558 with 100% identity. See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251

8091_at 98.4 A
non-annotated SAGE orf Found reverse in NC_001147 between 922939 and 923082 with 100% identity. See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251

8092_i_at 6218.1 P
non-annotated SAGE orf Found forward in NC_001147 between 1004376 and 1004510 with 100% identity. See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251

8093_r_at 3012.9 P
non-annotated SAGE orf Found forward in NC_001147 between 1004376 and 1004510 with 100% identity. See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251

8094_f_at 4752.4 P
non-annotated SAGE orf Found forward in NC_001147 between 1004376 and 1004510 with 100% identity. See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251

8095_at 61.3 A
non-annotated SAGE orf Found forward in NC_001147 between 301047 and 301238 with 100% identity. See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251

8096_at 531.2 P
non-annotated SAGE orf Found forward in NC_001147 between 413491 and 413682 with 100% identity. See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251

8097_i_at -18.3 A
non-annotated SAGE orf Found reverse in NC_001147 between 798316 and 798483 with 100% identity. See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251

8098_at 147.0 A
non-annotated SAGE orf Found forward in NC_001147 between 980859 and 981032 with 100% identity. See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251

8099_at 51.0 A
non-annotated SAGE orf Found reverse in NC_001147 between 17812 and 17970 with 100% identity. See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251

8100_at -40.2 A
non-annotated SAGE orf Found forward in NC_001147 between 18708 and 18944 with 100% identity. See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251

8101_at 327.6 A
non-annotated SAGE orf Found forward in NC_001147 between 27811 and 27948 with 100% identity.
See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251
8102_at 1868.6 P
non-annotated SAGE orf Found forward in NC_001147 between 136219 and 136404 with 100% identity.
See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251
8103_at 4.4 A
non-annotated SAGE orf Found forward in NC_001147 between 158885 and 159076 with 100% identity.
See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251
8104_at 1621.9 P
non-annotated SAGE orf Found forward in NC_001147 between 159172 and 159444 with 100% identity.
See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251
8105_at -10.1 A
non-annotated SAGE orf Found forward in NC_001147 between 226577 and 226801 with 100% identity.
See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251
8106_at 923.4 P
non-annotated SAGE orf Found forward in NC_001147 between 418190 and 418375 with 100% identity.
See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251
8107_at 464.1 P
non-annotated SAGE orf Found forward in NC_001147 between 438710 and 438853 with 100% identity.
See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251
8108_at -117.2 A
non-annotated SAGE orf Found reverse in NC_001147 between 682213 and 682368 with 100% identity.
See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251
8109_at -87.9 A
non-annotated SAGE orf Found reverse in NC_001147 between 682295 and 682447 with 100% identity.
See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251
8110_at 49.9 A
non-annotated SAGE orf Found reverse in NC_001147 between 759487 and 759765 with 100% identity.
See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251
8111_g_at 125.4 A
non-annotated SAGE orf Found reverse in NC_001147 between 759487 and 759765 with 100% identity.
See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251
8063_at 2302.3 P
non-annotated SAGE orf Found reverse in NC_001147 between 775471 and 775614 with 100% identity.
See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251
8064_at -46.0 A
non-annotated SAGE orf Found reverse in NC_001147 between 836569 and 836709 with 100% identity.
See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251
8065_at 56.9 A
non-annotated SAGE orf Found reverse in NC_001147 between 854174 and 854314 with 100% identity.
See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251
8066_at 582.4 A
non-annotated SAGE orf Found reverse in NC_001147 between 969027 and 969179 with 100% identity.
See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251
8067_i_at 3204.3 P
non-annotated SAGE orf Found reverse in NC_001147 between 974085 and 974252 with 100% identity.
See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251
8068_at 47.1 A
non-annotated SAGE orf Found reverse in NC_001147 between 978298 and 978459 with 100% identity.
See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251
8069_at -55.5 A
non-annotated SAGE orf Found reverse in NC_001147 between 978494 and 978640 with 100% identity.
See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251
8070_at 73.4 P
non-annotated SAGE orf Found reverse in NC_001147 between 979330 and 979470 with 100% identity.

See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251
8071_f_at 298.2 P
non-annotated SAGE orf Found reverse in NC_001147 between 1086064 and 1086357 with 100% identity. See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251
8072_i_at 293.9 P
non-annotated SAGE orf Found reverse in NC_001147 between 1086206 and 1086379 with 100% identity. See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251
8073_f_at 99.2 A
non-annotated SAGE orf Found reverse in NC_001147 between 1086206 and 1086379 with 100% identity. See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251
8074_s_at 965.7 P
non-annotated SAGE orf Found reverse in NC_001147 between 1089906 and 1090073 with 100% identity. See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251
8075_s_at 719.2 P
non-annotated SAGE orf Found reverse in NC_001147 between 1090615 and 1090749 with 100% identity. See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251
8076_at 155.7 A
non-annotated SAGE orf Found reverse in NC_001147 between 16559 and 16696 with 100% identity. See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251
8077_at -138.7 A
non-annotated SAGE orf Found reverse in NC_001147 between 16638 and 16781 with 100% identity. See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251
8078_at 150.0 A
non-annotated SAGE orf Found reverse in NC_001147 between 16760 and 16939 with 100% identity. See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251
8079_s_at 62.5 A
non-annotated SAGE orf Found forward in NC_001147 between 27083 and 27217 with 100% identity. See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251
8080_at 791.2 P
non-annotated SAGE orf Found forward in NC_001147 between 27147 and 27371 with 100% identity. See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251
8081_at -29.2 A
non-annotated SAGE orf Found forward in NC_001147 between 42706 and 42873 with 100% identity. See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251
8082_at 117.8 A
non-annotated SAGE orf Found forward in NC_001147 between 43030 and 43167 with 100% identity. See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251
8083_at 16.8 A
non-annotated SAGE orf Found forward in NC_001147 between 43142 and 43348 with 100% identity. See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251
8084_at -121.3 A
non-annotated SAGE orf Found forward in NC_001147 between 108972 and 109109 with 100% identity. See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251
8085_at 1258.0 P
non-annotated SAGE orf Found forward in NC_001147 between 180361 and 180495 with 100% identity. See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251
8086_at -67.4 A
non-annotated SAGE orf Found forward in NC_001147 between 193557 and 193784 with 100% identity. See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251
8087_at 240.8 A
non-annotated SAGE orf Found reverse in NC_001147 between 271475 and 271732 with 100% identity.

See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251
8039_at 292.5 P
non-annotated SAGE orf Found reverse in NC_001147 between 301017 and 301250 with 100% identity. See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251
8040_at 1180.4 P
non-annotated SAGE orf Found forward in NC_001147 between 524856 and 525080 with 100% identity. See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251
8041_at 1457.2 P
non-annotated SAGE orf Found reverse in NC_001147 between 609691 and 609825 with 100% identity. See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251
8042_at 280.1 A
non-annotated SAGE orf Found forward in NC_001147 between 690271 and 690495 with 100% identity. See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251
8043_at -10.7 A
non-annotated SAGE orf Found forward in NC_001147 between 692115 and 692309 with 100% identity. See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251
8044_at 7078.1 P
non-annotated SAGE orf Found forward in NC_001147 between 758077 and 758286 with 100% identity. See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251
8045_at -25.2 A
non-annotated SAGE orf Found forward in NC_001147 between 778364 and 778516 with 100% identity. See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251
8046_at 355.7 P
non-annotated SAGE orf Found forward in NC_001147 between 825297 and 825503 with 100% identity. See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251
8047_at 789.9 P
non-annotated SAGE orf Found forward in NC_001147 between 877184 and 877345 with 100% identity. See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251
8048_at 7534.3 P
non-annotated SAGE orf Found forward in NC_001147 between 1004147 and 1004431 with 100% identity. See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251
8049_at 30.2 A
non-annotated SAGE orf Found forward in NC_001147 between 1070794 and 1071003 with 100% identity. See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251
8050_at -76.4 A
non-annotated SAGE orf Found forward in NC_001147 between 1071000 and 1071164 with 100% identity. See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251
8051_i_at -10.2 A
non-annotated SAGE orf Found reverse in NC_001147 between 1074040 and 1074183 with 100% identity. See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251
8052_r_at 58.7 A
non-annotated SAGE orf Found reverse in NC_001147 between 1074040 and 1074183 with 100% identity. See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251
8053_at 715.2 A
snRNA
8054_at 1137.8 P
snRNA
8055_i_at -65.3 A
Centromere
8056_at 2639.0 P
snRNA

8057_i_at 194.0 P
snRNA
8058_r_at 248.5 P
snRNA
8059_at 684.7 P
snRNA
8060_at 1476.8 P
snRNA
8061_at 2313.8 P
snRNA
8062_at 7441.0 P
snRNA
8016_at 84.8 A
snRNA
8017_at 5244.7 P
snRNA
8018_i_at 165.3 P
strong similarity to hypothetical protein YOR389w/putative pseudogene
8019_s_at 316.7 P
strong similarity to hypothetical protein YOR389w/putative pseudogene
8020_s_at -14.1 A
putative formate dehydrogenase/putative pseudogene
8021_at 4755.2 P
strong similarity to amino-acid transport proteins
8022_at 3895.7 P
weak similarity to M.leprae metH2 protein, and strong similarity to hypothetical protein YLL062c
8023_at 73.4 A
hypothetical protein
8024_at 9326.5 P
nuclear gene for ATP synthase epsilon subunit
8025_at 2378.9 P
ATP-binding cassette (ABC) transporter family member
8026_at 698.1 P
Cortical protein required for cytoplasmic microtubule orientation\; localizes to the tip of shmoo projections and to the tip of budding cells in a cell-cycle dependent manner
8027_at 1186.8 P
phosphoinositide-specific phospholipase C
8028_at 753.6 P
weak similarity to C.elegans transcription factor unc-86
8029_at 7222.4 P
dimethyladenosine transferase
8030_at 10473.5 P
dicarboxylic amino acid permease
8031_at 666.8 P
strong similarity to YMR253c
8032_at 1387.4 P
similarity to Kel2p and Kel3p
8033_at 15353.9 P
mitochondrial and cytoplasmic fumarase (fumarate hydralase)
8034_at 198.7 A
questionable ORF
8035_at 2163.7 P
hypothetical protein
8036_at 1471.1 P
medium subunit of the clathrin-associated protein complex
8037_at 611.0 P

similarity to B.subtilis transcriptional activator tenA, and strong similarity to hypothetical proteins YOL055c and YPR121w
8038_at	86.4	A
weak similarity to YIL029c
7993_at	2902.2	P
G(sub)1 cyclin
7994_at	240.0	P
Involved in mitotic cell cycle and meiosis
7995_at	2247.3	P
transcription factor, member of Ada\/Gcn5 protein complex
7996_at	205.8	A
Cik1p homolog
7997_at	7544.4	P
iron-sulfur protein homologous to human adrenodoxin
7998_at	105.5	A
questionable ORF
7999_at	5371.4	P
weak similarity to YMR195w
8000_i_at	7473.5	P
Ribosomal protein L36B (L39) (YL39)
8001_at	93.8	P
similarity to mouse Tbc1 protein
8002_at	995.2	P
zinc-finger transcription factor of the Zn(2)-Cys(6) binuclear cluster domain type
8003_at	1410.0	P
similarity to human HAN11 protein and petunia an11 protein
8004_at	7379.0	P
weak similarity to mouse proteinase activated receptor 2
8005_at	3121.3	P
weak similarity to human mutL protein homolog
8006_at	3337.2	P
weak similarity to human UDP-galactose transporter related isozyme 1
8007_at	3120.1	P
component of signal recognition particle
8008_at	681.9	P
Homolog of the mammalian IQGAP1 and 2 genes\; probable regulator of cellular morphogenesis, inducing actin-ring formation in association with cytokinesis
8009_at	1606.9	P
involvement in microtubule function
8010_i_at	8150.1	P
heat shock protein
8011_at	7036.0	P
YAR1 encodes a 200-amino-acid protein with two ANK repeat motifs and an acidic C terminus rich in PEST-like sequences
8012_at	1521.5	P
questionable ORF
8013_at	8200.9	P
beta subunit of translation initiation factor eIF-2
8014_at	347.1	P
similarity to Prk1p, and serine/threonine protein kinase homolog from A. thaliana
8015_at	6324.7	P
strong similarity to TATA-binding protein-interacting protein 49 from rat
7970_at	8748.3	P
17-kDa subunit C of vacuolar membrane H(+)-ATPase
7971_at	559.2	P
hypothetical protein

7972_at 5996.7 P

SSO1 and SSO2 encode syntaxin homologs\; act in late stages of secretion

7973_at 9474.1 P

alpha subunit of fatty acid synthase

7974_at -22.3 A

Up in StarVation

7975_at 1211.3 P

weak similarity to YMR181c

7976_at 2233.5 P

mRNA capping enzyme beta subunit (80 kDa), RNA 5 -triphosphatase

7977_at 2632.1 P

UDP-glucose:dolichyl-phosphate glucosyltransferase

7978_at 11778.8 P

similarity to translation elongation factor eEF3

7979_at 6044.0 P

hypothetical protein

7980_at 2617.4 P

Protein involved in mitochondrial iron accumulation

7981_at 340.8 P

Induced by osmotic stress

7982_at 82.4 P

similarity to C.perfringens hypothetical protein

7983_at 5866.3 P

Bypass of PAM1

7984_s_at 9438.3 P

Ribosomal protein L1A, forms part of the 60S ribosomal subunit

7985_at 1028.2 P

PHO85 cyclin

7986_at 10175.7 P

GTP binding protein

7987_at 3192.8 P

similarity to human hypothetical protein KIAA0187

7988_at 201.2 P

similarity to YGL133w

7989_at 1447.0 P

Protein required for assembly of ubiquinol cytochrome-c reductase complex (cytochrome bc1 complex)

7990_at 1540.3 P

TMP pyrophosphorylase, hydroxyethylthiazole kinase

7991_at 604.4 P

similarity to A.thaliana U2 snRNP protein A

7992_at 5226.1 P

intranuclear protein which exhibits a nucleotide-specific intron-dependent tRNA pseudouridine synthase activity

7947_at 6503.5 P

Nip7p is required for 60S ribosome subunit biogenesis

7948_at 3088.4 P

component of signal recognition particle

7949_at 320.2 P

Protein kinase

7950_at 1228.7 P

similarity to YHL039w

7951_at 4133.6 P

similarity to hypthetical proteins from A. fulgidus, M. thermoautotrophicum and M. jannaschii

7952_at 7206.8 P

weak similarity to glycerophosphoryl diester phosphodiesterases

7953_at 441.1 P

questionable ORF
7954_at 5535.1 P
casein kinase I isoform
7955_at 2538.6 P
cAMP-dependent protein kinase catalytic subunit
7956_at 937.3 P
similarity to cell size regulation protein Rcs1p
7957_at 0.1 A
hypothetical protein
7958_at -39.7 A
hypothetical protein
7959_at 6730.4 P
weak similarity to T.cruzi p284 protein
7960_i_at 7361.5 P
Ribosomal protein L7B (L6B) (rp11) (YL8)
7961_f_at 7558.9 P
Ribosomal protein L7B (L6B) (rp11) (YL8)
7962_s_at 11296.9 P
Ribosomal protein L7B (L6B) (rp11) (YL8)
7963_at 391.1 P
questionable ORF
7964_at 1182.8 P
weak similarity to S.pombe hypothetical protein SPAC8C9
7965_at 1453.9 P
delta-like subunit of the yeast AP-3 adaptin component of the membrane-associated clathrin assembly complex
7966_at 782.7 P
DNA damage checkpoint gene
7967_at 484.2 P
weak similarity to human centromere protein E
7968_at 494.0 A
hypothetical protein
7969_at 219.7 P
strong similarity to YGL082w
7924_at 1721.8 P
polyadenylated RNA-binding protein
7925_at 181.0 P
strong similarity to YGL084c
7926_at 1591.3 P
similarity to Utr1p and YEL041w
7927_at 9515.8 P
mating factor alpha
7928_at 330.9 P
weak similarity to Xenopus protein xlgv7
7929_at 27.8 A
questionable ORF
7930_at 2357.4 P
weak similarity to Pub1p
7931_at 3951.1 P
ribosomal protein L36, mitochondrial
7932_at 4170.9 P
similarity to Taf90p
7933_at 645.9 P
questionable ORF
7934_at 570.5 P
weak similarity to YKR029c

7935_at 2353.3 P
weak similarity to human l-caldesmon I
7936_at 2541.6 P
protein phosphatase Q
7937_at 4429.2 P
Small subunit of nuclear cap-binding protein complex
7938_at 5528.6 P
putative DNA binding protein which shows similarity in homeobox domain to human proto-oncogene PBX1
7939_at 1900.7 P
similarity to chinese hamster transferrin receptor protein
7940_at 1569.7 P
N-acetylglucosaminyl-phosphatidylinositol biosynthetic protein
7941_at 217.2 P
Nuclear import protein
7942_at 2015.4 P
Mitochondrial ribosomal protein MRPL40 (YmL40)
7943_at 1827.6 P
Putative farnesyl transferase required for heme A synthesis
7944_at 616.3 P
NAD(P)H dehydrogenase
7945_at 2535.9 P
similarity to C.elegans LIM homeobox protein
7946_at 5251.9 P
INvolved in nuclear mRNA export, binds both poly(A)
7902_at 36.3 P
weak similarity to E.coli bfpB protein
7903_at 546.2 P
DNA polymerase
7904_at 39.2 A
weak similarity to paramyosins
7905_at -64.5 A
weak similarity to YHR207c
7906_at 486.6 A
similarity to mismatch repair protein Mlh1p
7907_at 10807.3 P
Serine and threonine rich protein.
7908_at 1151.5 P
hypothetical protein
7909_at 715.4 P
Involved in polarity establishment and bud emergence\; interacts with the Rho1p small GTP-binding protein
7910_at 9095.3 P
cytosolic leucyl tRNA synthetase
7911_at 1088.5 P
weak similarity to YPR151c
7912_at 4462.9 P
weak similarity to human nucleolin
7913_at 724.8 P
weak similarity to S.pombe hypothetical protein SPAC2G11.15c
7914_at 1067.7 P
weak similarity to YDL010w
7915_at 823.1 P
kinesin-related protein
7916_at 9834.9 P
vacuolar proteinase A

7917_at	217.3	P	protein kinase, Mec1p and Tel1p regulate rad53p phosphorylation
7918_at	1095.2	P	Resistant to Rapamycin Deletion 2
7919_at	2075.9	P	strong similarity to A.thaliana PRL1 and PRL2 proteins
7920_at	375.1	P	similarity to ser/thr protein kinases
7921_at	1535.5	P	involved in autophagy
7922_at	1209.0	P	Phosphopantetheine
7923_at	170.2	P	Pxa1p and Pxa2p appear to be subunits of a peroxisomal ATP-binding cassette transporter necessary for transport of long-chain fatty acids into peroxisomes
7879_at	1283.9	P	weak similarity to myosin heavy chain proteins
7880_at	6799.1	P	Homologous to human oxysterol-binding protein\; implicated in ergosterol biosynthesis and regulation of Golgi-derived transport vesicle biogenesis
7881_at	4587.4	P	encodes snRNA U3, SNR17A also encodes snRNA U3
7882_f_at	12365.3	P	Ribosomal protein L33A (L37A) (YL37) (rp47)
7883_at	639.4	P	questionable ORF
7884_at	1444.2	P	strong similarity to protein kinase Kin4p
7885_at	393.2	P	protein kinase
7886_at	443.3	P	Transcriptional modulator
7887_at	1300.4	P	weak similarity to fruit fly polycomblike nuclear protein
7888_at	1566.4	P	similarity to microtubule-interacting protein Mhp1p and to hypothetical protein YOR227w
7889_at	-226.8	A	questionable ORF
7890_at	5146.7	P	NifU-like protein A
7891_at	878.1	P	similarity to ADP/ATP carrier proteins
7892_at	924.7	P	weak similarity to transcription factors
7893_at	1883.3	P	Putative heme A biosynthetic enzyme involved in forming the formyl group at position 8 of the porphyrin ring
7894_at	9598.5	P	Ribosomal protein L5 (L1a)(YL3)
7895_at	208.2	P	hypothetical protein
7896_at	4410.2	P	TFIIF subunit (transcription initiation factor), 30 kD
7897_at	2196.7	P	TTAGGG repeat binding factor
7898_at	4319.6	P	

histone H1
7899_at 2241.4 P
weak similarity to fruit fly TFIID subunit p85
7900_at 2570.8 P
weak similarity to YDR395w and cellular apoptosis susceptibility protein
7901_at 265.3 P
Nuclear import protein
7857_at 236.2 P
similarity to ribonucleases
7858_at 1830.8 P
TFIIH subunit Tfb2\; has homology to CAK and human IIH subunits
7859_at -22.9 A
Meiotic protein required for synapsis and meiotic recombination
7860_at 1027.8 P
Required for sorting and delivery of soluble hydrolases to the vacuole.
7861_at 581.1 P
putative ATP-dependent RNA helicase\; Dead box protein
7862_at 2322.9 P
Component of small subunit of the mitochondrial ribosome
7863_at 5824.3 P
Isopentenyl diphosphate:dimethylallyl diphosphate isomerase (IPP isomerase)
7864_at 513.6 P
Protein with similarity to Hda1p, Rpd3p, Hos2p, and Hos1p
7865_at 4089.3 P
has GTPase-activating protein activity toward the essential bud-site assembly GTPase Cdc42
7866_at 801.0 P
questionable ORF
7867_at 274.1 P
similarity to glycerate dehydrogenases
7868_at 3571.3 P
weak similarity to YOR193w
7869_at 4575.8 P
arginase
7870_at 2450.7 P
similarity to C.elegans hypothetical protein, weak similarity to Pho81p
7871_at 452.8 P
similarity to aminoglycoside acetyltransferase regulator from P. stuartii
7872_at 1035.3 P
hypothetical protein
7873_at 544.3 P
hypothetical protein

7874_at 10211.3 P
HSP70 family member, highly homologous to Ssa1p and Sse2p
7875_at 3419.7 P
similarity to Smy2p
7876_at 2219.0 P
Aspartyl-tRNA synthetase, mitochondrial
7877_at 2480.0 P
similarity to hypothetical M. tuberculosis protein
7878_at 870.5 P
questionable ORF
7834_at 4044.0 P
hypothetical protein
7835_at 1353.5 P
similarity to YFR021w

7836_at	1432.9	P	weak similarity to Sulfolobus hypothetical protein
7837_at	8491.5	P	similarity to S.pombe hypothetical protein
7838_at	932.1	P	Tyrosyl-tRNA synthetase
7839_at	1836.9	P	hypothetical protein
7840_at	1141.2	P	strong similarity to YBR177c
7841_at	5746.8	P	membrane component of ER protein translocation apparatus
7842_at	8375.3	P	similarity to M.jannaschii GTP-binding protein, GTP1/OBG-family, weak similarity to other GTP-binding proteins
7843_at	1541.0	P	sensitive to sulfite
7844_at	7485.1	P	Glutathione oxidoreductase
7845_s_at	10991.6	P	Ribosomal protein S6A (S10A) (rp9) (YS4)
7846_at	3136.6	P	serum response factor-like protein
7847_at	1176.1	P	similarity to aryl-alcohol dehydrogenases
7848_at	5576.9	P	strong similarity to YBR183w
7849_at	2371.7	P	Histone and other Protein Acetyltransferase\; Has sequence homology to known HATs and NATs
7850_at	1898.3	P	multidomain vesicle coat protein that interacts with Sec23p
7851_at	878.6	P	BCK1-like resistance to osmotic shock
7852_at	722.2	P	54kDa subunit of the tetrameric tRNA splicing endonuclease
7853_at	2220.5	P	putative helicase
7854_i_at	6075.4	P	Ribosomal protein S9A (S13) (rp21) (YS11)
7855_f_at	7866.3	P	Ribosomal protein S9A (S13) (rp21) (YS11)
7856_at	182.6	P	hypothetical protein
7811_at	5245.7	A	Ribosomal protein L21B
7812_at	4984.4	P	F(1)F(0)-ATPase complex delta subunit, mitochondrial
7813_at	277.4	P	weak similarity to YBR197c
7814_at	1836.1	P	Required for synthesis of N-acetylglucoaminylphosphatidylinositol, the first intermediate in synthesis of glycosylphosphatidylinositol (GPI) anchors
7815_at	632.7	P	similarity to Vps4p and YER047c
7816_at	-52.4	A	questionable ORF

7817_at 484.6 P
encodes putative deubiquitinating enzyme
7818_at 675.4 P
hypothetical protein
7819_at 689.0 P
weak similarity to Vps9p
7820_at 738.8 P
geranylgeranyl diphosphate synthase
7821_at 815.6 P
hypothetical protein
7822_at 3031.1 P
hypothetical protein
7823_at 2135.0 P
hypothetical protein
7824_at 1497.3 P
soluble, hydrophilic protein involved in transport of precursors for soluble vauolar hydrolases from the late endosome to the vacuole
7825_at 1705.3 P
weak similarity to S.pombe peptidyl-prolyl cis-trans isomerase
7826_at 5249.1 P
similarity to hypothetical protein YLR019w, YLL010c and S.pombe hypothetical protein SPAC2F7.02c
7827_at 301.3 A
hypothetical protein
7828_at 12266.5 P
cytosolic aldehyde dehydrogenase
7829_at 284.2 P
strong similarity to Mrs2p
7830_at 4356.0 P
similarity to glutaredoxins
7831_at 6600.7 P
multidrug resistance transporter
7832_at 3656.9 P
Multicopy suppressor of cls2-2\; also suppresses rvs161 mutations
7833_at 1479.9 P
hypothetical protein
7788_at 968.6 P
hypothetical protein
7789_at 311.7 P
protein of unknown function
7790_at 6934.3 P
mannosylphosphate transferase
7791_at 3575.5 P
hypothetical protein
7792_at 1372.5 P
strong similarity to ADP-ribosylation factors
7793_at 3810.2 P
Protein required for complex glycosylation
7794_at 5318.4 P
MAP kinase-associated protein
7795_at 7557.4 P
Calcium and phospholipid binding protein homologous to translation elongation factor 1-gamma (EF-1gamma)
7796_at 2060.2 P
hypothetical protein
7797_at 1898.4 P
Elongin C transcription elongation factor

7798_at 1188.5 P
Vacuolar sorting protein
7799_at 348.0 P
questionable ORF
7800_at 5830.9 P
RNA recognition motif-containing protein
7801_at 1333.9 P a
cyclin(SSN8)-dependent serine\/threonine protein kinase
7802_at 1372.8 P
hypothetical protein
7803_at 1324.9 P
nuclear encoded mitochondrial isoleucyl-tRNA synthetase
7804_at 837.9 P
hypothetical protein
7805_at 764.5 P
zinc finger DNA binding factor, transcriptional regulator of sulfur amino acid metabolism, highly homologous to Met32p
7806_at 9580.9 P
GAL4 enhancer protein, has similarity to human transcription factor BTF3
7807_at 613.0 P
plasma membrane ATPase
7808_at 420.2 P
questionable ORF
7809_at 1056.0 P
questionable ORF
7810_at 75.1 A
weak similarity to YLR426w
7766_at 6397.2 P
styryl dye vacuolar localization
7767_at 4882.6 P
negative transcriptional regulator, protein kinase homolog
7768_at 1964.6 P
similarity to C.elegans hypothetical protein
7769_at 1018.1 P
putative ATP-dependent helicase
7770_at 7136.1 P
acetoacetyl CoA thiolase
7771_at 457.4 A
hypothetical protein
7772_at 1842.5 P
serine\/threonine protein kinase homologous to Ran1p
7773_at 109.2 A
questionable ORF
7774_at 528.1 P
(N)egative regulator of (C)ts1 (E)xpression
7775_at 3620.9 P
putative methylenetetrahydrofolate reductase (mthfr)
7776_at 615.7 P
UV endonuclease
7777_at 89.7 A
ExtraCellular Mutant\; similar to SRD1
7778_at 2773.7 P
weak similarity to Smt4p
7779_at 8429.0 P
strong similarity to YFL004w, similarity to YJL012c
7780_at 1123.5 P

Important for chromosome segregation
7781_at -59.9 A
strong similarity to Lpd1p and other dihydrolipoamide dehydrogenases
7782_at 1614.3 P
Zinc-finger transcription factor
7783_at 2109.0 P
Homolog of SIR2
7784_at 917.5 P
hypothetical protein
7785_at 3863.7 P
ribosomal protein S16, mitochondrial
7786_at 5988.9 P
hypothetical protein
7787_at 1195.0 P
Component of the TAF(II) complex (TBP-associated protein complex)
7743_at 5812.3 P
coatomer complex zeta chain
7744_at 3757.7 P
similarity to M.jannaschii hypothetical protein
7745_at 800.0 P
kinetochore protein in the DEAH box family
7746_at 1181.4 P
hypothetical protein
7747_at 4506.2 P
predicted transmembrane protein
7748_at 652.4 P
weak similarity to Nup2p
7749_at 10047.5 P
strong similarity to YGR086c
7750_at 427.6 P
Required for activation of RUB1 (ubiquitin-like protein) together with UBA3. Related to AOS1 and to N-terminus of UBA1. Collaborates with UBC12 in conjugation of RUB1 to other proteins. Required for modification of CDC53\/cullin with RUB1
7751_at 996.8 P
appears to be functionally related to SNF7
7752_at 1279.4 P
histone acetyltransferase
7753_at 147.2 A
Mitochondrial isoform of citrate synthase
7754_at 341.6 P
similarity to B.subtilis mmgE protein
7755_at 231.6 M
similarity to sulphate transporter proteins
7756_at 5320.2 P
strong similarity to electron transfer flavoproteins alpha chain
7757_at 436.6 A
polar 32k Da cytoplasmic protein
7758_at 1480.2 P
Isocitrate lyase, may be nonfunctional
7759_at -144.0 A
hypothetical protein
7760_at 1713.7 P
similarity to transcription factor
7761_at 2018.4 P
similarity to sterol uptake protein Sut1p
7762_at 10078.2 P

RNA polymerase I subunit A135
7763_at 2354.9 P
similarity to ADP/ATP carrier proteins and Graves disease carrier protein
7764_at 892.3 A
hypothetical protein
7765_at 1139.4 P
similarity to transcription factors
7721_at -1.7 A
hypothetical protein
7722_at 288.5 A
similarity to transcription factors
7723_at 8128.3 P
similar to human translation initiation factor 6 (eIF6)
7724_at 1451.8 P
GDP dissociation factor for Sec4p
7725_at 694.1 P
p90 subunit of yeast omatin Assembly Factor-I (CAF-I)
7726_at 1781.9 P
essential for initiation of DNA replication\; homolog of S. pombe CDC21
7727_at 3302.0 P
hypothetical protein
7728_at 510.2 P
similarity to human citrate transporter protein
7729_at 1020.6 P
weak similarity to fruit fly dorsal protein and Snf5p
7730_at 7081.4 P
similarity to human hypothetical protein
7731_at 2296.8 P
Mitochondrial protein of the CDC48\/PAS1\/SEC18 family of ATPases
7732_at 1196.9 P
novel cyclin gene\; encodes subunits of TFIIK, a subcomplex of transcription factor TFIIH
7733_at 361.4 P
null mutant is viable\; increased tolerance to dehydration, freezing, and toxic levels of ethanol
7734_at 242.3 A
similarity to YNL019c and YNL033w
7735_at 9209.4 P
Ypt Interacting Protein
7736_at 10744.6 P
Ypt Interacting Protein
7737_at 5376.1 P
Gamma-adaptin, large subunit of the clathrin-associated protein (AP) complex
7738_at 207.1 A
similarity to YBL101c
7739_at 630.2 P
similarity to human zinc-finger protein BR140
7740_at 1208.9 P
yeast homolog of the Drosphila tumor suppressor, lethal giant larvae
7741_at 9172.3 P
cytoplasmic and mitochondrial histidine tRNA synthetases
7742_at 1820.3 P
Actin-related protein
7698_at 13337.3 P
glutamine synthetase
7699_at 10247.5 P
54-kDa vacuolar H(+) ATPase subunit of V1 sector
7700_at 4682.4 P

similarity to Erv1p and rat ALR protein
7701_at 114.9 A
questionable ORF
7702_g_at 1243.7 P
questionable ORF
7703_at 629.8 A
questionable ORF
7704_at 1405.0 P
similarity to C.elegans C02C2.6 protein
7705_at 5727.6 P
Translation initiation factor eIF-5
7706_at 1903.7 P
similarity to Jsn1p
7707_i_at 16993.8 P
Ribosomal protein L43A
7708_f_at 8279.5 P
Ribosomal protein L43A
7709_at 434.8 P
questionable ORF
7710_at 396.1 P
similarity to C.elegans hypothetical protein
7711_at 869.9 P
Required for chromosome segregation
7712_at 602.5 P
alpha subunit of yeast mitochondrial phenylalanyl-tRNA synthetase
7713_at 2703.2 P
similarity to M.domestica NADPH--ferrihemoprotein reductase and mammalian nitric-oxide synthases
7714_at 1456.0 P
similarity to Uso1p
7715_at 581.4 P
questionable ORF
7716_at 4169.3 P
N-acetyltransferase
7717_at 8507.9 P
11-kDa nonhistone chromosomal protein
7718_g_at 8832.1 P
11-kDa nonhistone chromosomal protein
7719_at 1973.9 P
questionable ORF
7720_at -28.7 A
MAP kinase
7675_at 805.5 P
121 kDa component of the Exocyst complex, which is required for exocytosis, and which also contains the gene products encoded by SEC3, SEC5, SEC6, SEC10, SEC15, and EXO70
7676_at 2305.4 P
Component of RNA polymerase transcription initiation TFIIH (factor b), 37 kDa subunit
7677_at 1540.7 P
Protein involved in snRNP biogenesis
7678_at 6845.8 P
putative mitochondrial carrier protein
7679_at 338.3 P
questionable ORF
7680_at 7278.1 P
chorismate mutase
7681_at 210.1 P
weak similarity to Synechococcus sp. DnaJ protein

7682_at	7853.4	P	cytosine deaminase
7683_at	8459.6	P	hypothetical protein
7684_at	-21.7	A	hypothetical protein
7685_at	2306.0	P	site-specific DNA binding protein, repressor
7686_at	752.3	P	ubiquitin-like protein activating enzyme
7687_at	1307.5	P	weak similarity to F.alni nitrogen fixation protein
7688_at	219.5	P	Protein with similarity to Hda1p, Rpd3p, Hos2p, and Hos3p
7689_at	7418.3	P	putrescine aminopropyltransferase (spermidine synthase)
7690_at	813.3	P	hypothetical protein
7691_at	1587.8	P	strong similarity to YIL029c
7692_at	3336.3	P	member of the NOT complex, a global negative regulator of transcription
7693_at	1922.1	P	18-kDa phosphotyrosine phosphatase of unknown function
7694_at	11301.7	P	Transketolase 1
7695_at	1064.9	P	imparts Far- phenotype
7696_at	8.7	A	questionable ORF
7697_i_at	113.1	P	questionable ORF
7653_s_at	-115.3	A	questionable ORF
7654_at	129.7	A	hypothetical protein
7655_at	792.7	P	weak similarity to human insulin-like growth factor 2 receptor
7656_s_at	11700.0	P	translational elongation factor EF-1 alpha
7657_at	1324.7	P	strong similarity to glycyl-tRNA synthetases
7658_at	2272.2	P	S. pombe dim1+ in budding yeast
7659_at	611.5	P	hypothetical protein
7660_at	1309.9	P	hypothetical protein
7661_at	428.9	P	hypothetical protein
7662_at	6643.3	P	transcription factor TFIIB homolog
7663_at	475.0	P	questionable ORF
7664_at	7722.5	P	Signal recognition particle subunit (homolog of mammalian SRP54)

7665_at	1192.7	P	questionable ORF
7666_at	4801.6	P	hypothetical protein
7667_at	1337.9	P	weak similarity to C.elegans LIM homeobox protein
7668_at	169.1	M	questionable ORF
7669_at	584.1	P	weak similarity to zinc-finger proteins
7670_at	3572.0	P	weak similarity to chicken lim-3 protein
7671_at	616.2	P	Suppressor of Ypt3
7672_at	410.7	P	hypothetical protein
7673_at	3796.7	P	hypothetical protein
7674_at	8510.4	P	hypothetical protein
7629_at	175.2	P	questionable ORF
7630_at	3616.7	P	weak similarity to C.elegans hypothetical protein CEC25A1
7631_at	1097.9	P	splicing factor
7632_i_at	18948.0	P	Ribosomal protein L11A (L16A) (rp39A) (YL22)
7633_s_at	13348.9	P	Ribosomal protein L11A (L16A) (rp39A) (YL22)
7634_at	11142.5	P	proteasome subunit
7635_at	497.4	P	Protein with a domain similar to the fork head DNA-binding domain found in the developmental fork head protein of Drosophila melanogaster and in the HNF-3 family of hepatocyte mammalian transcription factors.
7636_at	2027.8	P	hypothetical protein
7637_at	794.0	P	protein kinase
7638_at	1382.4	P	Yeast 30kDa Homologue
7639_at	7222.1	P	Subunit of the regulatory particle of the proteasome
7640_at	844.0	P	weak similarity to human nicotinic acetylcholine receptor delta chain
7641_at	6668.9	P	RNA polymerase III (C) subunit
7642_at	114.9	A	kinase required for late nuclear division
7643_at	336.1	P	kinase required for late nuclear division
7644_at	1283.5	P	similarity to RNA-binding proteins
7645_at	11137.8	P	phosphatidylinositol synthase

7646_at 8639.8 P
similarity to YJR116w
7647_at 3590.4 P
similarity to probable transcription factor Ask10p, and to YNL047c and YIL105c
7648_at -307.5 A
hypothetical protein
7649_at 915.5 P
similarity to YLR454w
7650_at 1291.5 P
similarity to M.jannaschii translation initiation factor, eIF-2B
7651_at 1210.1 P
G(sub)2-specific B-type cyclin
7652_at 3596.5 P
B-type cyclin
7607_at 1110.3 P
similarity to B.subtilis transcriptional activator tenA, strong similarity to hypothetical proteins YPL258c and YOL055c
7608_at 1219.8 P
putative homolog of human insulin-degrading endoprotease
7609_at 1104.8 P
questionable ORF
7610_at 6737.2 P
High affinity copper transporter into the cell, probable integral membrane protein
7611_at 7336.1 P
suppressor of mrs2-1 mutation
7612_at 832.5 P
questionable ORF
7613_at 1655.6 P
similarity to C-term. of N.tabacum auxin-induced protein
7614_at 5180.0 P
similarity to carrier protein FLX1
7615_at 3207.0 P
multicopy suppressor of clathrin deficiency
7616_at 451.7 P
questionable ORF
7617_at 3123.0 P
similarity to N-acetyltransferases
7618_f_at 17445.1 P
Ribosomal protein S23B (S28B) (rp37) (YS14)
7619_s_at 7941.4 P
Ribosomal protein S23B (S28B) (rp37) (YS14)
7620_at 3286.9 P
similarity to C.elegans hypothetical protein
7621_at 11144.2 P
Translocase of the Outer Mitochondrial membrane
7622_at 1255.2 P
Protein involved in splicing intron a15beta of COX1
7623_at 1410.3 P
DNA polymerase alpha binding protein
7624_at 230.1 P
questionable ORF
7625_at 4942.2 P
weak similarity to Taf90p
7626_at 3417.9 P
NH4+ transporter, highly similar to Mep1p and Mep2p
7627_at 2251.6 P

hypothetical protein
7628_at 1341.4 P
similarity to human BTHS gene involved in Barth syndrome
7584_at 1143.4 P
kinesin-like nuclear fusion protein
7585_at 657.7 P
questionable ORF
7586_at 1941.9 P
hypothetical protein
7587_at 2398.8 P
similarity to YDR060w and C.elegans hypothetical protein
7588_at 10029.0 P
asparagine synthetase
7589_at 1305.4 P
questionable ORF
7590_at 2291.0 P
hypothetical protein
7591_at 3448.4 P
hypothetical protein
7592_at 8980.6 P
involved in secretion of proteins that lack classical secretory signal sequences
7593_at 125.1 A
questionable ORF
7594_at 693.5 P
weak similarity to YPL159c
7595_at 607.6 P
hypothetical protein
7596_at 647.5 P
hypothetical protein
7597_at 4474.2 P
similarity to chicken growth factor receptor-binding protein GRB2 homolog
7598_at 529.8 P
Regulates proper expression of subunits 6 (Atp6p) and 8 (Atp8p) of the Fo-F1 ATP synthase
7599_i_at 90.6 P
similarity to multidrug resistance proteins
7600_s_at 12252.7 P
similarity to multidrug resistance proteins
7601_at 452.4 P
strong similarity to YGR141w
7602_at 1295.9 P
similarity to YGR142w
7603_at 7540.6 P
potential beta-glucan synthase
7604_at 326.7 A
Glycogen phosphorylase
7605_at 1685.4 P
CDC28\/cdc2 related protein kinase
7606_at 2450.2 P
56-kDa subunit of origin recognition complex (ORC)
7561_at 10490.2 P
Translation initiation factor eIF-4B
7562_at 428.7 P
killed in mutagen, sensitive to diepoxybutane and\/or mitomycin C
7563_at 9391.4 P
GTP-binding protein of the rho subfamily of ras-like proteins
7564_at 4075.7 P

14 kDa mitochondrial ribosomal protein\; homologous to E. coli S14 protein
7565_at 756.6 P 3
phosphoadenylylsulfate reductase
7566_at 324.0 A
negative regulator of URS2 of the HO promoter
7567_at 4643.1 P
hypothetical protein
7568_at -8.9 A
hypothetical protein
7569_at 615.9 P
hypothetical protein
7570_at 874.6 P
strong similarity to YLR456w
7571_at 3694.0 P
defective in vacuolar protein sorting
7572_at 492.5 P
weak similarity to Nbp1p
7573_at 769.1 P
DNA polymerase epsilon, subunit B
7574_at 4526.2 P
Geranylgeranyltransferase Type II beta subunit
7575_at 294.7 A
questionable ORF
7576_at 1319.4 P
associated with the U4\/U6 snRNP
7577_at 388.1 P
hypothetical protein
7578_at 4144.7 P
Along with Uba2p forms a heterodimeric activating enzyme for Smt3p
7579_at 1591.9 P
cytoplasmic GTPase-activating protein
7580_at 6117.8 P
Sm or Sm-like snRNP protein
7581_at 10260.3 P
dolichol phosphate mannose synthase
7582_at 1386.9 P
similarity to human 4-alpha-glucanotransferase (EC 2.4.1.25)/amylo-1,6-glucosidase (EC 3.2.1.33)
7583_at 901.9 P
Autophagy
7538_at 216.1 P
Transcription factor IIIA (TFIIIA) with putative Zn-fingers
7539_at 9009.1 P
subunit common to RNA polymerases I, II, and III
7540_at 986.0 P
similarity to calmodulin and calmodulin-related proteins
7541_at 1241.9 P
Contains 8 copies of the TPR domain
7542_at 5191.9 P
82-kDa subunit of RNA polymerase III (C)
7543_at 10458.2 P
40 kDa ubiquinol cytochrome-c reductase core protein 2
7544_at 255.1 A
similarity to plasma membrane and water channel proteins
7545_at 94.2 A
Histone and other Protein Acetyltransferase\; Has sequence homology to known HATs and NATs
7546_at 194.8 A

similarity to S.pombe isp4 protein
7547_at 64.1 A
hypothetical protein
7548_at 263.1 P
strong similarity to regulatory protein Mal63p
7549_g_at 3760.4 P
strong similarity to regulatory protein Mal63p
7550_at 73.9 P
questionable ORF
7551_at 3139.2 P
multi-copy suppressor of gal11 null\; member of drug-resistance protein family
7552_at 1595.4 P
Similar to transcriptional regulatory elements YAP1 and cad1
7553_at 229.8 A
Required for arsenate but not for arsenite resistance
7554_at -22.1 A
involved in arsenite transport
7555_s_at 2171.7 P
trans-acting positive regulator of the enolase and glyceraldehyde-3-phosphate dehydrogenase gene families
7556_at 1110.9 P
non-annotated SAGE orf Found reverse in NC_001148 between 188306 and 188512 with 100% identity. See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251
7557_at 12262.5 P
non-annotated SAGE orf Found reverse in NC_001148 between 582456 and 582632 with 100% identity. See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251
7558_at 56.6 A
non-annotated SAGE orf Found forward in NC_001148 between 744172 and 744384 with 100% identity. See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251
7559_at 692.2 P
non-annotated SAGE orf Found forward in NC_001148 between 744464 and 744637 with 100% identity. See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251
7560_at 124.3 P
non-annotated SAGE orf Found reverse in NC_001148 between 824685 and 824921 with 100% identity. See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251
7512_at 4420.9 P
non-annotated SAGE orf Found reverse in NC_001148 between 132446 and 132580 with 100% identity. See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251
7513_f_at 245.8 P
non-annotated SAGE orf Found forward in NC_001148 between 809943 and 810116 with 100% identity. See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251
7514_at 512.6 P
non-annotated SAGE orf Found forward in NC_001148 between 810533 and 810709 with 100% identity. See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251
7515_f_at 27.5 A
non-annotated SAGE orf Found forward in NC_001148 between 853160 and 853345 with 100% identity. See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251
7516_at 1282.2 P
non-annotated SAGE orf Found reverse in NC_001148 between 212813 and 212956 with 100% identity. See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251
7517_at 775.6 P
non-annotated SAGE orf Found reverse in NC_001148 between 278112 and 278294 with 100% identity. See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251
7518_at 298.0 P
non-annotated SAGE orf Found forward in NC_001148 between 411416 and 411688 with 100% identity. See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251

7519_at 1711.9 P
non-annotated SAGE orf Found forward in NC_001148 between 431473 and 431622 with 100% identity.
See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251
7520_at 7275.5 P
non-annotated SAGE orf Found reverse in NC_001148 between 592171 and 592326 with 100% identity.
See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251
7521_at 5947.8 P
non-annotated SAGE orf Found reverse in NC_001148 between 624294 and 624434 with 100% identity.
See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251
7522_at -13.1 A
non-annotated SAGE orf Found forward in NC_001148 between 700058 and 700300 with 100% identity.
See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251
7523_at 524.7 P
non-annotated SAGE orf Found forward in NC_001148 between 706696 and 706830 with 100% identity.
See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251
7524_at 1523.2 P
non-annotated SAGE orf Found reverse in NC_001148 between 718768 and 718944 with 100% identity.
See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251
7525_at 1306.7 P
non-annotated SAGE orf Found forward in NC_001148 between 743828 and 743980 with 100% identity.
See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251
7526_i_at 4712.5 P
non-annotated SAGE orf Found reverse in NC_001148 between 773596 and 773742 with 100% identity.
See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251
7527_r_at 54.7 P
non-annotated SAGE orf Found reverse in NC_001148 between 773596 and 773742 with 100% identity.
See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251
7528_f_at 276.0 P
non-annotated SAGE orf Found reverse in NC_001148 between 773596 and 773742 with 100% identity.
See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251
7529_at 507.6 P
non-annotated SAGE orf Found forward in NC_001148 between 819135 and 819326 with 100% identity.
See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251
7530_s_at 1127.3 M
non-annotated SAGE orf Found forward in NC_001148 between 880290 and 880439 with 100% identity.
See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251
7531_at 6401.6 P
non-annotated SAGE orf Found forward in NC_001148 between 883373 and 883558 with 100% identity.
See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251
7532_at 1354.0 P
non-annotated SAGE orf Found forward in NC_001148 between 897142 and 897291 with 100% identity.
See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251
7533_at 8312.9 P
non-annotated SAGE orf Found forward in NC_001148 between 298197 and 298373 with 100% identity.
See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251
7534_i_at -633.6 A
non-annotated SAGE orf Found reverse in NC_001148 between 700274 and 700456 with 100% identity.
See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251
7535_f_at -55.3 A
non-annotated SAGE orf Found reverse in NC_001148 between 700274 and 700456 with 100% identity.
See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251
7536_at 608.4 P
non-annotated SAGE orf Found forward in NC_001148 between 754361 and 754570 with 100% identity.
See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251
7537_at 416.5 P
non-annotated SAGE orf Found reverse in NC_001148 between 812874 and 813047 with 100% identity.

See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251
7489_at 449.0 A
non-annotated SAGE orf Found forward in NC_001148 between 860478 and 860687 with 100% identity.
See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251
7490_at 591.6 P
non-annotated SAGE orf Found reverse in NC_001148 between 927488 and 927640 with 100% identity.
See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251
7491_at 88.2 P
non-annotated SAGE orf Found forward in NC_001148 between 14739 and 14888 with 100% identity.
See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251
7492_at 335.5 P
non-annotated SAGE orf Found reverse in NC_001148 between 85401 and 85580 with 100% identity.
See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251
7493_at 6799.8 P
non-annotated SAGE orf Found reverse in NC_001148 between 296871 and 297017 with 100% identity.
See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251
7494_at 187.5 A
non-annotated SAGE orf Found forward in NC_001148 between 297125 and 297292 with 100% identity.
See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251
7495_at -54.6 A
non-annotated SAGE orf Found reverse in NC_001148 between 411982 and 412140 with 100% identity.
See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251
7496_at 594.8 P
non-annotated SAGE orf Found reverse in NC_001148 between 445295 and 445444 with 100% identity.
See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251
7497_at 0.2 A
non-annotated SAGE orf Found reverse in NC_001148 between 588920 and 589057 with 100% identity.
See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251
7498_at -5.6 A
non-annotated SAGE orf Found reverse in NC_001148 between 588994 and 589242 with 100% identity.
See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251
7499_at 818.5 A
non-annotated SAGE orf Found reverse in NC_001148 between 678411 and 678614 with 100% identity.
See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251
7500_at 123.1 P
non-annotated SAGE orf Found reverse in NC_001148 between 769132 and 769359 with 100% identity.
See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251
7501_at -187.7 A
non-annotated SAGE orf Found forward in NC_001148 between 775843 and 775980 with 100% identity.
See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251
7502_at 264.4 P
non-annotated SAGE orf Found forward in NC_001148 between 822144 and 822302 with 100% identity.
See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251
7503_i_at 2637.4 P
non-annotated SAGE orf Found reverse in NC_001148 between 880229 and 880366 with 100% identity.
See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251
7504_r_at 244.7 P
non-annotated SAGE orf Found reverse in NC_001148 between 880229 and 880366 with 100% identity.
See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251
7505_at 177.6 A
non-annotated SAGE orf Found reverse in NC_001148 between 921211 and 921453 with 100% identity.
See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251
7506_at 1205.8 P
non-annotated SAGE orf Found reverse in NC_001148 between 324023 and 324286 with 100% identity.
See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251
7507_at 588.2 M

non-annotated SAGE orf Found reverse in NC_001148 between 408869 and 409009 with 100% identity. See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251
7508_at 411.7 P
non-annotated SAGE orf Found forward in NC_001148 between 408896 and 409066 with 100% identity. See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251
7509_at 357.0 P
non-annotated SAGE orf Found reverse in NC_001148 between 409022 and 409276 with 100% identity. See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251
7510_at 1393.8 M
non-annotated SAGE orf Found forward in NC_001148 between 427735 and 427896 with 100% identity. See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251
7511_at -386.8 A
non-annotated SAGE orf Found forward in NC_001148 between 497768 and 497959 with 100% identity. See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251
7466_at 69.8 P
non-annotated SAGE orf Found forward in NC_001148 between 560044 and 560235 with 100% identity. See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251
7467_at 163.4 A
non-annotated SAGE orf Found forward in NC_001148 between 596567 and 596728 with 100% identity. See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251
7468_at 20.1 A
non-annotated SAGE orf Found forward in NC_001148 between 633787 and 633930 with 100% identity. See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251
7469_at 45.0 M
non-annotated SAGE orf Found forward in NC_001148 between 703978 and 704121 with 100% identity. See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251
7470_at 10756.8 P
non-annotated SAGE orf Found reverse in NC_001148 between 733362 and 733532 with 100% identity. See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251
7471_at 66.7 A
non-annotated SAGE orf Found forward in NC_001148 between 780342 and 780503 with 100% identity. See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251
7472_at 545.9 P
non-annotated SAGE orf Found forward in NC_001148 between 831698 and 831880 with 100% identity. See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251
7473_at 1520.3 P
snRNA
7474_at 2197.7 P
snRNA
7475_at 4989.4 P
snRNA
7476_at 2306.4 P
snRNA
7477_at 658.9 P
snRNA
7478_s_at 768.9 P
similarity to subtelomeric encoded proteins
7479_at 1286.3 P
hypothetical protein
7480_at 800.7 P
yeast homolog of the Drosphila tumor suppressor, lethal giant larvae
7481_at 1692.6 P
putative protein kinase
7482_at 1977.3 P
hypothetical protein
7483_at 966.8 P

Probable cytochrome c subunit, copper binding
7484_at 6929.5 P
suppressor of sed5 ts mutants
7485_at 1748.5 P
ExtraCellular Mutant
7486_at 205.7 A
questionable ORF
7487_at 8445.3 P
mitochondrial F1F0-ATPase alpha subunit
7488_at 2267.1 P
similarity to human and D.melanogaster kynurenine 3-monooxygenase
7443_at 53.7 P
BARREN, a gene with sequence similarity to Drosophila barren and Xenopus XCAP-H, and a functional homolog of human BRRN1
7444_at 2862.3 P
questionable ORF
7445_at 1562.9 P
similarity to C.albicans hypothetical protein
7446_at 679.4 P
questionable ORF
7447_at 1884.6 P
RNA polymerase II holoenzyme\/mediator subunit
7448_at 11201.3 P
Ribosomal protein L32
7449_at 2886.8 P
weak similarity to SCS2
7450_at 10489.6 P
methionine aminopeptidase 2
7451_at 343.7 P
Component of the small subunit of mitochondrial ribosomes
7452_at 2133.0 P
weak similarity to A.thaliana aminoacid permease AAP3
7453_at 921.8 P
putative phosphatidylinositol kinase
7454_s_at 11606.7 P
Ribosomal protein L23A (L17aA) (YL32)
7455_at 606.6 P
involved in sugar metabolism
7456_at 2798.5 P
BEM1-binding protein
7457_at 3107.4 P
component of the anaphase-promoting complex
7458_i_at 188.4 P
questionable ORF
7459_s_at 3253.9 P
questionable ORF
7460_at 4043.6 P
putative Dol-P-Man dependent alpha(1-3) mannosyltransferase involved in the biosynthesis of the lipid-linked oligosaccharide
7461_at 2073.0 P
hypothetical protein
7462_at 425.7 P
62-kDa protein
7463_at 2490.0 P
Nucleoporin highly similar to Nup157p and to mammalian Nup155p (nup170 mutant can be complemented with NUP155)

7464_at 3311.8 P
Form a protein complex with Aut2p, to mediate attachment of autophagosomes to microtubules. Aut7p shows homologies to LC3, a microtubule-associated protein from rat. AUT7 was identified as a suppressor of mutant phenotypes of aut2-1 cells. Uptake of precursor Aminopeptidase I into the vacuole depends on Aut2p and Aut7p.
7465_at 407.1 P
questionable ORF
7421_at 10216.3 P
cytoplasmic isoleucyl-tRNA synthetase
7422_at 376.8 P
heat-inducible cytosolic member of the 70 kDa heat shock protein family
7423_at 600.7 P
splices pre mRNA of the MATa1 cistron
7424_at 108.0 A
questionable ORF
7425_s_at 11696.7 P
Ribosomal protein S8A (S14A) (rp19) (YS9)
7426_at 641.8 P
hypothetical protein
7427_at -13.6 A
questionable ORF
7428_at 7139.9 P
ribose-phosphate pyrophosphokinase 4
7429_at 1306.8 P
ubiquitin carboxyl-terminal hydrolase
7430_at 180.1 A
putative transcription factor
7431_at 233.9 A
questionable ORF
7432_at 2365.9 P
Homolog to thiol-specific antioxidant
7433_at 196.9 P
kinesin related protein
7434_at 472.4 P
questionable ORF
7435_at 2143.3 P
protoplast regeneration and killer toxin resistance gene, may be a post-translational regulator of chitin synthase III activity, interacts with Chs3p
7436_at 387.5 P
hypothetical protein
7437_at 208.1 P
weak similarity to hypothetical protein YER093c-a
7438_at 1125.6 P
weak similarity to hypothetical protein YER093c-a
7439_at 7927.2 P
isolated as a suppressor of the lethality caused by overexpression of the phosphoprotein phosphatase 1 catalytic subuniut encoded by GLC7
7440_at 2316.9 P
strong similarity to hypothetical S.pombe protein
7441_at 2074.1 P
protein phosphatase type 2C
7442_at 2520.4 P
similarity to hypothetical S.pombe protein
7398_at 3120.0 P
Homolog to myb transforming proteins
7399_at 1694.6 A

questionable ORF
7400_at 603.8 P
SAS3 for Something about silencing, gene 3. Influences silencing at HMR.
7401_at 3696.5 P
similarity to S.pombe Z66568_C protein
7402_at 3529.3 P
peripheral membrane protein required for vesicular transport between ER and Golgi
7403_at 143.6 P
hypothetical protein
7404_at 194.0 P
hypothetical protein
7405_at 4480.2 P
USO1 homolog (S. cerevisiae), cytoskeletal-related transport protein, Ca++ binding
7406_at 2785.5 P
weak similarity to hypothetical protein YOR054c
7407_at 8159.9 P
44 kDa core protein of yeast coenzyme QH2 cytochrome c reductase
7408_at 49.5 A
hypothetical protein
7409_at 916.0 P
ExtraCellular Mutant
7410_at 10029.7 P
uridine permease
7411_at 8599.9 P
proteasome subunit
7412_at 3543.3 P
encodes the HDEL receptor required for retention of ER proteins
7413_at 9581.1 P
CTP synthase, highly homologus to URA8 CTP synthase
7414_at 1240.9 P
Mitochondrial ribosomal protein MRPL16
7415_at 1083.5 P
clathrin Associated Protein complex Large subunit
7416_at 3115.1 P
Homolog to twitching motility protein (P. aeroginosa)
7417_at 2119.6 P B
subunit of DNA polymerase alpha-primase complex
7418_at 1845.1 P
suppressor of cold-sensitive tub2 mutation\; shown to be a component of the mitotic spindle
7419_at 5134.1 P
GTP cyclohydrolase II
7420_at 7389.7 P
weak similarity to hnRNP complex protein homolog YBR233w
7374_at 241.6 P
hypothetical protein
7375_at 12610.6 P
mitochondrial ADP\/ATP translocator
7376_at 1058.0 P
hypothetical protein
7377_at 3356.7 P
involved in mating-type regulation
7378_s_at 14742.0 P
Ribosomal protein L19B (YL14) (L23B) (rpl5L)
7379_i_at 315.1 P
snRNA-associated protein of the Sm class
7380_f_at 150.8 P

snRNA-associated protein of the Sm class
7381_at 3652.1 P
snRNA-associated protein of the Sm class
7382_at 730.0 P
Upstream activation factor subunit
7383_at 7343.5 P
Probable proliferating-cell nucleolar antigen (human p120)
7384_at 3757.0 P
Minichromosome maintenance protein, transcription factor
7385_at 8780.8 P
mitochondrial ATP-dependent protease
7386_at 1542.8 P
transcriptional activator protein of CYC1
7387_at 3976.6 P
67 kDa integral membrane protein
7388_at 339.3 P
AP endonuclease
7389_at 3189.4 P
integral subunit of RNase P and apparent subunit of RNase MRP
7390_at 6020.6 P
carboxypeptidase Y sorting receptor in late Golgi\; Type I integral membrane protein 166aa cytoplasmic tail, 1300 aa lumenal domain
7391_at 4855.0 P
cdc2+\/CDC28 related kinase with positive role in conjugation
7392_at 2477.9 P
acetyl CoA hydrolase
7393_at 1003.0 P
member of yeast Pol I core factor (CF) also composed of Rrn11p, Rrn7p and TATA-binding protein
7394_at 871.4 A
Probable met-tRNA formyltransferase, mitochondrial
7395_at 155.4 A
questionable ORF
7396_at 4405.6 P
High copy suppresor of choline-transport mutants
7397_at 563.6 P
hypothetical protein
7352_at 2326.7 P
strong similarity to DNA damage responsive Alk1p
7353_at 729.8 P
putative repressor protein homologous to yeast Tup1p and mammalian retinal transducin\; contains nuclear targeting signal
7354_at 4956.0 P
contains 3 SH3 domains, interacts with Bee1p
7355_at 3428.4 P
hypothetical protein
7356_at 748.3 P
Pleiotropic drug resistance protein 3
7357_at 4020.5 P
weak similarity to Papaya ringspot virus polyprotein
7358_s_at 17772.9 P
Histone H2A (HTA1 and HTA2 code for nearly identical proteins)
7359_at 13773.8 P
Histone H2B (HTB1 and HTB2 code for nearly identical proteins)
7360_at 6745.6 P
ExtraCellular Mutant
7361_at 1512.2 P

Neutral trehalase, highly homologous to Nth1p		
7362_at	2768.0	P
strong similarity to hypothetical protein YMR101c		
7363_at	5478.5	P
hexaprenyl pyrophosphate synthetase		
7364_at	3292.9	P
similarity to S.pombe hypothetical protein SPAC18B11.05		
7365_at	1743.9	P
strong similarity to hypothetical protein YDR003w		
7366_at	1443.4	P
hypothetical protein		
7367_at	1737.7	P
Major Facilitator Transporter		
7368_i_at	8192.7	P
Histone H3 (HHT1 and HHT2 code for identical proteins)		
7369_s_at	9057.7	P
Histone H3 (HHT1 and HHT2 code for identical proteins)		
7370_at	13904.4	P
Inorganic pyrophosphatase		
7371_at	1193.3	P
hypothetical protein		
7372_at	990.6	P
hypothetical protein		
7373_at	2538.8	P
Glutaredoxin homolog		
7328_at	5038.0	P
Type II transmembrane protein		
7329_at	8090.0	P
strong similarity to hypothetical proteins YDL012c and YDR210w		
7330_at	3803.7	P
karyopherin beta 2, yeast transportin		
7331_at	157.2	A
galactose-1-phosphate uridyl transferase		
7332_at	15.8	M
UDP-glucose 4-epimerase		
7333_at	152.0	A
galactokinase		
7334_at	4241.6	P
uracil permease		
7335_at	1620.6	P
hypothetical protein		
7336_at	7788.9	P
chitin synthase 3		
7337_at	1427.3	P
SCO1 protein homolog (S. cerevisiae)		
7338_at	9156.6	P
probable purine nucleotide-binding protein		
7339_at	1481.2	P
Nuclear protein that binds to T-rich strand of core consensus sequence of autonomously replicating sequence		
7340_at	433.0	P
hypothetical protein		
7341_at	969.3	P
Probable ser\/thr-specific protein kinase, homolog to YKR2 and YPK1 (S. cerevisiae)		
7342_at	5223.0	P
CDP-diacylglycerol synthase, CTP-phosphatidic acid cytidylyltransferase, CDP-diglyceride synthetase		

7343_at 1460.8 P
involved in inositol biosynthesis
7344_i_at 1615.4 P
Ribosomal protein L4A (L2A) (rp2) (YL2)
7345_s_at 13508.1 P
Ribosomal protein L4A (L2A) (rp2) (YL2)
7346_at 854.3 P
hypothetical protein
7347_at 90.9 A
Probable regulatory Zn-finger protein,\/ homolog to YKL251\/
7348_at 5980.5 P
nuclear protein arginine methyltransferase (mono- and asymmetrically dimethylating enzyme)
7349_at 5900.6 P
pyridoxine (pyridoxiamine) phosphate oxidase
7350_at 6107.9 P
contains 9 or 10 putative membrane spanning regions\; putative Ca2+ binding protein (homology to EF-hand Ca2+ binding site)
7351_at 3170.6 P
inner mitochondrial membrane protein
7306_at 1958.7 P
chitin synthase 2
7307_at 10584.3 P
gamma subunit of mitochondrial ATP synthase
7308_at 648.4 P
integral membrane protein
7309_at 2260.9 P
Fatty acid transporter
7310_at 2144.3 P
Probable membrane-bound small GTPase
7311_at 2569.2 P
similarity to benomyl/methotrexate resistance protein
7312_at 1119.3 A
similarity to chaperonin HSP60 proteins
7313_at 49.4 A
Glc7-interacting protein.
7314_at 1695.2 P
Homolog to quinone oxidoreductase (E. coli)
7315_at 782.5 P
hypothetical protein
7316_s_at 9254.6 P
Ribosomal protein S11B (S18B) (rp41B) (YS12)
7317_at 1306.0 P
RNA polymerase I enhancer binding protein
7318_at 654.9 P
Possible regulatory subunit for the PP1 family protein phosphatase Glc7p
7319_at 216.5 A
questionable ORF
7320_at 8000.3 P
Homolog to YCR004, obr1 (S. pombe), trp repressor binding protein (E. coli)
7321_at 1423.0 P
similarity to rat regucalcin
7322_at 2665.8 P
Homolog to HSP30 heat shock protein YRO1 (S. cerevisiae) 7
7323_at 1917.3 P
RNA splicing factor
7324_at 512.6 P

Homolog to glucan-1,3--glucosidase (EC 3.2.1.5\; S. cerevisiae) 2
7325_at 854.4 P
Muddled Meiosis
7326_at 1954.1 P
Ubiquitin-specific protease
7327_at 1442.3 P
Probable protein kinase
7283_at 2929.8 P
origin recognition complex subunit 2
7284_at 4949.2 P
Homolog to ftsJ protein (E. coli) ,\/ YCR054\/
7285_at 6596.7 P
similarity to rat neurodegeneration associated protein 1
7286_at 826.6 P
Probable phosphopanthethein-binding protein
7287_at 85.1 A
questionable ORF
7288_at 312.3 A
ExtraCellular Mutant
7289_at 1564.0 P
Probable Zn-finger protein
7290_at 9476.2 P
cell wall mannoprotein
7291_at 8980.4 P
probable amino acid permease for leucine, valine, and isoleucine
7292_at 3806.4 P
Probable amino acid transport protein
7293_at 2020.7 P
osmotolerance protein
7294_at 1321.0 P
hypothetical protein
7295_at 835.6 P
heat shock protein 26
7296_at 2495.6 P
Putative helicase similar to RAD54
7297_at 2404.5 P
Homolog to aminopeptidase Y (S. cerevisiae)
7298_at 1633.4 P
hypothetical protein
7299_at 139.7 A
ExtraCellular Mutant
7300_at 3025.7 P
hypothetical protein
7301_at 10728.3 P
Homolog to sporulation specific protein SPS2 (S. cerevisiae)
7302_at 9201.6 P
Homolog to sporulation specific protein SPS2 (S. cerevisiae)
7303_at 7585.5 P
Exhibits significant sequence similarity with a subunit of the mammalian translation initiation factor 3
7304_at 4270.2 P
cytoplasmic protein involved in protein transport between ER and Golgi\; ATPase
7305_at 1949.6 P
transcription factor, member of the histone acetyltransferase SAGA complex
7260_at 12374.3 P
ubiquitin-conjugating enzyme
7261_at 9134.0 P

			transcription factor of the TEA\/ATTS DNA-binding domain family, regulator of Ty1 expression
7262_at	8550.1	P	mitochondrial C1-tetrahydroflate synthase
7263_at	2455.4	P	mitochondrial ADP\/ATP translocator
7264_at	7409.4	P	Probable transmembrane protein
7265_at	2485.5	P	Subunit 5 of Replication Factor C\; homologous to human RFC 38 kDa subunit
7266_at	6396.0	P	profilerating cell nuclear antigen (PCNA)\; accessory factor for DNA polymerase delta, mRNA increases in G1, peaks in S in mitosis, and increases prior to DNA synthesis in meiosis
7267_at	-7.4	A	questionable ORF
7268_at	2487.5	P	11-kDa nonhistone chromosomal protein
7269_g_at	2729.2	P	11-kDa nonhistone chromosomal protein
7270_i_at	10930.1	P	questionable ORF
7271_at	176.1	A	questionable ORF
7272_at	2843.0	P	Nuclear protein involved in mitochondrial intron splicing
7273_at	9738.1	P	Acid phosphatase, constitutive
7274_at	5898.0	P	Acid phosphatase, repressible
7275_at	1173.5	P	weak similarity to pig tubulin-tyrosine ligase
7276_at	3527.8	P	hypothetical protein
7277_at	2410.7	P	hypothetical protein
7278_at	1879.5	P	Myristoylated Serine\/threonine protein kinase involved in vacuolar protein sorting
7279_at	176.4	P	putative transcriptional (co)activator for DNA damage
7280_at	237.2	P	weak similarity to T.brucei mitochondrion hypothetical protein 6
7281_at	335.2	P	questionable ORF
7282_at	8695.6	P	weak similarity to S.pombe hypothetical protein SPBC3B9.01
7238_at	270.3	P	hypothetical protein
7239_at	1689.5	P	weak similarity to human U3 snoRNP associated 55 kDa protein
7240_at	3019.9	P	mitochondrial carrier protein
7241_at	1703.1	P	involved in fructose-1,6-bisphosphatase degradation
7242_at	16004.1	P	May be a membrane protein involved in inorganic phosphate transport and regulation of Pho81p function
7243_at	526.0	P	weak similarity to N.crassa chitin synthase

7244_at	431.3	P	Probable transcription factor
7245_at	8045.9	P	Calmodulin
7246_at	2673.8	P	beta-1,4-mannosyltransferase
7247_at	10449.4	P	Homolog to serendipity protein (D. melanogaster)
7248_at	3139.5	P	Transcription regulatory protein
7249_at	446.8	A	questionable ORF
7250_at	459.5	P	Radiation repair protein, putative DNA helicase
7251_at	8470.6	P	alpha aminoadipate reductase
7252_at	573.5	P	questionable ORF
7253_g_at	688.3	P	questionable ORF
7254_at	91.6	A	transketolase, homologous to tkl1
7255_at	1776.0	P	U1 snRNP A protein
7256_at	1105.1	P	Translational activator of COB mRNA
7257_at	11909.8	P	Glycyl-tRNA synthase
7258_at	2543.0	P	Mitochondrial ribosomal protein MRPL36 (YmL36)
7259_at	2370.3	P	transcription factor tau (TFIIIC) subunit 95
7215_at	-164.8	A	questionable ORF
7216_at	1399.9	P	Probable phosphoprotein phosphatase (EC 3.1.3.16)
7217_at	5451.2	P	56 kD synthase subunit of trehalose-6-phosphate synthase\/phosphatase complex
7218_at	11370.6	P	H+-transporting ATPase, vacuolar (EC 3.6.1.35)
7219_at	66.6	A	required for autophagy
7220_at	819.0	P	imparts Far- phenotype
7221_at	4721.8	P	cytoplasmic protein involved in mother-specific HO expression
7222_at	1194.9	P	Calcium Caffeine Zinc sensitivity
7223_at	290.9	A	Amino acid permease
7224_at	2347.6	P	Negative regulator of swe1 kinase (which regulates cdc28)
7225_at	23.8	M	questionable ORF
7226_at	4362.7	P	subunit of the Cdc28 protein kinase

7227_at	1265.7	P
similar to phosphatidylinositol(PI)3-kinases required for DNA damage induced checkpoint responses in G1, S\/M, intra S, and G2\/M in mitosis
7228_at	2518.5	P
hypothetical protein
7229_at	82.8	P
Unknown
7230_at	3375.2	P
Probable serine-type carboxypeptidase (EC 3.4.16.1)
7231_at	1766.8	P
GTPase activating protein
7232_at	1977.2	P
hypothetical protein
7233_at	3187.1	P
Probable pre-mRNA splicing RNA-helicase
7234_at	9387.9	P
Ominipotent suppressor protein of nonsense codons
7235_at	159.2	P
hypothetical protein
7236_at	3497.7	P
alcohol dehydrogenase isoenzyme V
7237_at	2839.4	P
Probable mitochondrial ribosomal protein S9
7193_at	645.8	P
strong similarity to hypothetical protein YOL092w
7194_at	85.3	P
Spore-specific protein
7195_at	3996.2	P
D-arabinose dehydrogenase
7196_at	1155.1	P
Probable Zn-finger protein
7197_at	3455.3	P
weak similarity to potato sucrose cleavage protein
7198_at	125.5	P
U4\/U6.U5-associated snRNP protein\; contains a PEST proteolysis motif
7199_at	3344.5	P
Riboflavin biosynthesis protein
7200_at	8288.9	P
25-kDa RNA polymerase subunit (common to polymerases I, II and III)
7201_at	2779.0	P
Stress-inducible riboflavin biosynthetic protein homolog
7202_at	687.8	P
weak similarity to myosins
7203_at	400.3	P
hypothetical protein
7204_at	8374.2	P
hypothetical protein
7205_at	7501.4	P
similarity to human 17-beta-hydroxysteroid dehydrogenase
7206_at	5630.0	P
protein kinase catalytic subunit
7207_at	688.7	P
Homolog to suppressor of reduced viability of starvation (SUR1, S. cerevisiae)
7208_at	10344.3	P
similarity to hypothetical protein YJL171c
7209_at	5105.6	P

Protein that participates in secretory pathway
7210_at 2248.3 P
hypothetical protein
7211_at 6202.1 P
ADP-ribosylation factor-like protein 1
7212_at 1398.2 P
General positive regulator of CDC34\; Suppress some cdc34 mutations when over-expressed
7213_at 3103.9 P
Prephenate dehydrogenase (NADP+)
7214_at 1123.0 P
Pop7 protein, an integral subunit of RNase P and apparent subunit of RNase MRP
7170_at -46.0 P
weak similarity to hypothetical protein YLR324w
7171_at 1498.9 P
HSP70 family member, highly homologous to Sse1p
7172_at 1866.7 P
Suppressor of SEC63 (S.cerevisiae), novel ER translocation component
7173_at 6706.6 P
glycoprotein complexed with Sec62p and Sec63p in the Sec63 complex, an integral endoplasmic reticulum membrane protein complex required for translocation of presecretory proteins
7174_at 1640.6 P
Kinesin-related protein suppressing myosin defects (MYO2)
7175_at 1357.9 P
20S proteasome maturation factor
7176_at 11.1 A
questionable ORF
7177_at 3040.1 P
Probable GTP-binding protein
7178_at 2541.9 P
Alpha-Ketoisovalerate Hydroxymethyltransferase
7179_at 6864.8 P
Probable membrane receptor
7180_at -1.3 A
questionable ORF
7181_at 1324.0 P
homolog of Drosophila melanogaster fuzzy onions gene\; integral protein of the mitochondrial outer membrane which can be isolated as part of a high molecular weight complex
7182_at 54.1 A
Probable resistance protein
7183_at 409.5 P
Probable DNA-binding transcription factor, Homolog to SRF\/SL-2
7184_at 4824.5 P
strong similarity to hypothetical protein YPL087w
7185_at 216.8 P
alpha-galactosidase
7186_at 1393.0 P
respiratory chain assembly protein
7187_at 18.3 A
Putative ATPase
7188_at 9432.1 P
probable membrane protein
7189_at 1059.1 P
splicing factor
7190_i_at 11782.5 P
Ribosomal protein S9B (S13) (rp21) (YS11)
7191_f_at 10417.4 P

Ribosomal protein S9B (S13) (rp21) (YS11)
7192_at 253.7 P
questionable ORF
7147_at 4803.1 P
Ribosomal protein L21A
7148_at 2067.8 P
Probable carrier protein, mitochondrial
7149_at 293.0 P
Stoichiometric member of mediator complex
7150_at 1621.9 P
hypothetical protein
7151_at 2603.4 P
p50 subunit of the yeast omatin Assembly Factor-I (CAF-I) negative regulator of ras-mediated cAMP induction\; homologous to beta subunit of GTP-binding proteins
7152_at 12695.2 P
Glucose-6-phosphate isomerase
7153_at 749.5 P
weak similarity to hypothetical protein YPL077c
7154_at 4556.9 P
Probable transcription-associated factor protein, probable -transducin type
7155_at 4423.4 P
Putative alpha-1,2-mannosyltransferase
7156_at 497.2 P
contains two SH3 domains
7157_at 2944.2 P
MCM3 protein homolog (S. cerevisiae)
7158_at 172.1 P
hypothetical protein
7159_at 2117.3 P
Probable serine-active lipase, peroxisomal (EX 3.1.1.-)
7160_at 5550.4 P
Putative alpha-1,2-mannosyltransferase
7161_g_at 6831.1 P
Putative alpha-1,2-mannosyltransferase
7162_at 3617.9 P
questionable ORF
7163_at 3577.9 P
probable membrane protein
7164_at 1268.4 P
Urea amidolyase (contains urea carboxylase and allophanate hydrolase)
7165_at -56.0 A
hypothetical protein
7166_at 3577.4 P
strong similarity to D.melanogaster cornichon protein
7167_at 397.3 P
regulator of microtubule stability
7168_at 2310.0 P
negative growth regulatory protein
7169_at 2820.9 P
Effector in the expression of PAPS reductase and sulfite reductase
7124_at 1608.5 P
strong similarity to hypothetical protein YGL056c
7125_at 1069.8 P
highly charged, basic protein
7126_at 718.9 P
strong similarity to hypothetical protein YGL060w

7127_at	604.3	P	autophagy
7128_at	10356.8	P	pyruvate carboxylase
7129_at	2031.0	P	similarity to human acetyl-coenzyme A transporter
7130_g_at	2356.2	P	similarity to human acetyl-coenzyme A transporter
7131_at	9133.6	P	beta subunit of pyruvate dehydrogenase (E1 beta)
7132_at	5257.4	P	Probable AMP-binding protein
7133_at	1725.7	P	hypothetical protein
7134_at	508.1	P	questionable ORF
7135_at	1338.2	P	hypothetical protein
7136_at	221.6	A	questionable ORF
7137_at	1866.4	P	Homolog to ATP-binding protein clpX (E.coli)
7138_at	712.9	P	similarity to hypothetical A.thaliana protein
7139_at	2270.3	P	Homolog to 1,4-a-glucosidase (S.cerevisiae) (EC 3.2.1.3) 3
7140_at	3619.3	P	hypothetical protein
7141_at	704.2	P	similarity to human p97 homologous protein
7142_at	242.7	A	questionable ORF
7143_at	944.3	P	Homolog to human hnRNP complex K protein
7144_at	6281.7	P	similarity to human Arp2/3 protein complex subunit p41-Arc and to human Sop2p-like protein
7145_at	1185.2	P	similarity to bumetanide-sensitive Na-K-Cl cotransport protein
7146_at	3980.6	P	RNA (guanine-7-)methyltransferase (cap methyltransferase)
7102_at	662.9	P	RNA helicase homolog
7103_at	1770.5	P	strong similarity to general chromatin factor Spt16p
7104_at	1488.6	P	Probable Zn-finger protein
7105_at	353.7	P	Probable Zn-finger protein
7106_at	4116.7	P	Probable sugar transport protein
7107_at	2218.6	P	Probable ATP\/GTP-binding protein
7108_at	5985.8	P	UDP-N-acetyl-glucosamine-1-P transferase (GPT)
7109_at	1252.3	P	Probable glutathione peroxidase (EC 1.11.1.9)

7110_at 3270.0 P
Homolog to SNF2\/SWI2 DNA-binding regulatory protein
7111_at 5314.3 P
hypothetical protein
7112_at 7955.8 P
Putative 57 kDa protein with an apparent MW of 70 kDa by SDS-PAGE
7113_at 7417.8 P
glutamine amidotransferase:cyclase
7114_at 9905.5 P
3-deoxy-D-arabino-heptulosonate 7-phosphate (DAHP) synthase isoenzyme
7115_at 44.9 M
hypothetical protein
7116_at 1593.3 P
Probable mitochondrial ribosomal protein S5
7117_at 10774.1 P
dUTP pyrophosphatase (dUTPase)
7118_at 303.2 P
transcription factor, part of Srb\/Mediator complex
7119_at 2043.7 P
probable membrane protein
7120_at 287.5 P
hypothetical protein
7121_at 768.3 P
Riboflavin synthase alpha-chain
7122_at 1068.8 P
Required for normal 5.8S rRNA processing and for tRNA processing\; associated with RNase MRP and RNase P
7123_at 627.8 P
hypothetical protein
7079_at 584.4 P
hypothetical protein
7080_at 2526.3 P
similarity to C.elegans GTPase-activating protein
7081_at 7430.3 P
similarity to hypothetical S. pombe protein
7082_at 3816.9 P
questionable ORF
7083_at 10928.2 P
Serine hydroxymethyltransferase, mitochondrial
7084_at 2261.5 P
Probable small GTP-binding protein
7085_at 8026.1 P
probable membrane protein
7086_at 2990.2 P
Probable mitochondrial protein L37
7087_at 1597.2 P
hypothetical protein
7088_at 298.2 P
Probable ATP\/GTP-binding protein
7089_at 1986.6 P
weak similarity to S.pombe uvi22 protein and hypothetical protein YNL024c
7090_at 835.9 P
Hsm3p may be a member of the yeast MutS homolog family
7091_at 2776.9 P
similarity to hypothetical protein YJL048c
7092_at 1158.3 P

Probable protein kinase (growth factor & cytokine receptor family)
7093_at 592.1 A
RAP1-interacting factor, involved in establishment of repressed chromatin
7094_at 3379.0 P
dual specificity protein phosphatase
7095_at 109.9 P
questionable ORF
7096_at 1251.2 P C
and C subunits of DNA polymerase II
7097_at 2269.2 P
RNA polymerase II-associated, nuclear protein that may serve as both a positive and negative regulator of a subset of genes, perhaps operating in parallel with Gal11p
7098_at 1678.4 P
hypothetical protein
7099_at 1491.2 P
Probable G-protein, -transducin type
7100_at 3737.2 P
Mitochondrial ribosomal protein MRPL27 (YmL27)
7101_at 8455.8 P
Probable SEC61 protein homolog
7057_at 207.3 P
similarity to AMP deaminase
7058_at 55.5 A
hypothetical protein
7059_at 14505.5 P
Aminopeptidase yscIII
7060_at 5798.2 P
similarity to hypothetical S. pombe protein
7061_at 2291.3 P
clathrin associated protein medium chain
7062_at 1798.8 P
transcriptional activator
7063_at 1678.2 P
metal homeostasis protein\; putative membrane protein
7064_at 7006.2 P
citrate tranporter in mitochondrial inner membrane
7065_at 1099.1 P
hypothetical protein
7066_at 1456.4 P
Probable multidrug resistance protein
7067_at 144.4 A
Probable sulfate transport protein
7068_at 828.8 P
Putative P-type Cu(2+)-transporting ATPase
7069_at 1915.2 P
Homolog to phosphate-repressible phosphate permease
7070_at 523.6 P
Maltose fermentation regulatory protein
7071_s_at 515.2 P
maltose permease
7072_s_at 89.1 A
Maltase (EC 3.2.1.20)
7073_at 288.1 P
strong similarity to hypothetical protein YGR293c
7074_f_at 1664.0 P
YKL224 c homolog

7075_at -11.6 A
hypothetical membrane protein
7076_at 1118.2 P
identified by SAGE
7077_at 5258.9 P
identified by SAGE
7078_at 1254.7 P
hypothetical protein
7033_at 257.1 P
questionable ORF - upstream ORF of ALG1
7034_i_at 8200.0 P
identified by SAGE
7035_s_at 11458.7 P
identified by SAGE
7036_s_at 2245.6 P
Protein involved in targeting of plasma membrane [H+]ATPase
7037_s_at 675.9 P
Probable aldehyde dehydrogenase (EC 1.2.1.-)
7038_s_at 1986.9 P
Degradation in the Endoplasmic Reticulum
7039_at 102.1 A
probable membrane protein
7040_g_at 201.5 P
probable membrane protein
7041_s_at 3650.2 P
Probable Zn-finger protein (C2H2 type)
7042_at 928.0 P
non-annotated SAGE orf Found forward in NC_001134 between 46929 and 47189 with 100% identity. See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251
7043_at 2077.7 P
non-annotated SAGE orf Found reverse in NC_001134 between 164451 and 164735 with 100% identity. See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251
7044_at 116.5 A
non-annotated SAGE orf Found reverse in NC_001134 between 164788 and 164997 with 100% identity. See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251
7045_i_at 5008.7 P
non-annotated SAGE orf Found forward in NC_001134 between 490774 and 490932 with 100% identity. See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251
7046_s_at 8476.2 P
non-annotated SAGE orf Found forward in NC_001134 between 490774 and 490932 with 100% identity. See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251
7047_at 3405.1 P
non-annotated SAGE orf Found forward in NC_001134 between 680321 and 680521 with 100% identity. See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251
7048_i_at 743.8 P
non-annotated SAGE orf Found forward in NC_001134 between 680595 and 680834 with 100% identity. See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251
7049_s_at 725.9 P
non-annotated SAGE orf Found forward in NC_001134 between 680595 and 680834 with 100% identity. See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251
7050_at 4148.0 P
non-annotated SAGE orf Found reverse in NC_001134 between 680739 and 680900 with 100% identity. See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251
7051_at 26.3 A
non-annotated SAGE orf Found forward in NC_001134 between 36284 and 36424 with 100% identity. See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251

7052_at 211.4 A
non-annotated SAGE orf Found reverse in NC_001134 between 101483 and 101674 with 100% identity.
See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251
7053_at -31.4 A
non-annotated SAGE orf Found reverse in NC_001134 between 196846 and 196992 with 100% identity.
See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251
7054_i_at -769.0 A
non-annotated SAGE orf Found forward in NC_001134 between 592971 and 593117 with 100% identity.
See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251
7055_f_at -193.4 A
non-annotated SAGE orf Found forward in NC_001134 between 592971 and 593117 with 100% identity.
See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251
7056_at -76.6 A
non-annotated SAGE orf Found forward in NC_001134 between 767702 and 767938 with 100% identity.
See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251
7010_at 399.8 P
non-annotated SAGE orf Found reverse in NC_001134 between 88277 and 88447 with 100% identity.
See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251
7011_g_at 2702.0 P
non-annotated SAGE orf Found reverse in NC_001134 between 88277 and 88447 with 100% identity.
See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251
7012_at 8145.5 P
non-annotated SAGE orf Found reverse in NC_001134 between 88345 and 88512 with 100% identity.
See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251
7013_at -203.1 A
non-annotated SAGE orf Found reverse in NC_001134 between 101183 and 101410 with 100% identity.
See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251
7014_at 2247.0 P
non-annotated SAGE orf Found reverse in NC_001134 between 115345 and 115482 with 100% identity.
See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251
7015_at 585.8 P
non-annotated SAGE orf Found reverse in NC_001134 between 143662 and 143892 with 100% identity.
See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251
7016_at 911.7 P
non-annotated SAGE orf Found forward in NC_001134 between 172044 and 172202 with 100% identity.
See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251
7017_at 1282.2 P
non-annotated SAGE orf Found reverse in NC_001134 between 241413 and 241568 with 100% identity.
See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251
7018_at 4430.2 P
non-annotated SAGE orf Found reverse in NC_001134 between 256812 and 256976 with 100% identity.
See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251
7019_at 1416.4 P
non-annotated SAGE orf Found forward in NC_001134 between 270737 and 270898 with 100% identity.
See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251
7020_at 4722.0 P
non-annotated SAGE orf Found reverse in NC_001134 between 305964 and 306119 with 100% identity.
See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251
7021_at 9733.8 P
non-annotated SAGE orf Found reverse in NC_001134 between 373567 and 373737 with 100% identity.
See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251
7022_at -201.4 A
non-annotated SAGE orf Found forward in NC_001134 between 391411 and 391557 with 100% identity.
See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251
7023_at 1758.7 P
non-annotated SAGE orf Found forward in NC_001134 between 407263 and 407424 with 100% identity.

See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251
7024_at -68.0 A
non-annotated SAGE orf Found reverse in NC_001134 between 480941 and 481075 with 100% identity.
See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251
7025_at 145.9 P
non-annotated SAGE orf Found reverse in NC_001134 between 553502 and 553690 with 100% identity.
See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251
7026_at 2115.3 P
non-annotated SAGE orf Found reverse in NC_001134 between 553777 and 553935 with 100% identity.
See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251
7027_at 6318.7 P
non-annotated SAGE orf Found reverse in NC_001134 between 562982 and 563116 with 100% identity.
See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251
7028_at 40.5 A
non-annotated SAGE orf Found forward in NC_001134 between 592774 and 592914 with 100% identity.
See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251
7029_g_at -363.7 A
non-annotated SAGE orf Found forward in NC_001134 between 592774 and 592914 with 100% identity.
See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251
7030_at -193.5 A
non-annotated SAGE orf Found forward in NC_001134 between 592832 and 593005 with 100% identity.
See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251
7031_at 550.1 P
non-annotated SAGE orf Found reverse in NC_001134 between 615895 and 616062 with 100% identity.
See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251
7032_at 2282.6 P
non-annotated SAGE orf Found forward in NC_001134 between 649944 and 650114 with 100% identity.
See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251
6985_at -12.8 A
non-annotated SAGE orf Found reverse in NC_001134 between 741739 and 741900 with 100% identity.
See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251
6986_i_at 35.7 A
non-annotated SAGE orf Found forward in NC_001134 between 35606 and 35800 with 100% identity.
See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251
6987_at 230.8 A
non-annotated SAGE orf Found reverse in NC_001134 between 66854 and 67036 with 100% identity.
See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251
6988_at -107.2 A
non-annotated SAGE orf Found forward in NC_001134 between 181316 and 181477 with 100% identity.
See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251
6989_at 21.6 P
non-annotated SAGE orf Found reverse in NC_001134 between 593218 and 593355 with 100% identity.
See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251
6990_at 796.9 M
non-annotated SAGE orf Found forward in NC_001134 between 622942 and 623106 with 100% identity.
See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251
6991_i_at 803.0 P
non-annotated SAGE orf Found reverse in NC_001134 between 694564 and 694710 with 100% identity.
See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251
6992_r_at -24.5 A
non-annotated SAGE orf Found reverse in NC_001134 between 694564 and 694710 with 100% identity.
See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251
6993_f_at 5283.9 P
non-annotated SAGE orf Found reverse in NC_001134 between 694564 and 694710 with 100% identity.
See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251
6994_at 1499.1 P

non-annotated SAGE orf Found reverse in NC_001134 between 747849 and 748010 with 100% identity.
See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251
6995_at 1427.4 P
non-annotated SAGE orf Found forward in NC_001134 between 143356 and 143535 with 100% identity.
See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251
6996_at 322.6 A
non-annotated SAGE orf Found reverse in NC_001134 between 159883 and 160056 with 100% identity.
See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251
6997_at 298.4 P
non-annotated SAGE orf Found forward in NC_001134 between 164491 and 164637 with 100% identity.
See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251
6998_at 47.6 A
non-annotated SAGE orf Found forward in NC_001134 between 165623 and 165823 with 100% identity.
See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251
6999_at 1004.1 P
non-annotated SAGE orf Found forward in NC_001134 between 165783 and 165998 with 100% identity.
See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251
7000_i_at 6.9 A
non-annotated SAGE orf Found reverse in NC_001134 between 197442 and 197720 with 100% identity.
See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251
7001_r_at 95.8 A
non-annotated SAGE orf Found reverse in NC_001134 between 197442 and 197720 with 100% identity.
See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251
7002_at 620.5 P
non-annotated SAGE orf Found reverse in NC_001134 between 235796 and 235936 with 100% identity.
See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251
7003_at -45.3 A
non-annotated SAGE orf Found reverse in NC_001134 between 351253 and 351459 with 100% identity.
See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251
7004_at 123.7 A
non-annotated SAGE orf Found reverse in NC_001134 between 363544 and 363771 with 100% identity.
See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251
7005_at 115.0 P
non-annotated SAGE orf Found forward in NC_001134 between 419296 and 419436 with 100% identity.
See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251
7006_at -140.2 A
non-annotated SAGE orf Found forward in NC_001134 between 477095 and 477283 with 100% identity.
See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251
7007_at -302.9 A
non-annotated SAGE orf Found forward in NC_001134 between 480969 and 481103 with 100% identity.
See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251
7008_at 961.4 P
non-annotated SAGE orf Found reverse in NC_001134 between 554862 and 555011 with 100% identity.
See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251
7009_g_at 825.7 P
non-annotated SAGE orf Found reverse in NC_001134 between 554862 and 555011 with 100% identity.
See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251
6962_at 56.7 A
non-annotated SAGE orf Found reverse in NC_001134 between 554921 and 555088 with 100% identity.
See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251
6963_at 1033.5 P
non-annotated SAGE orf Found forward in NC_001134 between 555545 and 555691 with 100% identity.
See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251
6964_s_at 2195.9 P
non-annotated SAGE orf Found forward in NC_001134 between 555685 and 555879 with 100% identity.
See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251

6965_i_at 23.8 A

non-annotated SAGE orf Found forward in NC_001134 between 555695 and 555919 with 100% identity. See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251

6966_r_at 79.2 P

non-annotated SAGE orf Found forward in NC_001134 between 555695 and 555919 with 100% identity. See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251

6967_at 1287.7 P

non-annotated SAGE orf Found reverse in NC_001134 between 624453 and 624656 with 100% identity. See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251

6968_at 931.3 P

non-annotated SAGE orf Found reverse in NC_001134 between 681184 and 681420 with 100% identity. See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251

6969_at 3966.8 P

non-annotated SAGE orf Found reverse in NC_001134 between 681366 and 681578 with 100% identity. See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251

6970_at 142.4 A

non-annotated SAGE orf Found reverse in NC_001134 between 681785 and 681940 with 100% identity. See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251

6971_at 573.4 P

non-annotated SAGE orf Found forward in NC_001134 between 697768 and 697947 with 100% identity. See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251

6972_at 57.9 P

non-annotated SAGE orf Found forward in NC_001134 between 744626 and 744784 with 100% identity. See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251

6973_at -120.4 A

non-annotated SAGE orf Found forward in NC_001134 between 9384 and 9605 with 100% identity. See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251

6974_at -100.6 A

non-annotated SAGE orf Found forward in NC_001134 between 9785 and 9922 with 100% identity. See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251

6975_at 1852.2 P

non-annotated SAGE orf Found forward in NC_001134 between 133720 and 133872 with 100% identity. See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251

6976_at 8491.0 P

non-annotated SAGE orf Found reverse in NC_001134 between 167284 and 167427 with 100% identity. See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251

6977_at 1904.2 P

non-annotated SAGE orf Found forward in NC_001134 between 283360 and 283566 with 100% identity. See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251

6978_at 252.3 P

non-annotated SAGE orf Found reverse in NC_001134 between 308633 and 308923 with 100% identity. See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251

6979_at 2456.4 P

non-annotated SAGE orf Found forward in NC_001134 between 333970 and 334104 with 100% identity. See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251

6980_at -56.3 A

non-annotated SAGE orf Found reverse in NC_001134 between 376102 and 376293 with 100% identity. See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251

6981_at 2436.7 P

non-annotated SAGE orf Found reverse in NC_001134 between 398333 and 398488 with 100% identity. See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251

6982_at 77.7 A

non-annotated SAGE orf Found forward in NC_001134 between 479146 and 479289 with 100% identity. See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251

6983_at 283.8 A

non-annotated SAGE orf Found forward in NC_001134 between 741104 and 741241 with 100% identity.

See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251

6984_at	147.8	P	non-annotated SAGE orf Found forward in NC_001134 between 741803 and 741964 with 100% identity. See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251
6938_at	1907.4	P	Saccharomyces cerevisiae chromosome II, complete chromosome sequence. Found forward in NC_001134 between 1 and 1000 with 100% identity.
6939_g_at	1449.3	P	Saccharomyces cerevisiae chromosome II, complete chromosome sequence. Found forward in NC_001134 between 1 and 1000 with 100% identity.
6940_s_at	62.5	A	Saccharomyces cerevisiae chromosome II, complete chromosome sequence. Found forward in NC_001134 between 1001 and 2000 with 100% identity.
6941_s_at	401.1	P	Saccharomyces cerevisiae chromosome II, complete chromosome sequence. Found forward in NC_001134 between 2001 and 3000 with 100% identity.
6942_at	375.0	A	Saccharomyces cerevisiae chromosome II, complete chromosome sequence. Found forward in NC_001134 between 3001 and 4000 with 100% identity.
6943_g_at	635.1	P	Saccharomyces cerevisiae chromosome II, complete chromosome sequence. Found forward in NC_001134 between 3001 and 4000 with 100% identity.
6944_at	78.1	A	Saccharomyces cerevisiae chromosome II, complete chromosome sequence. Found forward in NC_001134 between 4001 and 5000 with 100% identity.
6945_g_at	1730.9	P	Saccharomyces cerevisiae chromosome II, complete chromosome sequence. Found forward in NC_001134 between 4001 and 5000 with 100% identity.
6946_at	2619.0	P	Saccharomyces cerevisiae chromosome II, complete chromosome sequence. Found forward in NC_001134 between 5001 and 6000 with 100% identity.
6947_g_at	4030.8	P	Saccharomyces cerevisiae chromosome II, complete chromosome sequence. Found forward in NC_001134 between 5001 and 6000 with 100% identity.
6948_i_at	112.0	A	Saccharomyces cerevisiae chromosome II, complete chromosome sequence. Found forward in NC_001134 between 6001 and 6215 with 100% identity.
6949_f_at	372.1	P	Saccharomyces cerevisiae chromosome II, complete chromosome sequence. Found forward in NC_001134 between 6001 and 6215 with 100% identity.
6950_at	3732.8	P	snRNA
6951_at	6421.7	P	telomerase RNA component
6952_at	5007.2	P	telomerase RNA component
6953_at	43.2	M	snRNA
6954_at	158.3	P	snRNA
6955_s_at	89.5	A	putative pseudo-TY5
6956_s_at	305.8	P	Reverse transcriptase
6957_s_at	847.7	P	Bud site selection

6958_s_at 2850.3 P
Mating type protein alpha-2
6959_s_at 4897.5 P
transcripton factor involved in the regulation of the alpha-specific genes
6960_at -66.7 A
questionable ORF
6961_g_at 7517.7 P
questionable ORF
6915_at 3066.8 P
catabolic serine (threonine) dehydratase
6916_at 2636.1 P
weak similarity to yeast translation regulator Gcd6p
6917_at 736.4 P
similarity to myosin heavy chain form b from Chicken and Xenopus
6918_at 4571.6 P
strong similarity to human Rev interacting protein Rip-1
6919_at 820.6 A
hypothetical protein
6920_at 3804.6 P
Saccharolysin (oligopeptidase yscD)
6921_at 5470.4 P
hypothetical protein
6922_at 1991.6 P
May assist Ste12p in pheromone-dependent expression of KAR3 and CIK1
6923_at 2241.8 P
Methyltransferase
6924_at 2504.9 P
Protease B Non-derepressible
6925_at 1562.7 P
involved in laminarinase resistance
6926_at 6975.3 P
diadenosine 5 ,5 -P1,P4-tetraphosphate phosphorylase I
6927_at 4009.5 P
hypothetical protein
6928_at -93.9 A
strong similarity to sporulation-specific protein Sps2p
6929_at 1060.9 P
hypothetical protein
6930_at 2821.1 P
weak similarity to human ORF
6931_at 79.0 A
questionable ORF
6932_at 1928.0 P
hypothetical protein
6933_at 11798.6 P
protein disulfide isomerase
6934_at 384.9 P
questionable ORF
6935_at 1101.3 P
questionable ORF
6936_g_at 5254.2 P
questionable ORF
6937_at 8083.1 P
Glucokinase
6893_at 886.1 P
regulatory protein

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6894_at	1196.8	P
Membrane transporter
6895_at	8116.1	P
SRO9 may overlap in function with tropomyosin and may be involved in organization of actin filaments
6896_at	6830.6	P
similarity to hypothetical protein YDR514c
6897_at	7388.4	P
Glutaredoxin (thiol-transferase)
6898_at	4969.1	P
similarity to hypothetical S.pombe protein
6899_at	2512.4	P
Transcription regulator
6900_at	343.5	P
possesses a SAM (sterile alpha motif)\; interacts with G protein and Ste11p
6901_at	1906.0	P
involved in pre-rRNA processing and ribosome assembly
6902_at	11568.2	P
histidinol dehydrogenase
6903_at	475.3	P
Microtubule-binding protein
6904_at	6711.8	P
weak similarity to glutenins, high molecular weight chain
6905_at	3207.0	P
serine\/threonine-rich membrane protein
6906_at	762.5	P
Protein involved in the integration of lipid signaling pathways with cellular homeostatis
6907_at	2711.0	P
Amino acid permease
6908_at	195.6	P
questionable ORF
6909_at	8683.6	P
beta-IPM (isopropylmalate) dehydrogenase
6910_at	7500.5	P
NifS-like protein
6911_at	903.8	P
hypothetical protein
6912_at	891.8	P
Cell cycle regulated protein required for axial bud formation\; co-assembles with Bud4p at bud sites
6913_at	1456.2	P
part of budding protein Bud3p due to frameshift in DNA sequence
6914_at	6352.5	P
Protein with RNA recognition motifs
6870_at	781.8	P
strong similarity to Saccharomyces pastorianus hypothetical protein LgYCL010c
6871_at	9773.0	P
Small regulatory subunit of Acetolactate synthase
6872_at	267.5	P
Calcofluor White Hypersensitivity
6873_at	335.7	P
questionable ORF
6874_at	1800.7	P
strong similarity to Saccharomyces pastorianus hypothetical protein LgYCL005w
6875_at	266.3	P
17-kDa phosphatidylserine synthase
6876_at	2222.3	P
strong similarity to Saccharomyces pastorianus hypothetical protein LgYCL002c
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6877_at 4800.1 P

Protein involved in retention of membrane proteins, including Sec12p, in the ER\; localized to Golgi, where it may function in returning membrane proteins to the ER

6878_at -22.6 A

similarity to Dom34p

6879_at 121.7 A

hypothetical protein

6880_at 6054.1 P

conserved potential GTP-ginding protein

6881_at 2993.3 P

Mitochondrial ribosomal protein MRPL32 (YmL32)

6882_at 8771.3 P

FMN-binding protein

6883_at 8017.1 P

non-mitochondrial citrate synthase

6884_at 111.5 M

hypothetical protein

6885_at 6180.1 P

Ser\/Thr protein kinase

6886_at 7293.8 P

Reduced viability on starvation protein RVS161

6887_at 349.2 P

strong similarity to Y.lipolytica GPR1 protein and Fun34p

6888_at 4225.7 P

Active transport ATPase

6889_at 2.9 A

weak similarity to M.leprae B1496_F1_41 protein

6890_at 5868.1 P

3-phosphoglycerate kinase

6891_at 341.3 P

DNA polymerase IV

6892_at 878.8 P

hypothetical protein

6848_at 1354.2 P

hypothetical protein

6849_at 5295.8 P

similarity to hypothetical S.pombe protein

6850_at 2126.1 P

Transcription regulator

6851_at 1293.1 P

MAK32 sugar kinase

6852_at 424.5 A

Transcription regulator

6853_at 4871.1 P

MAK31 snRNP

6854_at 287.5 P

Protein induced by heat shock, ethanol treatment, and entry into stationary phase\; located in plasma membrane

6855_at 309.8 A

hypothetical protein

6856_at 2022.1 P

Membrane transporter

6857_at 778.2 P

Asn-tRNA synthetase

6858_f_at 11990.2 P

Proteolipid associated with plasma membrane H(+)-ATPase (Pma1p)

6859_at	-36.8	A	hypothetical protein
6860_at	405.5	P	Membrane phospho-diesterase
6861_at	409.0	P	GTPase (RAS-related)
6862_at	1707.1	P	Amino acid permease
6863_at	7458.9	P	required for mitochondrial DNA replication
6864_at	8470.5	P	required for mitochondrial DNA replication
6865_at	1478.8	P	weak similarity to S.pombe hypothetical protein SPBC4C3.06
6866_at	11960.0	P	Ribosomal protein S14A (rp59A)
6867_at	947.9	P	Beige Protein Homologue 1
6868_at	2963.4	P	similarity to mouse nuclear receptor co-repressor N-Cor
6869_at	9216.9	P	Probable subunit of 1,3-beta-glucan synthase\; homolog of ELO1
6825_at	2662.5	P	Component of the exosome 3->5 exoribonuclease complex with Rrp4p, Rrp41p, Rrp42p and Dis3p (Rrp44p).
6826_at	3270.6	P	ribokinase
6827_at	2578.0	P	May collaborate with Pho86p and Pho84p in inorganic phosphate uptake\; protein contains 12 predicted transmembrane domains
6828_at	496.7	P	GTP\/GDP exchange factor for Rsr1 protein
6829_at	18.4	A	questionable ORF
6830_at	666.2	P	TATA binding protein-associated factor (TAF)
6831_at	2384.2	P	hypothetical protein
6832_at	3130.2	P	involved in manganese homeostasis
6833_at	-147.0	A	Protease
6834_at	4286.3	P	required for respiration and maintenance of mitochondrial genome
6835_at	3403.0	P	Protein carboxyl methylase
6836_at	85.3	A	questionable ORF
6837_at	7010.3	P	Acyl-CoA cholesterol acyltransferase (sterol-ester synthetase)
6838_at	-5.3	A	questionable ORF
6839_at	2865.8	P	weak similarity to ankyrins
6840_at	2466.9	P	a subunit of RSC, a fifteen-protein chromatin remodeling complex and related to the Swi\/snf Complex.

6841_at	8187.7	P	threonine synthase
6842_at	573.7	P	CTR86 shares a terminator region with THR4. CTR86 contains aGCN4 responsive site suggesting it may also be involved in amino acid biosynthesis.
6843_at	1866.9	P	regulatory protein
6844_at	5047.5	P	weak similarity to hypothetical protein YDL177c
6845_at	3782.1	P	regulatory protein
6846_at	2872.5	P	hypothetical protein
6847_g_at	4051.8	P	hypothetical protein
6803_at	1864.3	P	similarity to Ytp1p protein
6804_at	-12.0	A	questionable ORF
6805_at	1249.5	P	G10-like protein
6806_at	3499.7	P	Transcription factor (fork head domain)
6807_at	314.7	P	Zn finger protein, putative ATPase
6808_at	4198.1	P	Intracellular transport protein
6809_at	899.1	P	similarity to hypothetical S.pombe protein
6810_g_at	678.0	P	similarity to hypothetical S.pombe protein
6811_at	5297.3	P	cyclophilin homolog
6812_at	1442.3	P	(required for) Integrity of Mitochondrial Genome 2
6813_at	6414.9	P	regulatory protein
6814_at	715.7	P	protein kinase
6815_at	7312.8	P	shows similarity to glucose-6-phosphate dehydrogenase non-catalytic domains\; homologous to Sol1p and Sol3p
6816_at	1902.5	P	ERS1 protein, ER defect supressor
6817_at	1832.8	P	hypothetical protein
6818_at	4968.3	P	Necessary for accurate chromosome transmission during cell division
6819_at	719.5	P	weak similarity to A.thaliana protein phosphatase 2C
6820_at	1191.7	P	activation mediator subcomplex of RNA polymerase I holoenzyme
6821_at	5441.1	P	weak similarity to Rbk1p
6822_at	1828.1	P	Thioredoxin type II

6823_at	6619.6	P	glucose repression regulatory protein, exhibits similarity to beta subunits of G proteins
6824_at	228.6	P	hypothetical protein
6780_at	1858.2	P	hypothetical protein
6781_at	1168.3	P	questionable ORF
6782_at	2933.9	P	nucleic acid-binding protein
6783_at	3704.8	P	Actin binding protein
6784_at	2333.9	P	predicted GPI-anchored cell wall protein
6785_at	3438.0	P	hypothetical protein
6786_at	23.4	A	Putative serine\/threonine protein kinase most similar to cyclic nucleotide-dependent protein kinase subfamily and the protein kinase C subfamily
6787_at	328.5	P	mutS homolog, forms a complex with Msh2p to repair insertion-deletion mispairs\; redundant with Pms3\/Msh6p in repair of insertion-deletion mispairs
6788_at	1836.1	P	nuclear protein that negatively regulates basal transcription
6789_at	2959.3	P	Cell Division Cycle mutant
6790_at	403.6	P	hypothetical protein
6791_s_at	-23.1	A	Homeobox-domain containing protein which, together with alpha2, represses transcription of haploid-specific genes in diploid cells
6792_s_at	-47.1	A	Homeobox-domain containing protein which, together with alpha2, represses transcription of haploid-specific genes in diploid cells
6793_at	254.3	P	permease involved in the uptake of glycerophosphoinositol (GroPIns)
6794_at	284.9	A	strong similarity to Pep1p
6795_at	959.6	P	strong similarity to Pep1p
6796_at	1.6	A	strong similarity to Pep1p
6797_at	1950.2	P	Alcohol dehydrogenase
6798_f_at	1232.0	P	member of the seripauperin protein\/gene family (see Gene_class PAU)
6799_at	497.1	P	Alcohol dehydrogenase
6800_at	665.8	P	Transcription regulator
6801_at	14.7	A	hypothetical protein
6802_at	367.5	P	hypothetical protein
6755_i_at	30.7	P	hypothetical protein

6756_at 217.3 P
high-temperature lethal
6757_i_at -46.2 A
Homeobox-domain containing protein which, together with alpha2, represses transcription of haploid-specific genes in diploid cells
6758_at 91.3 P
hypothetical protein identified by SAGE
6759_at 6487.8 P
identified by SAGE
6760_g_at 12495.2 P
identified by SAGE
6761_at 458.8 A
similarity to starvation induced pSI-7 protein of C. fluvum
6762_s_at 650.5 P
Ser\/Thr protein kinase
6763_at 2184.1 P
homologous to mouse and human Tsg101 tumor susceptibility genes
6764_g_at 1024.2 P
homologous to mouse and human Tsg101 tumor susceptibility genes
6765_at -377.1 A
non-annotated SAGE orf Found forward in NC_001135 between 41465 and 41704 with 100% identity. See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251
6766_at 119.6 A
non-annotated SAGE orf Found forward in NC_001135 between 157511 and 157669 with 100% identity. See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251
6767_at 1075.2 P
non-annotated SAGE orf Found forward in NC_001135 between 171344 and 171496 with 100% identity. See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251
6768_at 1776.1 P
non-annotated SAGE orf Found reverse in NC_001135 between 175695 and 175841 with 100% identity. See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251
6769_at 62.8 P
non-annotated SAGE orf Found forward in NC_001135 between 289916 and 290113 with 100% identity. See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251
6770_i_at 763.2 P
non-annotated SAGE orf Found forward in NC_001135 between 127315 and 127521 with 100% identity. See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251
6771_s_at 137.2 P
non-annotated SAGE orf Found forward in NC_001135 between 127315 and 127521 with 100% identity. See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251
6772_at -181.6 A
non-annotated SAGE orf Found forward in NC_001135 between 127457 and 127678 with 100% identity. See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251
6773_at 487.5 P
non-annotated SAGE orf Found forward in NC_001135 between 18548 and 18736 with 100% identity. See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251
6774_at 910.8 P
non-annotated SAGE orf Found forward in NC_001135 between 109969 and 110139 with 100% identity. See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251
6775_at 8680.2 P
non-annotated SAGE orf Found reverse in NC_001135 between 130174 and 130308 with 100% identity. See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251
6776_at 695.4 P
non-annotated SAGE orf Found reverse in NC_001135 between 171326 and 171487 with 100% identity. See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251
6777_at 1556.9 P

non-annotated SAGE orf Found reverse in NC_001135 between 172336 and 172488 with 100% identity. See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251

6778_i_at 5524.4 A

non-annotated SAGE orf Found reverse in NC_001135 between 204772 and 204939 with 100% identity. See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251

6779_r_at 60.9 P

non-annotated SAGE orf Found reverse in NC_001135 between 204772 and 204939 with 100% identity. See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251

6731_at 163.5 P

non-annotated SAGE orf Found reverse in NC_001135 between 286677 and 286817 with 100% identity. See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251

6732_at 8849.3 P

non-annotated SAGE orf Found reverse in NC_001135 between 162144 and 162278 with 100% identity. See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251

6733_at 11654.4 P

non-annotated SAGE orf Found reverse in NC_001135 between 162307 and 162573 with 100% identity. See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251

6734_at 8.8 A

non-annotated SAGE orf Found reverse in NC_001135 between 205411 and 205581 with 100% identity. See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251

6735_i_at 150.2 P

non-annotated SAGE orf Found forward in NC_001135 between 258696 and 258884 with 100% identity. See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251

6736_r_at 9.4 A

non-annotated SAGE orf Found forward in NC_001135 between 258696 and 258884 with 100% identity. See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251

6737_at -65.3 A

non-annotated SAGE orf Found reverse in NC_001135 between 8959 and 9150 with 100% identity. See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251

6738_at 518.9 A

non-annotated SAGE orf Found reverse in NC_001135 between 9263 and 9469 with 100% identity. See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251

6739_at 74.5 A

non-annotated SAGE orf Found forward in NC_001135 between 15484 and 15642 with 100% identity. See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251

6740_at 294.8 P

non-annotated SAGE orf Found forward in NC_001135 between 24097 and 24348 with 100% identity. See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251

6741_at -162.8 A

non-annotated SAGE orf Found reverse in NC_001135 between 41458 and 41649 with 100% identity. See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251

6742_at 1772.2 A

non-annotated SAGE orf Found reverse in NC_001135 between 41640 and 41792 with 100% identity. See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251

6743_at 185.8 P

non-annotated SAGE orf Found reverse in NC_001135 between 123477 and 123677 with 100% identity. See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251

6744_at -4.5 A

non-annotated SAGE orf Found forward in NC_001135 between 125368 and 125520 with 100% identity. See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251

6745_at 1193.5 P

non-annotated SAGE orf Found reverse in NC_001135 between 168999 and 169175 with 100% identity. See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251

6746_at 1955.8 P

non-annotated SAGE orf Found forward in NC_001135 between 288361 and 288519 with 100% identity. See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251

6747_at	5579.9	P	non-annotated SAGE orf Found reverse in NC_001135 between 209220 and 209360 with 100% identity. See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251
6748_at	43.5	A	non-annotated SAGE orf Found reverse in NC_001135 between 213543 and 213719 with 100% identity. See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251
6749_at	-13.0	P	non-annotated SAGE orf Found forward in NC_001135 between 265724 and 265873 with 100% identity. See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251
6750_i_at	400.0	P	TY5-1
6751_at	593.3	P	snRNA
6752_i_at	-147.3	A	Centromere
6753_at	3442.7	P	snRNA
6754_at	-12.4	A	snRNA
6708_at	564.9	P	snRNA
6709_i_at	181.1	A	strong similarity to sugar transport proteins
6710_at	1372.2	P	Hypothetical aryl-alcohol dehydrogenase
6711_at	-2.3	A	strong similarity to hypothetical protein YPR079w
6712_at	1012.2	P	hypothetical protein
6713_at	1120.6	P	Protein similar to LIM-domain proteins and to rho\/rac GTPase-activating family of proteins
6714_at	265.4	P	hypothetical protein
6715_at	294.4	P	similarity to E.coli hypothetical protein and to chlorohydrolases
6716_at	3938.8	P	hypothetical protein
6717_at	9512.7	P	p-nitrophenyl phosphatase
6718_at	2467.1	P	Two-component phosphorelay intermediate
6719_at	792.6	P	protein of unknown function
6720_at	467.8	P	hypothetical protein
6721_at	9508.4	P	3.6-kDa protein, probably membrane-located
6722_at	863.7	P	hypothetical protein
6723_at	2960.6	P	phosphotyrosine-specific protein phosphatase
6724_at	275.8	P	similarity to A.klebsiana glutamate dehydrogenase
6725_at	5903.8	P	Homothallic switching endonuclease
6726_at	3794.3	P	

ADP-ribosylation factor GTPase-activating protein (ARF GAP)
6727_at 3026.7 P
similarity to Cdc11p, Cdc3p and human CDC10 protein
6728_at 2591.2 P
Possible RNA binding protein. Homolog of Whi3.
6729_at 733.1 P
weak similarity to mucin
6730_at 402.3 P
strong similarity to hypothetical protein YNL194c and similarity to YML052w
6686_at -102.9 A
questionable ORF
6687_at 1316.3 P
binds to single-stranded TG1-3 telomere G-tails
6688_at 4151.2 P
strong similarity to S.equisimilis hypothetical protein
6689_at 4901.3 P
strong similarity to S.equisimilis hypothetical protein
6690_at 118.9 P
weak similarity to hypothetical protein YNR061c
6691_at 3352.4 P
Mitochondrial inner membrane protein involved in import of proteins of the ADP\/ATP carrier (AAC) family
6692_at 275.8 P
similarity to Jun activation domain binding protein homologue of A. thaliana
6693_at 1660.3 P
NAD-dependent glutamate dehydrogenase
6694_at -147.8 A
strong similarity to putative protein kinase NPR1
6695_at 2692.1 P
has an RNA recognition domain in the N-terminal region
6696_at 10640.5 P
Integral membrane component of the endoplasmic reticulum
6697_at 147.9 P
similarity to hypothetical protein YNL176c
6698_at -60.9 A
GABA-specific transport protein
6699_at 1352.6 P
similarity to hypothetical S. pombe protein
6700_at 12102.5 P
HMG-like nuclear protein
6701_at 906.0 P
Nuclear-export-signal (NES)-containing protein
6702_at 399.9 P
weak similarity to transporter proteins
6703_at 112.3 A
phorphobilinogen deaminase (uroporphyrinogen synthase), the third step in heme biosynthesis
6704_at 131.7 P
similarity to hypothetical protein YDR233c
6705_at 320.0 P
similarity to Skt5p
6706_at 961.3 P
Mitochondrial ribosomal protein MRPL11 (YmL11)
6707_at 4203.5 P
strong similarity to human D1075-like protein
6663_at 626.0 A
6-O-methylguanine-DNA methylase
6664_at 191.1 P

similarity to sugar transporter proteins
6665_at 5965.0 P
high copy suppressor of abf2 lacking the HMG1-like mitochondrial HM protein\; putative mitochondrial carrier protein
6666_at 1540.2 P
Anti-silencing protein that causes depression of silent loci when overexpressed
6667_at 241.9 A
hypothetical protein
6668_at 11068.6 P
involved in protein transport from endoplasmic reticulum to Golgi
6669_at 234.7 P
glucose transporter
6670_at 1778.0 P
similarity to N.crassa hypothetical 32 kDa protein
6671_at 3359.4 A
ADP-ribosylation factor
6672_s_at 8632.5 P
Ribosomal protein L35A
6673_at 3517.2 P
ubiquitin fusion degradation protein
6674_at 520.6 P
hypothetical protein
6675_at 800.4 P
hypothetical protein
6676_at 3434.5 P
serine-threonine protein phosphatase 2A
6677_at 210.6 P
questionable ORF
6678_at 116.0 A
hypothetical protein
6679_at 10391.8 P
encodes a protein with three regions (ABC) that is spliced to yield the extein AC and the intein B\; AC is a 69K vacuolar (H+)-ATPase, and B is a 50K site-specfic endonuclease named VDE (PI-SceI) that is homologous to HO. Cleavage is meiosis-specific and induces gene conversion at the TFP1 locus.
6680_s_at 5180.1 P
Ribosomal protein L41A (YL41) (L47A)
6681_at 354.2 P
weak similarity to S.pombe hypothetical protein SPAC23H3
6682_at 13986.7 P
homocitrate synthase, highly homologous to YDL131W
6683_g_at 14955.4 P
homocitrate synthase, highly homologous to YDL131W
6684_at 1538.7 P
ATPase inhibitor
6685_at 1861.8 P
hypothetical protein
6641_at 1277.6 P
PHO85 cyclin
6642_at 4776.5 P
D-Lactate Dehydrogenase (Cytochrome)
6643_at 401.7 P
similarity to hypothetical protein YCR059c
6644_at 151.4 P
hypothetical protein
6645_at 833.0 P
strong similarity to hypothetical protein YIL079c and weak similarity to cellular nucleic acid binding

proteins
6646_at 8853.5 P
mitochondrial enzyme D-lactate ferricytochrome c oxidoreductase
6647_at 3361.5 P
hypothetical protein
6648_at 657.2 A
questionable ORF
6649_at 7474.1 P
Glutamate synthase (NADPH)
6650_at 471.0 P
zinc-finger transcription factor of the Zn(2)-Cys(6) binuclear cluster domain type
6651_at 234.3 P
protein of unknown function
6652_at 3364.7 P
Long-chain alcohol dehydrogenase (glutathione-dependent formaldehyde dehydrogenase)
6653_at 2348.4 P
Asparagine-rich protein
6654_at 4697.8 P
weak similarity to Pyrococcus horikoshii hypothetical protein PHBJ019
6655_at 4334.3 P
nuclear protein that negatively regulates basal transcription
6656_at 1987.1 P
DNA ligase
6657_at -186.0 A
questionable ORF
6658_at -49.6 A
hypothetical protein
6659_at 1262.8 P
strong similarity to hypothetical protein YLR206w and to human KIAA0171 protein
6660_at 1695.8 P
Putative RNA helicase of DEAD box family, required for Rap1p localization to telomeres
6661_at 1327.6 P
MEK homolog
6662_at 1541.0 P
questionable ORF
6618_at 7718.0 P
hypothetical protein
6619_at 156.0 A
weak similarity to Pas7p
6620_at 2565.7 P
G(sub)2-specific B-type cyclin
6621_at 459.9 P
MutS homolog involved in chromosome exchange
6622_at 6678.2 P
Something About Silencing 10
6623_at 254.6 P
questionable ORF
6624_at 126.9 A
questionable ORF
6625_at 2771.9 P
RNA polymerase III (C) subunit, homologus to human BN51 protein
6626_at 214.2 A
hypothetical protein
6627_at 2796.9 P
similarity to human mRNA clone RES4-25
6628_at 6559.2 P

Subunit of the regulatory particle of the proteasome
6629_at 301.5 P
weak similarity to Orc3p
6630_at 11311.1 P
alpha subunit of the coatamer complex\; gamma-alpha-COP
6631_at 3622.0 P
hypothetical protein
6632_at 6991.6 P
Cytoplasmic chaperonin subunit required for actin cytoskeleton assembly or function
6633_at 1231.3 P
Cardiolipin synthase
6634_at 1714.2 P
Biotin:apoprotein ligase
6635_at 10234.0 P
RNA polymerase II large subunit
6636_at 368.7 P
hypothetical protein
6637_at 668.6 P
suppressor of snf3 mutant
6638_at 13815.9 P
ADP-ribosylation factor 2
6639_at 6815.4 P
Rho GDP dissociation inhibitor with activity toward Rho1p
6640_at 703.8 P
serine-threonine protein phosphatase 2A
6595_at 2185.9 P
hypothetical protein
6596_at 2357.9 P
Acts together with Cdc4p and Cdc34p to control the G1-S phase transition, assists in mediating the proteolysis of the Cdk inhibitor Sic1p in late G1
6597_at 11666.9 P
homocitrate synthase, highly homologous to YDL182W
6598_at 4558.8 P
ATPase stabilizing factor
6599_at 11018.0 P
Ribosomal protein P1B (L44) (YP1beta) (Ax)
6600_at 4835.6 P
Ribosomal protein P1B (L44) (YP1beta) (Ax)
6601_at 1345.8 P
hypothetical protein
6602_at 7250.6 P
vacuolar H+\/Ca2+ exchanger
6603_at 1922.9 P
G1 cyclin
6604_at 10697.4 P
Microsomal protein of CDC48\/PAS1\/SEC18 family of ATPases\; full length homology to mammalian protein VCP\; involved in secretion, peroxisome formation and gene expression
6605_at 10234.1 P
Yeast member of the Histidine Triad protein family (HIT)
6606_at 522.6 A
Yeast member of the Histidine Triad protein family (HIT)
6607_at 2824.6 P
similarity to aldose reductases
6608_at 1859.7 P
similarity to hypothetical protein YJL151c
6609_at 5505.1 P

Ubiquitin-specific protease
6610_at 1723.6 P
hypothetical protein
6611_at 2300.9 P
Mitochondrial protein that regulates mitochondrial iron accumulation iron accumulation
6612_at 1707.2 P
similarity to bovine Graves disease carrier protein
6613_at -45.9 A
questionable ORF
6614_at 3980.9 P
similarity to hypothetical S. pombe protein
6615_at 5013.1 P
Protein with homology to mammalian Nup107p
6616_at 483.5 P
hypothetical protein
6617_at -141.1 A
weak similarity to Rhizobium nodulation protein nodG
6573_at 341.5 P
similarity to hypothetical protein YDR425w
6574_at 2961.2 P
similarity to C-terminus of human TRP-185 protein
6575_at 3924.4 P
Component of the exosome 3->5 exoribonuclease complex with Rrp4p, Rrp41p, Rrp43p and Dis3p (Rrp44p).
6576_at 1381.4 P
hypothetical protein
6577_at 445.3 P
strong similarity to thiamine-repressed protein Thi4p
6578_at 1257.2 P
serine-threonine kinase, subunit of transcription factor TFIIK, a subcomplex of TFIIH
6579_at 257.8 P
cox1 pre-mRNA splicing factor
6580_at 168.8 A
Homeobox-domain containing protein which is a positive regulator of PHO5 and other genes
6581_at 261.9 P
protein of unknown function
6582_at 79.2 P
similarity to H.influenzae sialoglycoprotease (gcp)
6583_at 2701.0 P
UDP-N-acetylglucosamine pyrophosphorylase
6584_at 988.7 P
largest and catalytic subunit of DNA polymerase III (delta)
6585_at 964.8 P
protein kinase
6586_at 6728.6 P
similarity to E.coli arsenical pump-driving ATPase
6587_at 4299.1 P
weak similarity to myosin heavy chain proteins
6588_at 1314.9 P
hypothetical protein
6589_at 8082.7 P
Subunit of the regulatory particle of the proteasome
6590_at 332.9 P
questionable ORF
6591_at 9811.5 P
dolichyl phosphate-D-mannose:protein O-D-mannosyltransferase

6592_at	83.2	P	questionable ORF
6593_at	1794.3	P	dolichyl phosphate-D-mannose:protein O-D-mannosyltransferase
6594_at	5168.1	P	Signal recognition particle subunit
6550_at	377.3	P	weak similarity to mouse FAF1 protein
6551_at	2668.4	P	beta subunit of farnesyltransferase
6552_at	1846.8	P	hypothetical protein
6553_at	1981.9	P	Suppressor of thermosensitive mutations in the DNA polymerase delta gene
6554_at	756.5	P	Living Under Cap-binding complex expression
6555_at	11451.9	P	similarity to hypothetical Synechocystis protein
6556_at	-250.1	A	strong similarity to NADH dehydrogenase (ubiquinone)
6557_at	9521.0	P	suppressor of the cold-sensitive snRNP biogenesis mutant brr1-1
6558_i_at	12404.9	P	Ribosomal protein S16B (rp61R)
6559_f_at	10974.7	P	Ribosomal protein S16B (rp61R)
6560_at	14732.0	P	Ribosomal protein L13A
6561_at	6810.6	P	Acidic ribosomal protein P1A (YP1alpha) (A1)
6562_at	1452.4	P	positive regulatory factor with thiamin pyrophosphate-binding motif for thiamin metabolism
6563_at	489.3	P	MDS1 related protein kinase
6564_at	71.8	A	MDS1 related protein kinase
6565_at	5019.6	P	malate dehydrogenase
6566_at	1255.3	P	Required for the vacuolar morphogenesis in yeast
6567_at	1618.3	P	hypothetical protein
6568_f_at	16874.7	P	Ribosomal protein L31A (L34A) (YL28)
6569_at	8304.9	P	Ribosomal protein L31A (L34A) (YL28)
6570_at	2037.2	P	weak similarity to spindle pole body protein NUF1
6571_at	1196.3	P	weak similarity to Cyprinus carpio calcium channel protein
6572_at	5106.2	P	weak similarity to hypothetical protein YMR040w
6527_at	2254.3	P	questionable ORF
6528_at	5483.6	P	Bromodomain protein, homolog of Bdf1

6529_at 975.1 P
translational activator of cytochrome b

6530_at 122.7 P
questionable ORF

6531_at 7696.3 P
Subunit VIIa of cytochrome c oxidase

6532_at 8469.2 P
Mitochondrial form of NADP-specific isocitrate dehydrogenase

6533_at 1032.6 P
40 kDa farnesylated protein associated with peroxisomes

6534_at 5921.5 P
ubiquitin-conjugating enzyme

6535_at 3900.7 P
weak similarity to human estrogen-responsive finger protein

6536_at 152.4 P
questionable ORF

6537_f_at 11320.7 P
Ribosomal protein S29B (S36B) (YS29)

6538_at 9023.1 P
similarity to C.elegans hypothetical protein

6539_at 208.9 P
A mutation in this gene results in RADiation sensitivity and recombination defects, which are general properties of the RAD52 epistasis group mutants. rad59 is epistatic to rad52 for its repair and recombination defects. The RAD59 gene product has homology to the Rad52 protein.

6540_at 1497.9 P
Integrin analogue gene

6541_at 978.0 P
hypothetical protein

6542_at 859.8 P
transcription factor

6543_at 13798.4 P
mannose-1-phosphate guanyltransferase, GDP-mannose pyrophosphorylase

6544_at 1909.6 P
hypothetical protein

6545_at 4237.4 P
hypothetical protein

6546_at 6794.2 P
putative 1-acyl-sn-gylcerol-3-phosphate acyl transferase

6547_at 4744.0 P
Protein homologous to human La (SS-B) autoantigen

6548_at 758.2 P
questionable ORF

6549_at 438.8 P
KRE9 homolog

6504_at 2297.1 P
SIT4 suppress mutations in DBF2

6505_at 8396.9 P
hypothetical protein

6506_at 3589.3 P
homologous to Yml37p, component of the 37 S subunit of mitochondrial ribosomes

6507_at 1070.8 P
FAD synthetase

6508_at 1225.2 P
Necessary for the stability and\/or processing of some large mitochondrial transcripts

6509_at 969.5 P
snRNA-associated protein

6510_at	1694.8	P	regulator of silent mating loci
6511_at	656.0	P	questionable ORF
6512_at	4478.9	P	N-terminal acetyltransferase
6513_at	7473.1	P	questionable ORF
6514_at	3760.2	P	similarity to mucin proteins
6515_at	3839.3	P	strong similarity to glucan 1,4-alpha-glucosidase
6516_at	3060.8	P	strong similarity to RIB2 protein
6517_at	1511.6	P	G-protein coupled receptor
6518_at	106.9	A	questionable ORF
6519_at	1953.4	P	similarity to H.influenzae hypothetical protein HI0174
6520_at	702.9	P	questionable ORF
6521_at	4808.0	P	DEAD box protein 10
6522_at	1045.7	P	RNA splicing factor
6523_at	7318.6	P	actin-related protein
6524_at	594.9	P	serine\/threonine\/tyrosine protein kinase (dual specificity), able to autophosphorylate itself as well as Mad1p. A mutation predicted to abolish kinase function not only eliminates in vitro protein kinase activity, but also behaves like a null mutation in vivo, suggesting that kinase activity contributes to the essential function of the protein.
6525_at	401.4	P	hypothetical protein
6526_at	139.2	A	questionable ORF
6482_at	1164.8	P	ser/thr protein kinase of the DEAD/DEAH box family
6483_at	846.6	P	strong similarity to acid phosphatase
6484_at	-124.4	A	questionable ORF
6485_at	3393.3	P	glycerol-3-phosphate dehydrogenase
6486_at	191.1	P	Similar to GPM1 (phosphoglycerate mutase)
6487_at	2155.2	P	involved in ubiquitin degradation pathway
6488_at	3893.6	P	similarity to Osh1p
6489_at	829.7	P	p24 protein involved in membrane trafficking
6490_at	1402.1	P	serine\/threonine protein kinase
6491_at	-154.1	A	

questionable ORF
6492_at 8005.1 P
similarity to rat synaptic glycoprotein SC2
6493_at 10629.7 P
nucleolar protein, homologous to mammalian fibrillarin
6494_at 3019.2 P
Protein involved in hexose metabolism
6495_at 6894.1 P
strong similarity to hypothetical protein YBR016w and YDR210w
6496_at 354.4 P
questionable ORF
6497_at 1232.6 P
similarity to hypothetical protein YBR014c and glutaredoxins
6498_at 709.6 P
questionable ORF
6499_at 2593.1 P
subunit of the anaphase promoting complex (APC)
6500_at 4589.0 P
Probable 26S protease subunit and member of CDC48\/PAS1\/SEC18 family of ATPases
6501_at 399.9 P
serine-threonine protein phosphatase
6502_at 572.6 P
Stoichiometric member of mediator complex
6503_at 7628.0 P
ATP synthase delta subunit
6459_at 1460.2 P
Mitotic omosome Determinant\; similar to S. pombe RAD21\; may function in chromosome morphogenesis from S phase through mitosis
6460_at 1353.4 P
HMG1-box containing protein
6461_at 815.8 P
similarity to hypothetical protein YFR048w, YDR282c and S.pombe hypothetical protein SPAC12G12.14
6462_at 1761.4 P
neutral trehalase (alpha,alpha-trehalase)
6463_at 11492.8 P
Yeast Ran Binder #1\; suppressor of FUS1\; homolog of mouse HTF9a and human RanBP1
6464_at 767.8 P
strong similarity to hypothetical protein YBR005w
6465_at 1829.2 P
RecA homolog (similar to DMC1, RAD51, and RAD55), interacts with Rad 55p by two-hybrid analysis
6466_at 1612.8 P
required for sorting of Mod5p
6467_at 1445.0 P
gene dosage suppressors of the conditional growth defect of several temperature-sensitive A kinase mutants
6468_at 2033.4 P
n-(5 -phosphoribosyl)-anthranilate isomerase
6469_at 125.9 P
questionable ORF
6470_at 405.5 P
galactokinase
6471_at 125.1 A
hypothetical protein
6472_at 4732.6 P
ABC transporter
6473_i_at 17905.0 P

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Ribosomal protein L4B (L2B) (rp2) (YL2)
6474_at	779.6	P
similarity to human hypothetical KIAA0186 protein
6475_at	214.1	P
weak similarity to chicken neurofilament triplet M protein
6476_at	117.2	P
hypothetical protein
6477_at	2136.5	P
hypothetical protein
6478_at	3141.7	P
Shows homology to basic leucine zipper family of transcription factors
6479_at	69.3	A
strong similarity to hypothetical protein YBR042c
6480_at	1574.3	P
glycine cleavage T protein (T subunit of glycine decarboxylase complex
6481_at	78.9	M
weak similarity to uridine kinases and phosphoribulokinases
6436_at	1438.4	P
DEAD-box protein, putative RNA helicase
6437_at	649.1	P
cik1 suppressor
6438_at	10414.4	P
seryl-tRNA synthetase
6439_at	76.4	P
hypothetical protein
6440_at	1860.1	P
strong similarity to DNA-binding protein Reb1p
6441_at	2329.4	P
Loss Upsets Vacuole
6442_at	1174.4	P
regulatory subunit for protein phosphatase Glc7p
6443_at	497.6	P
hypothetical protein
6444_at	333.9	P
Protein involved in the same pathway as Rad26p, has beta-transducin (WD-40) repeats
6445_at	1843.5	P
hypothetical protein
6446_at	10228.9	P
strong similarity to S.pombe obr1
6447_at	9624.4	P
strong similarity to putative heat shock protein YRO2
6448_at	833.1	P
Transcriptional activator of lysine pathway genes with 2-aminoadipate semialdehyde as co-inducer\;
saccharopine reductase synthesis
6449_at	1310.0	P
identified by SAGE expression analysis
6450_at	10190.3	P
DAHP synthase\; a.k.a. phospho-2-dehydro-3-deoxyheptonate aldolase, phenylalanine-inhibited\;
phospho-2-keto-3-deoxyheptonate aldolase\; 2-dehydro-3-deoxyphosphoheptonate aldolase\;
3-deoxy-D-arabine-heptulosonate-7-phosphate synthase
6451_at	3728.4	P
similarity to enoyl CoA hydratase
6452_at	14642.8	P
lysyl-tRNA synthetase
6453_at	3169.5	P
P-type ATPase involved in Na+ efflux
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6454_g_at 5525.2 P
P-type ATPase involved in Na+ efflux
6455_s_at 4525.7 P
plasma membrane protein\; putative Na+ pump\; P-type ATPase
6456_at 2583.2 P
weak similarity to bacterial ribosomal S10 proteins
6457_at 121.6 P
hypothetical protein
6458_at 490.6 P
Suppressor of SNf
6413_at 5131.3 P
Coproporphyrinogen III oxidase
6414_at 6052.5 P
strong similarity to S.acidocaldarius transcription elongation factor tfs
6415_at 6414.0 P
Valine transporter
6416_at 5151.3 P
uroporphyrinogen decarboxylase
6417_at -17.5 A
questionable ORF
6418_at 572.8 P
similarity to C.elegans K06H7.3 protein
6419_at 8466.1 P
triosephosphate isomerase
6420_at 3963.8 P
similarity to hypothetical A. thaliana protein BAC F7G19
6421_at 96.7 P
cyclin-like kinase required for late nuclear division
6422_at -151.2 A
questionable ORF
6423_at 1282.6 P
ubiquitin-conjugating enzyme, E2
6424_at 4407.2 P
strong similarity to SPS2 protein
6425_at 3212.5 P
hypothetical protein
6426_at 363.4 P
weak similarity to L.lactis mleR protein
6427_at 576.0 P
TriGlyceride Lipase
6428_at 1033.5 P
ubiquitin-conjugating enzyme
6429_at 3086.1 P
similarity to mouse putative CCAAT binding factor CBF1 and CBF2
6430_at 2290.1 P
similarity to E.coli modF and photorepair protein phrA
6431_at 9888.7 P
Probable component of serine palmitoyltransferase, which catalyzes the first step in biosynthesis of long-chain sphingolipids
6432_at 3670.5 P
weak similarity to glia maturation factor beta
6433_at 10710.4 P
Ribosomal protein S13 (S27a) (YS15)
6434_at 303.0 P
hypothetical protein
6435_at 344.6 P

similarity to hypothetical protein YER139c
6391_at 871.8 P
similarity to YNL099c
6392_at 2411.4 P
involved in genome stability
6393_at 990.7 P
ubiquitin isopeptidase
6394_at 298.7 P
hypothetical protein
6395_at 7309.1 P
similarity to O.aries arylalkylamine N-acetyltransferase
6396_at 2904.3 P
inositolphosphotransferase 1
6397_at 1059.9 P
component of SWI\/SNF global transcription activator complex
6398_at 3690.4 P
Trehalose-6-phosphate phosphatase
6399_at 1361.3 P
protein phosphatase type 2A
6400_at 171.6 A
RecA homolog (related to DMC1, RAD51, RAD57), interacts with Rad51p and Rad57p by two-hybrid analysis
6401_at 9857.8 P
putative cell surface glycoprotein
6402_at 938.4 P
Preferential Use of Neither donor locus during mating type switching.
6403_at 2742.0 P
cytochrome c oxidase-specific assembly factor
6404_at 386.1 P
vacuolar protein sorting
6405_at 3133.5 P
Asparagine and serine-rich protein
6406_at 598.1 P
Involved in telemere length regulation, may be functional in telemere metabolism during late S phase
6407_at 5741.4 P
similarity to hypothetical S.pombe protein
6408_at 4112.4 P
similarity to hypothetical C.elegans protein
6409_at 923.2 P
coordinates regulation of alpha-factor receptor signalling and induction of morphogenesis during conjugation
6410_at 8056.6 P
endoplasmic reticulum protein that is part of the Sec61 trimeric complex and the Ssh1 trimeric complex
6411_at 2433.6 P
involved in processing rRNA precursor species to mature rRNAs
6412_at 747.1 P
involved in 3 splice site choices and 2nd step of splicing
6368_at 1604.0 P
weak similarity to Streptococcus transposase
6369_at 2408.9 P
weak similarity to YRO2 protein
6370_at 9663.7 P
strong similarity to human RNase L inhibitor and M.jannaschii ABC transporter protein
6371_at 9540.4 P
ubiquitin-conjugating enzyme
6372_at 2336.8 P

similarity to P.falciparum ATPase 2

6373_g_at	6594.8	P	similarity to P.falciparum ATPase 2
6374_at	1016.7	P	questionable ORF
6375_at	490.0	P	hypothetical protein
6376_at	834.8	P	putative zinc finger protein
6377_at	2702.2	P	Homolog of the human GTBP protein, forms a complex with Msh2p to repair both single-base and insertion-deletion mispairs, redundant with Msh3p in repair of insertion-deletion mispairs
6378_at	4756.6	P	similarity to Legionella glutaredoxin-like protein
6379_at	8135.8	P	Homolog of mammalian 14-3-3 proteins
6380_at	5998.9	P	similarity to Dictyostelium development-specific membrane protein
6381_at	7004.0	P	weak similarity to proliferation-associated protein
6382_at	109.3	A	hypothetical protein
6383_at	1951.6	P	Protein of the pheromone pathway
6384_at	545.1	P	hypothetical protein
6385_at	2469.7	P	similarity to mouse hypothetical protein
6386_at	595.7	P	Actin-related protein
6387_at	1012.1	P	strong similarity to Emp70 protein
6388_at	385.6	P	Probably has role late in meiosis following DNA replication
6389_at	582.7	P	similarity to Mpa43p
6390_at	401.7	P	DNA replication fork blocking protein
6346_at	569.1	P	strong similarity to alanine transaminase
6347_at	4.8	A	questionable ORF
6348_at	296.7	P	42-kDa nuclear protein
6349_at	112.4	A	questionable ORF
6350_at	4527.7	P	similarity to bacterial ribosomal L34 proteins
6351_at	2065.5	P	similarity to bacterial ribosomal L1 proteins
6352_at	2358.4	P	similarity to mouse ligatin, a trafficking receptor for phosphoglycoproteins
6353_at	426.1	P	subunit of the anaphase promoting complex (APC)
6354_at	4182.8	P	similarity to B.subtilis tetracyclin resistance

6355_at 4120.4 P
N2,N2-dimethylguanosine-specific tRNA methyltransferase
6356_at 1825.5 P
weak similarity to YNC2beta protein
6357_at 1178.8 P
Serine\/threonine protein kinase
6358_at 837.3 P
helix-loop-helix protein
6359_at 28.7 A
hypothetical protein
6360_at -58.1 A
ExtraCellular Mutant
6361_at 1215.8 P
similarity to hypothetical protein YLR246w and YOL003c
6362_at 10265.9 P
pentafunctional arom polypeptide (contains: 3-dehydroquinate synthase, 3-dehydroquinate dehydratase (3-dehydroquinase), shikimate 5-dehydrogenase, shikimate kinase, and epsp synthase)
6363_at 2553.5 P
weak similarity to Sec27p, YMR131c and human retinoblastoma-binding protein
6364_at 6426.0 P
fibrim homolog (actin-filament bundling protein)
6365_at 765.7 P
weak similarity to sea urchin myosin heavy chain
6366_at 293.5 P
similarity to hypothetical protein YJL149w
6367_at 398.9 P
strong similarity to hypothetical protein YLR108c
6323_at 10144.3 P
questionable ORF
6324_g_at 12319.7 P
questionable ORF
6325_at 3108.8 P
Metal resistance protein with similarity to human cystic fibrosis protein CFTR and multidrug resistance proteins
6326_at 176.2 P
questionable ORF
6327_at 2368.1 P
Reduced growth phenotype
6328_at 405.0 P
Hyperrecombination protein that suppresses intrachromosomal excision recombination
6329_at 6449.6 P
ubiquitin-like protein
6330_at 6042.7 P
ubiquitin-like protein
6331_at 3047.4 P
weak similarity H.influenzae protoporphyrinogen oxidase (hemK) homolog
6332_at 1366.9 P
hypothetical protein
6333_at 406.0 P
Member of beta-transducin-related (WD-40) protein family
6334_at 2738.1 P
mating-type regulation protein
6335_at 6954.4 P
aspartyl protease related to Yap3p
6336_at 1155.4 P
TFIID subunit

6337_at 1720.9 P
transcriptional activator
6338_at 468.6 P
Ethanolamine Kinase
6339_at 6462.9 P
dihydrolipoyl transsuccinylase component of alpha-ketoglutarate dehydrogenase complex in mitochondria
6340_at -18.6 A
questionable ORF
6341_at 2014.5 P
Protein with variable number of tandem repeats of a 64 amino-acid polypeptide, potential Ca2+-binding site, and pleckstrin homology domain
6342_at 724.2 P
member of the CCCH zinc finger protein family that has two or more repeats of a novel zinc finger motif consisting of Cys and His residues in the form Cx8Cx5Cx3H [where x is a variable amino acid (aa)]
6343_at 2524.2 P
weak similarity to C.elegans hypothetical protein CET26E3
6344_at 2799.9 P
hypothetical protein
6345_at 6852.2 P
questionable ORF
6300_g_at 10270.0 P
questionable ORF
6301_at 10023.4 P
cyclophilin peptidyl-prolyl cis-trans isomerase
6302_at 10554.0 P
RNA polymerase I subunit A14
6303_at 2325.3 P
questionable ORF
6304_at 8144.0 P
aspartic beta semi-aldehyde dehydrogenase
6305_at 2251.1 P
Leucine permease transcriptional regulator
6306_at 597.2 P
Ssy1p controls expression of several transporter genes, including BAP2, TAT1, PTR2 and YDR046c
6307_at 2393.4 P
protein phosphatase Two C-Interacting protein
6308_at 487.5 P
Nap1p-binding protein
6309_at 918.7 P
weak similarity to S.pombe hypothetical protein
6310_at 945.1 P
Hydrophilic protein involved at the late stage of secretion
6311_at 2544.1 P
weak similarity to hypothetical C.elegans protein
6312_at 2297.9 P
107 kDa component of the Exocyst complex\; required for exocytosis.
6313_at 3910.2 P
TFIID subunit
6314_at 6139.5 P
Cell cycle protein necessary for passage through START
6315_at 539.7 P
Binds Sin3p in two-hybrid assay
6316_at 9332.3 P
Guanine nucleotide exchange protein for ARF
6317_at 2398.2 P
Similar to HSP26\; expression is regulated by stress conditions

6318_at 6907.8 P
putative translation factor
6319_at 618.6 P
Regulator of arginine-responsive genes with ARG80 and ARG81
6320_at 7232.0 P
Non-histone protein
6321_at 2159.4 P
similarity to S.pombe hypothetical protein SPAC2F7.15
6322_at 894.9 P
transcription factor\; genetic and mutant analyses suggest that Ngg1p (Ada3p) is part of two transcriptional adaptor\/HAT (histone acetyltransferase complexes, the 0.8 MD ADA complex and the 1.8 MD SAGA complex
6278_at 7983.6 P
ubiquitin-conjugating enzyme
6279_at 5978.1 P
succinate dehydrogenase membrane anchor subunit
6280_at 130.6 P
hypothetical protein
6281_at 277.3 P
hypothetical protein
6282_at 1659.8 P
Sister chromatid cohesion protein
6283_at 791.3 P
Involved in silencing at telomeres, HML and HMR
6284_at 3057.7 P
Protein that affects bud emergence, intrachromosomal recombination, and nuclear division
6285_at 887.3 P
weak similarity to thioredoxin
6286_at 2987.9 P
Aip Three Complex\; interacts with AIP3, localized to the nucleus
6287_at 377.1 P
strong similarity to Msf1p
6288_at 450.4 P
hypothetical protein
6289_at 113.4 A
questionable ORF
6290_at 7946.0 P
Cytoplasmic chaperonin of the Cct ring complex (previously called TCP1 or TRiC), distantly related to Tcp1p and to Hsp60
6291_at 1393.1 P
Hydrophilic suppressor of ypt1 involved in vesicle trafficking between ER and Golgi
6292_at 7714.9 P
strong similarity to TATA-binding protein-interacting protein 49 - rat
6293_at 713.9 P
Homolog of SIR2
6294_at 979.1 P
nucleoporin
6295_at 148.9 A
questionable ORF
6296_at 6879.6 P
Mitochondrial RNA helicase of the DEAD box family
6297_at 1444.7 P
RNA-binding protein involved in cleavage step of mRNA 3 -end formation, prior to polyadenylation
6298_at 1418.2 P
similarity to C.elegans hypothetical protein T05G5.5
6299_at 802.3 P

cytochrome b translational activator
6255_at 1208.1 P
hypothetical protein
6256_at 188.4 A
questionable ORF
6257_at 420.2 P
similarity to hypothetical protein YLR238w
6258_at 1808.5 P
component of spindle pole
6259_at 1022.8 P
hypothetical protein
6260_at 51.9 A
questionable ORF
6261_at 3395.4 P
Involved in ubiquinone biosynthesis
6262_at 848.1 P
similarity to A.eutrophus cation efflux system membrane protein czcD, rat zinc transport protein ZnT-1 and Cot1p
6263_at 1498.2 P
EST1-like bcy1 Suppressor
6264_at 1851.0 P
Ume6p is a C6 zinc finger URS1-binding protein that is a key regulator required for both repression and induction of early meiotic genes, and for sporulation\; Ume6p rquires Ume4 for mitotic repression and interacts with and requires Ime1p and Rim11p for induction of meiosis-specific transcription
6265_at 2836.9 P
Phosphatidylinositol 4-phosphate kinase
6266_at 1032.4 P
questionable ORF
6267_at 10029.2 P
strong similarity to hypothetical protein YBR016w
6268_at 5308.4 P
Translation initiation factor eIF-2B epsilon subunit
6269_at 8544.5 P
chaperonin subunit alpha
6270_at 293.8 P
regulatory protein involved in control of sterol uptake
6271_at 7144.8 P
similarity to hypothetical protein YNL281w
6272_at 343.4 A
hypothetical protein
6273_at 676.6 P
positive transcriptional regulator of ADH2 and peroxisomal protein genes
6274_at 649.6 P
cell cycle arrest protein
6275_at 111.1 P
Septin-related protein expressed during sporulation
6276_at 284.1 P
hypothetical protein
6277_at 877.6 P
questionable ORF
6232_at 692.7 P
weak similarity to the beta subunit of an ER luminal alpha-glucosidase from mouse
6233_at 3089.7 P
strong similarity to hypothetical protein YLR225c
6234_at 57.8 P
similarity to Ifh1p

6235_at 11383.6 P
Histone H2B (HTB1 and HTB2 code for nearly identical proteins)
6236_i_at 18587.4 P
Histone H2A (HTA1 and HTA2 code for nearly identical proteins)
6237_at 10372.9 P
cytosolic adenylate kinase
6238_at 400.1 P
regulator of silent mating loci
6239_at 772.7 P
Component of pre-mRNA cleavage and polyadenylation factor I, interacts with Rna14p and Rna15p
6240_at 624.7 P
hypothetical protein
6241_at 305.1 P
questionable ORF
6242_at 1859.6 P
hypothetical protein
6243_at 5253.5 P
5-aminolevulinate synthase
6244_at 11330.9 P
similarity to hypothetical protein YDL204w
6245_at 7890.6 P
homoaconitase
6246_at 1368.6 P
U1 snRNP protein that shares 50\% sequence similarity with Prp39p U1 snRNP protein and has multiple copies of the crn-like TPR motif
6247_at 1286.8 P
similarity to hypothetical A. thaliana protein
6248_at 785.8 P
Mitochondrial ribosomal protein MRPL7 (YmL7)
6249_at 10410.0 P
encodes a subunit of yeast coatomer
6250_at 2162.0 P
hypothetical protein
6251_at 738.5 P
Snurp = Small nuclear ribonucleoprotein particle of MW 56 kDa. Associated with the U1 snRNP\; no counterpart in mammalian U1 snRNP. Serine-rich.
6252_at 2.6 A
questionable ORF
6253_at 510.7 P
putative amidase
6254_at 838.9 P
Required for the first step of splicing in vitro
6209_at 517.4 P
69-kDa protein containing tetratricopeptide repeat (TPR)
6210_at 5159.1 P
galactosyltransferase
6211_at 3577.9 P
involved in targeting and fusion of ER to golgi transport vesicles
6212_at 439.9 P
strong similarity to Sks1p
6213_at 1864.8 P
strong similarity to E.coli thermoresistant gluconokinase
6214_at 1652.9 P
weak similarity to cytochrome b
6215_at 168.0 P
hypothetical protein

6216_at 2077.6 P
coiled-coil protein multicopy suppressor of loss of PP2A
6217_at 993.1 P
Negative effect on expression of several genes transcribed by RNA polymerase II\; BTF3 homolog
6218_at 180.0 A
zinc finger DNA binding factor, transcriptional regulator of sulfur amino acid metabolism, highly homologous to Met31p
6219_at 143.2 P
Protein necessary for stability of ARS-CEN plasmids\; suggested to be required for kinetochore function
6220_at 824.5 P
weak similarity to hypothetical S.pombe hypothetical protein SPBC29A3
6221_at 339.6 P
catalase A
6222_at 1318.2 P
Transcription regulator
6223_at 2050.0 P
Mitochondrial heat shock protein 78 kDa
6224_at 203.0 A
bZIP protein
6225_at 1420.7 P
hypothetical protein
6226_at 2070.5 P
Exo-1,3-b-glucanase
6227_at 2848.1 P
hypothetical protein
6228_at 563.0 P
DNA-damage inducible gene
6229_at 2279.6 P
Ankyrin repeat-containing protein
6230_at 658.2 P
C3HC4 zinc-binding integral peroxisomal membrane protein
6231_at 2523.8 P
similarity to hypothetical C.elegans protein
6187_at 2126.0 P
weak similarity to human TAFII100 and other WD-40 repeat containing proteins
6188_at 1089.1 P
mitochondrial tryptophanyl-tRNA synthetase
6189_at 99.1 A
questionable ORF
6190_at 3071.4 P
Copper-transporting P-type ATPase with similarity to human Menkes and Wilsons genes
6191_at 138.6 A
questionable ORF
6192_at 1605.4 P
Cytoplasmic glyoxylase-II
6193_at 186.7 P
weak similarity to YOR042w
6194_at 466.9 A
hypothetical protein
6195_at 1676.4 P
weak similarity to YOR042w
6196_at 11295.4 P
strong similarity to Hordeum vulgare blt101 protein
6197_at 593.2 P
Protein is 61\% identical to Msn3p
6198_at 68.0 A

hypothetical protein
6199_at	878.1	P
hypothetical protein
6200_at	4450.3	P
Putative 3 ->5 exoribonuclease\; component of exosome complex of 3 ->5 exonucleases
6201_at	1634.1	P
hypothetical protein
6202_at	887.4	P
similarity to hypothetical protein YDL001w, YFR048w and S.pombe hypothetical protein SPAC12G12.14
6203_at	1028.6	P
eukaryotic initiation factor 2 alpha (eIF2-alpha) kinase
6204_at	3521.1	P
Diacylglycerol Pyrophosphate Phosphatase
6205_at	245.4	P
Synaptonemal complex protein, component of the central element
6206_at	1427.6	P
hypothetical protein
6207_at	1473.4	P
similarity to inositolmonophosphatases
6208_at	308.8	P
hypothetical protein
6163_at	364.5	P
hypothetical protein
6164_at	-22.0	A
questionable ORF
6165_at	1753.9	P
similarity to B.subtilis helicases
6166_at	3163.0	P
signal recognition particle receptor - alpha subunit
6167_at	3687.8	P
putative protein phosphatase
6168_at	8290.1	P
dihydrosphingosine phosphate lyase (also known as sphingosine phosphate lyase)
6169_at	430.5	A
weak similarity to Uso1p, YPR179c and fruit fly tropomyosin
6170_at	3538.3	P
hypothetical protein
6171_at	6087.1	P
Syringomycin response protein 2
6172_at	5265.0	P
ATP synthase subunit 5\; oligomycin sensitivity-conferring protein
6173_at	3157.0	P
involved in protein transport step at the Brefeldin A blocks
6174_at	4568.5	P
gamma-glutamyl kinase
6175_at	3030.2	P
Component of pre-mRNA cleavage factor II (CFII)\; 150-kDa protein associated with polyadenylation factor 1 (PF I)
6176_at	5357.5	P
weak similarity to human GPI-anchor biosynthesis protein
6177_at	854.1	P
similarity to transcriptional regulator proteins
6178_at	9574.1	P
Cyclophilin D, Peptidyl-prolyl cis-trans isomerase D
6179_at	2993.2	P
Yeast member of the Histidine Triad protein family (HIT)

6180_i_at 140.4 P
Yeast member of the Histidine Triad protein family (HIT)
6181_r_at 34.5 A
Yeast member of the Histidine Triad protein family (HIT)
6182_f_at 195.5 P
Yeast member of the Histidine Triad protein family (HIT)
6183_at 1815.5 P
weak similarity to S.pombe hypothetical protein SPAC6F6
6184_at 2653.0 P
similarity to Pmt1p, Pmt2p, Pmt3p and Pmt5p
6185_at 2030.3 P
RNA polymerase II holoenzyme component
6186_at 7195.0 P
GTPase-interacting component 2
6140_at 4493.5 P
Suppresor of mar1-1 (sir2) mutation
6141_at 1039.1 P
Component of transcription initiation factor IIb, 75 kDa subunit
6142_i_at 218.4 P
high copy suppressor of G beta subunit temperature sensitive mutation
6143_f_at 1206.1 P
high copy suppressor of G beta subunit temperature sensitive mutation
6144_at 835.4 P
Phosphatidylinositol(3)-phosphate binding
6145_at 73.5 A
weak similarity to hypothetical S.pombe protein
6146_at 287.1 A
hypothetical protein
6147_at 1776.3 P
hypothetical protein
6148_at 109.8 A
hypothetical protein
6149_at 888.1 P
Involved in minichromosome maintenance
6150_at 1942.7 P
hypothetical protein
6151_at 289.8 P
similarity to hypothetical S. pombe protein and weak similarity to bovine auxilin
6152_at 9358.4 P
Asparaginase I, intracellular isozyme
6153_at 1546.1 P
Mitochondrial ribosomal protein MRPL35 (YmL35)
6154_at 10082.6 P
subunit e of mitochondrial F1F0-ATPase
6155_at 116.5 A
cytosolic and peripheral membrane protein with three zinc fingers\; cysteine rich regions of amino acids are essential for function
6156_at 4093.0 P
weak similarity to beta transducin from S. pombe and other WD-40 repeat containing proteins
6157_at 678.9 P
weak similarity to S.pombe hypothetical protein SPAC1B9
6158_at 770.9 P
strong similarity to YHR080c, similarity to YFL042c and YLR072w
6159_at 487.1 P
questionable ORF
6160_at 7041.6 P

Skp1p encodes Cbf3d, a 29 Kd kinetochore protein subunit of CBF3, a multiprotein complex which binds to the CDE III element of centromeres. In addition, Skp1p is a subunit of the SculCdc4 (also termed SCFCdc4p) complex, which also contains the ubiquitin ligase Cdc34p, the cullin Cdc53p, and Cdc4p. SculCdc4 complexes transfer ubiquitin to phosphorylated Sic1p, and substrate recognition is thought to involve the Cdc4p and Skp1p subunits. Following the SculCdc4-mediated monoubiquitination of Sic1p, a polyubiquitin chain is added, andubiquitinated Sic1p is then degraded by the 26S proteosome.
6161_at 1088.0 P
48-kDa peroxisomal integral membrane protein
6162_at 1201.6 P
similarity to hypothetical S. pombe protein
6117_at 2643.7 P
Protein involved in the attachment of glycosylphosphatidylinositol (GPI) anchors to proteins
6118_at 408.5 P
similarity to E.coli hypothetical protein and weak similarity to RNA helicase MSS116 / YDR194c
6119_at 1817.9 P
similarity to hypothetical S. pombe protein
6120_at 1273.3 P
similarity to nuclear Sth1p, Snf2p and related proteins
6121_at 4903.6 P
Multicopy suppressor of snf1 mutation
6122_at 1613.6 P
weak similarity to B.subtilis hypothetical protein X
6123_at 2382.4 P
Mitochondrial ribosomal protein MRPS28 (E. coli S15)
6124_at 1571.9 P
similarity to Erc1p
6125_at 6977.0 P
weak similarity to hypothetical protein YOR004w
6126_at 44.5 A
questionable ORF
6127_at 13025.0 P
strong similarity to arginine-tRNA ligase
6128_f_at 10321.2 P
Hexose transporter
6129_f_at 9812.9 P
Hexose transporter
6130_at 139.6 A
hypothetical protein
6131_at 13690.3 P
High-affinity glucose transporter
6132_at 3156.4 P
similarity to hypothetical S.pombe protein
6133_at 2597.4 P
37 kDa mitochondrial ribosomal protein
6134_at 1501.6 P
similarity to hypothetical protein YHR097c
6135_at 4109.0 P
GPI-anchored aspartic protease
6136_at 774.1 P
protein of unknown function
6137_at 2629.3 P
required for bud growth
6138_at 1262.6 P
weak similarity to hypothetical proteins YOL092w, YBR147w and YMR010w
6139_at 7986.9 P
Thioredoxin reductase

6095_at 3398.7 P
anthranilate phosphoribosyl transferase
6096_at -32.2 A
questionable ORF
6097_at 633.8 P
component of the spindle pole body that interacts with Spc42p, calmodulin, and a 35 kDa protein
6098_at 1329.3 P
hypothetical protein
6099_at 900.6 P
strong similarity to hypothetical protein YHR108w and weak similarity to signal transducing adaptor from mouse and man
6100_at 937.0 P
hypothetical protein
6101_at -234.9 A
questionable ORF
6102_at 2476.9 P
hypothetical protein
6103_at 1106.4 P
91 kDa tau91 subunit of transcription factor IIIC (TFIIIC)
6104_at 1362.2 P
Establishes Silent omatin
6105_at 4629.4 P
Homolog of DSS1\; similar to hypothetical protein from S. pombe
6106_at 1978.7 P
Member of the beta transducin family
6107_at 1908.1 P
weak similarity to Streptococcus M protein
6108_at 166.3 A
similarity to YOL106w and YER181c
6109_at 2187.7 P
hypothetical protein
6110_at 5091.7 P
homologous to the aldo-keto reductase protein family
6111_at 293.8 A
DNA repair protein
6112_at 2017.1 P
hypothetical protein
6113_at 78.4 P
similarity to chitinases
6114_at 2788.9 P
similarity to hypothetical S. pombe protein
6115_at 4452.5 P
strong similarity to human BDR-1 protein and other calcium binding proteins
6116_at 75.9 A
similarity to hypothetical A. thaliana protein BAC F21M12
6072_at 1115.2 P
Mitochondrial protein of the CDC48\/PAS1\/SEC18 ATPase family, required for expression of functional Rieske iron-sulfur protein
6073_at 1718.1 P
adrenodoxin oxidoreductase homolog
6074_at 5246.4 P
ATP synthase subunit f
6075_at 4073.6 P
Sm-like protein
6076_at 255.9 P
Contains a Rho-GAP domain and two LIM domains. Has strong similarity to Rga1p. Has some similarity

to all known Rho-GAPs.
6077_at 8106.2 P
similarity to Pdc6p, Thi3p and to pyruvate decarboxylases
6078_at 9192.3 P
Nuclear RNA-binding RNA annealing protein
6079_at 7846.7 P
Nuclear RNA-binding RNA annealing protein
6080_at 6721.0 P
Ribosomal protein P2B (YP2beta) (L45)
6081_at 4.0 A
weak similarity to S.pombe paramyosin
6082_at 6796.4 P
strong similarity to Y.lipolytica GPR1 gene
6083_at 281.6 P
MMS and UV Sensitive\; Mus81p and Rad54p are found together in a complex from whole-cell extracts
6084_at 502.8 P
similarity to Itr1p and Itr2p and E.coli araE
6085_at 9919.8 P
involved in endocytosis
6086_at 1209.2 P
GTPase activating protein (GAP) for RHO1
6087_at 1066.3 P
Protein with homology to mammalian ubiquitin activating (E1) enzyme
6088_at 1127.8 P
strong similarity to hypothetical protein YOR013w
6089_at 883.7 P
transcription factor, member of the histone acetyltransferase SAGA complex
6090_at 325.5 P
mRNA (identified by a library screen) that causes growth arrest when overexpressed
6091_at 3785.6 P
probable 26S protease subunit and member of the CDC48\/PAS1\/SEC18 family of ATPases
6092_at 4432.7 P
Sxm1p
6093_at 373.1 P
hypothetical protein
6094_at 2109.8 P
repressor of class II transcription
6049_at 6887.9 P
similarity to human KIAA0007 gene
6050_at 5708.1 P
Hypoxanthine Phosphoribosyltransferase
6051_at 6801.3 P
similarity to C. fasciculata inosine-uridine preferring nucleoside hydrolase (EC 3.2.2.1)
6052_at -104.1 A
Cytochrome P450 56, Dit2p catalyzes oxidation of N-formyl tyrosine to N,N-bisformyl dityrosine in vitro
6053_at -107.5 A
questionable ORF
6054_at 140.4 A
first enzyme in dityrosine synthesis in the outer layer of the spore wall pathway converting L-tyrosine to N-formyl-L-tyrosine, expressed late (10-16 hr) in sporulation
6055_at 5916.2 P
dissociable subunit of RNA polymerase II
6056_at 916.2 P
263-amino acid mitochondrial ribosomal large subunit protein\; similar to L23 family of ribosomal proteins
6057_at 791.0 P
probable multidrug resistance transporter

6058_at 1910.7 P
weak similarity to Myo1p
6059_at 5743.3 P
glycinamide ribotide transformylase
6060_at 426.4 P
similarity to Nfi1p
6061_at 5495.3 P
farnesyl cysteine-carboxyl methyltransferase
6062_at 2743.3 P
weak similarity to Der1p
6063_at 344.7 P
weak similarity to NADH dehydrogenase
6064_at 1441.0 P
questionable ORF
6065_at 1223.3 P
Protein required for retention of luminal ER proteins
6066_at 2527.0 P
strong similarity to bacterial leucyl aminopeptidase
6067_at 1258.2 P
SYnthetic lethal with cdcForty
6068_at 370.9 P
questionable ORF
6069_i_at 15936.0 P
Ribosomal protein L12B (L15B) (YL23)
6070_s_at 12061.3 P
Ribosomal protein L12B (L15B) (YL23)
6071_at 275.8 P
similar to E. coli DinB and S. cerevisiae REV1
6026_at 2177.4 P
Type 1 membrane protein with EF hand motif
6027_at 247.7 P
hypothetical protein
6028_at 1600.3 P
SNF1 protein kinase substrate
6029_at 2744.0 P
Transcriptional activator involved in resistance to 1,10-phenanthroline\; member of yeast Jun-family of transcription factors related to mammalian c-jun
6030_at 7647.2 P
putative light chain of dynein
6031_at 391.5 P
similarity to hypothetical protein YDL113c
6032_at 122.9 A
questionable ORF
6033_at 6226.1 P
Subunit of the regulatory particle of the proteasome
6034_at 2035.8 P
hypothetical protein
6035_at 9020.1 P
Translation initiation factor 3 p33 subunit
6036_at 2066.8 P
similarity to C.perfringens hypothetical hypA protein
6037_at 55.0 A
questionable ORF
6038_at 7982.6 P
nuclear shuttling protein with an RNA recognition motif
6039_g_at 14916.3 P

nuclear shuttling protein with an RNA recognition motif
6040_i_at 18958.6 P
questionable ORF
6041_at 2331.6 P
similarity to S.pombe hypothetical protein
6042_at 1192.1 P
similarity to YOL141w and hypothetical C.elegans protein
6043_at 631.4 A
serine-threonine phosphatase Z
6044_at -80.8 A
hypothetical protein
6045_at 525.9 P
strong similarity to hypothetical protein YML018c
6046_at 439.6 P
Loss of rDNA silencing
6047_at 923.4 P
Pachytene CHeckpoint
6048_at 2245.3 P
Adenine phosphoribosyltransferase
6003_at -49.3 A
questionable ORF
6004_at 2393.1 P
RNA polymerase II holoenzyme component
6005_at 642.2 P
similarity to hypothetical protein YGL144c and YDL109c
6006_at 31.0 A
questionable ORF
6007_at 56.3 A
ExtraCellular Mutant
6008_at 1412.6 P
transcription factor, member of ADA and SAGA, two transcriptional adaptor\/HAT (histone acetyltransferase)complexes
6009_at 1985.2 P
hypothetical protein
6010_at 1173.1 P
strong similarity to Yox1p
6011_at 4453.6 P
similarity to human sphingomyelin phosphodiesterase
6012_at 882.5 P
strong similarity to thiol-specific antioxidant proteins
6013_at 11104.3 P
guanylate kinase
6014_at 13.2 A
questionable ORF
6015_at 2094.0 P
Na+\/H+ exchanger
6016_at 5509.3 P
hect-domain-containing protein, required for G2\/M transition\; similar to RSP5\; contains motifs typical of protein kinases
6017_at 523.9 P
similarity to hypothetical protein YML034w and YML033w
6018_at 1186.6 P
weak similarity to YNL326c
6019_at 1074.5 P
TFIIH subunit Tfb3 , contains ring finger motif\; similar to mammalian CAK subunit
6020_r_at 645.8 M

a-factor mating pheromone precursor
6021_f_at 119.7 A
a-factor mating pheromone precursor
6022_at 2720.7 P
Mitochondrial ribosomal protein MRPL28 (YmL28)
6023_at 1822.1 P
Nuclear-localized protein containing zinc finger motifs
6024_at 900.5 P
negative regulator of prp genes
6025_at 6155.1 P
Protein arginine methyltransferase
5980_at 1914.1 P
similarity to ser/thr protein kinase
5981_at 245.9 A
questionable ORF
5982_at 995.6 P
tSNARE that affects a Late Golgi compartment
5983_at 661.3 P
hypothetical protein
5984_at 365.7 P
similarity to chromosome segregation protein Cse1p
5985_at 14859.8 P
Ribosomal protein L27B
5986_at 2311.9 P
similarity to P.falciparum 41-2 protein antigen
5987_at 812.7 P
essential splicing factor
5988_at 1123.5 P
similarity to C-terminal region of YOR019w
5989_at 198.2 A
hypothetical protein
5990_at 6964.9 P
hypothetical protein
5991_at 2705.0 P
protein serine\/threonine kinase
5992_at 1992.4 P
RNAse MRP protein component
5993_at 621.5 P
weak similarity to YHR150w
5994_at 458.3 A
MAP kinase-associated protein
5995_at 2889.9 P
repressible alkaline phosphatase
5996_at 225.1 P
hypothetical protein
5997_at 7214.0 P
alpha-1,2-mannosyltransferase
5998_at 525.6 P
May interact with actin as a component or controller of the assembly or stability of the actin cytoskeleton
5999_at 2443.4 P
similarity to trichohyalin
6000_at 1673.1 P
weak similarity to Snf7p
6001_at 8239.7 P
3,4-dihydroxy-2-butanone 4-phosphate synthase
6002_at 1655.3 P

Protein required in the absence of Cin8p
5958_at 515.8 P
hypothetical protein
5959_at 1230.5 P
Ser\/Thr protein kinase
5960_at 126.0 A
questionable ORF
5961_at 8942.3 P
strong similarity to hypothetical protein YOL002c
5962_at 1142.6 P
hypothetical protein
5963_at 2784.6 P
hypothetical protein
5964_at 154.9 P
Vacuolar sorting protein
5965_at 5771.8 P
similarity to hypothetical human and C.elegans proteins
5966_at 11427.6 P
myo-inositol transporter
5967_at 2510.4 P
membrane glycoprotein, sorted by HDEL retrieval system
5968_at 752.2 P
weak similarity to hypothetical C.elegans protein, M.genitalium peptide chain release factor 1 and YJL149w
5969_at 13170.2 P
60S ribosomal protein L37B (L43) (YL35)
5970_at 96.4 M
similarity to hypothetical protein YLR183c
5971_at 8058.8 P
S-adenosylmethionine synthetase
5972_at 1442.5 P
Lipid phosphate phosphatase
5973_at 3961.1 P
similarity to hypothetical T.brucei protein
5974_at 1744.9 P
high copy suppressor of ts mutations in DNA polymerase alpha
5975_at 2220.1 P
similarity to FET3, YFL041w and F.floriforme diphenol oxidase
5976_at 3044.5 P
putative serine\/threonine kinase
5977_at 8905.3 P
high-affinity glutamine permease
5978_at 328.4 P
questionable ORF
5979_at 5307.3 P
may be involved in function and\/or structure of the eukaryotic kinetochore
5935_at 3582.7 P
weak similarity to C. elegans protein F25H9.7 and to the human complement 3 precursor
5936_at 2561.5 P
questionable ORF
5937_at 7440.5 P
Glutaredoxin (thioltransferase) (glutathione reductase)
5938_at 2550.9 P
strong similarity to hypothetical protein YCL036w
5939_at 618.4 P
regulates the copper-dependent mineralization of copper sulfide complexes on the cell surface in cells

cultured in medium containing copper salts
5940_at 2428.9 P
strong similarity to glucokinase
5941_at 1514.5 P
weak similarity to hypothetical S.pombe protein
5942_at 1856.8 P
Protein disulfide isomerase homolog
5943_at 6014.6 P
FKBP (FK506 binding protein) 13\; peptidylprolyl cis-trans isomerase activity
5944_at 948.1 P
weak similarity to transcription factors of the zinc finger class
5945_at -26.4 A
questionable ORF
5946_at -249.9 A
Middle\/late gene of meiosis
5947_at 311.4 P
serine\/threonine kinase homologous to Ste20p\; expressed in middle\/late meiosis
5948_at 646.8 P
similarity to hypothetical human protein and YIL044c
5949_at 29.4 A
hypothetical protein
5950_at 408.1 P
questionable ORF
5951_at 2786.2 P
weak similarity to Plasmodium yoelii rhoptry protein
5952_at 536.5 P
similarity to Lre1p
5953_at 8609.2 P
ubiquinol-cytochrome c oxidoreductase subunit 7 (14 kDa)
5954_at 1434.0 P
5 ,5 -P-1,P-4-tetraphosphate phosphorylase II
5955_at 2976.4 P
similarity to hypothetical A. thaliana and C. elegans proteins
5956_at 115.9 P
weak similarity Plasmodium repeat organellar protein
5957_at 9286.1 P
strong similarity to hypothetical proteins YPL280w, YOR391c and YMR322c
5913_at 580.4 P
similarity to YOR383c,Sta1p and pig mucin
5914_at 256.1 P
hypothetical protein
5915_at -150.2 A
sugar transporter-like protein
5916_at 522.3 P
questionable ORF
5917_at 3534.2 P
Phenylacrylic acid decarboxylase
5918_at 4622.9 P
similarity to E.coli hypothetical 55.3 kDa protein in rfah-rfe intergenic region
5919_at 187.7 A
hypothetical protein
5920_at 758.0 P
similarity to dihydroflavonol-4-reductases
5921_at 9169.0 P
hypothetical protein identified by SAGE
5922_s_at 4955.2 P

homing endonuclease with protein splicing activity
5923_at 2085.0 P
identified by SAGE
5924_at 331.1 P
identified by SAGE
5925_at 5051.0 A
identified by SAGE
5926_g_at 0.0 A
identified by SAGE
5927_at 2596.0 P
Involved in pre-tRNA splicing and in uptake of branched-chain amino acids
5928_at 334.3 P
non-annotated SAGE orf Found forward in NC_001136 between 169497 and 169697 with 100% identity. See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251
5929_at 1802.4 P
non-annotated SAGE orf Found reverse in NC_001136 between 340810 and 340977 with 100% identity. See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251
5930_at 804.6 P
non-annotated SAGE orf Found reverse in NC_001136 between 372033 and 372221 with 100% identity. See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251
5931_at 2397.8 P
non-annotated SAGE orf Found forward in NC_001136 between 578355 and 578501 with 100% identity. See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251
5932_at 3130.0 P
non-annotated SAGE orf Found reverse in NC_001136 between 603587 and 603805 with 100% identity. See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251
5933_at -47.2 P
non-annotated SAGE orf Found forward in NC_001136 between 691007 and 691207 with 100% identity. See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251
5934_at 1328.0 P
non-annotated SAGE orf Found reverse in NC_001136 between 1108272 and 1108490 with 100% identity. See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251
5887_i_at 5261.5 P
non-annotated SAGE orf Found reverse in NC_001136 between 1489561 and 1489731 with 100% identity. See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251
5888_at -6.0 A
non-annotated SAGE orf Found reverse in NC_001136 between 169634 and 169786 with 100% identity. See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251
5889_at 152.7 A
non-annotated SAGE orf Found reverse in NC_001136 between 436971 and 437174 with 100% identity. See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251
5890_i_at -211.9 A
non-annotated SAGE orf Found forward in NC_001136 between 437405 and 437677 with 100% identity. See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251
5891_f_at -16.0 A
non-annotated SAGE orf Found forward in NC_001136 between 437405 and 437677 with 100% identity. See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251
5892_at 342.1 A
non-annotated SAGE orf Found reverse in NC_001136 between 512499 and 512651 with 100% identity. See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251
5893_at -20.4 A
non-annotated SAGE orf Found forward in NC_001136 between 629245 and 629457 with 100% identity. See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251
5894_at 59.2 A

non-annotated SAGE orf Found reverse in NC_001136 between 1301069 and 1301203 with 100% identity. See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251

5895_at 810.5 P

non-annotated SAGE orf Found forward in NC_001136 between 31938 and 32096 with 100% identity. See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251

5896_at 453.9 P

non-annotated SAGE orf Found forward in NC_001136 between 54150 and 54302 with 100% identity. See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251

5897_at 417.8 P

non-annotated SAGE orf Found reverse in NC_001136 between 76964 and 77110 with 100% identity. See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251

5898_at 786.1 P

non-annotated SAGE orf Found reverse in NC_001136 between 104660 and 104806 with 100% identity. See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251

5899_i_at -39.2 A

non-annotated SAGE orf Found forward in NC_001136 between 130177 and 130317 with 100% identity. See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251

5900_at -160.7 A

non-annotated SAGE orf Found forward in NC_001136 between 130499 and 130633 with 100% identity. See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251

5901_at 4567.3 P

non-annotated SAGE orf Found forward in NC_001136 between 192383 and 192544 with 100% identity. See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251

5902_at -59.1 A

non-annotated SAGE orf Found forward in NC_001136 between 217255 and 217434 with 100% identity. See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251

5903_at -176.8 A

non-annotated SAGE orf Found forward in NC_001136 between 241211 and 241405 with 100% identity. See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251

5904_at 6123.9 P

non-annotated SAGE orf Found forward in NC_001136 between 370713 and 370868 with 100% identity. See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251

5905_i_at 264.5 P

non-annotated SAGE orf Found forward in NC_001136 between 370892 and 371032 with 100% identity. See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251

5906_r_at 2138.6 P

non-annotated SAGE orf Found forward in NC_001136 between 370892 and 371032 with 100% identity. See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251

5907_at 13.7 A

non-annotated SAGE orf Found forward in NC_001136 between 473863 and 474021 with 100% identity. See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251

5908_at 6749.7 P

non-annotated SAGE orf Found forward in NC_001136 between 509189 and 509365 with 100% identity. See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251

5909_at 37.5 P

non-annotated SAGE orf Found reverse in NC_001136 between 542450 and 542596 with 100% identity. See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251

5910_at 6274.3 P

non-annotated SAGE orf Found forward in NC_001136 between 654446 and 654610 with 100% identity. See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251

5911_at 986.7 P

non-annotated SAGE orf Found reverse in NC_001136 between 683771 and 683923 with 100% identity. See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251

5912_at 682.5 A

non-annotated SAGE orf Found forward in NC_001136 between 886950 and 887105 with 100% identity.

See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251
5864_at 384.7 P
non-annotated SAGE orf Found forward in NC_001136 between 930871 and 931032 with 100% identity. See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251
5865_at 14.0 A
non-annotated SAGE orf Found reverse in NC_001136 between 971521 and 971670 with 100% identity. See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251
5866_at 432.6 P
non-annotated SAGE orf Found reverse in NC_001136 between 971619 and 971783 with 100% identity. See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251
5867_at 609.8 P
non-annotated SAGE orf Found reverse in NC_001136 between 1014227 and 1014367 with 100% identity. See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251
5868_at 573.2 P
non-annotated SAGE orf Found forward in NC_001136 between 1021700 and 1021852 with 100% identity. See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251
5869_at 159.4 A
non-annotated SAGE orf Found reverse in NC_001136 between 1078478 and 1078672 with 100% identity. See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251
5870_at 35.4 A
non-annotated SAGE orf Found reverse in NC_001136 between 1149727 and 1149861 with 100% identity. See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251
5871_at -33.1 A
non-annotated SAGE orf Found reverse in NC_001136 between 1162667 and 1162810 with 100% identity. See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251
5872_at 877.1 P
non-annotated SAGE orf Found forward in NC_001136 between 1224746 and 1225015 with 100% identity. See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251
5873_at 414.4 P
non-annotated SAGE orf Found reverse in NC_001136 between 1276382 and 1276564 with 100% identity. See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251
5874_at 919.2 A
non-annotated SAGE orf Found forward in NC_001136 between 1385570 and 1385815 with 100% identity. See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251
5875_s_at -19.1 A
non-annotated SAGE orf Found forward in NC_001136 between 1385623 and 1385760 with 100% identity. See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251
5876_at 5822.9 P
non-annotated SAGE orf Found reverse in NC_001136 between 1410191 and 1410346 with 100% identity. See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251
5877_i_at 713.0 P
non-annotated SAGE orf Found reverse in NC_001136 between 34050 and 34184 with 100% identity. See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251
5878_r_at 2859.5 A
non-annotated SAGE orf Found reverse in NC_001136 between 34050 and 34184 with 100% identity. See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251

5879_at 2566.2 P
non-annotated SAGE orf Found forward in NC_001136 between 160791 and 160925 with 100% identity. See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251
5880_at 1740.0 P
non-annotated SAGE orf Found reverse in NC_001136 between 217125 and 217325 with 100% identity. See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251
5881_at 276.8 A
non-annotated SAGE orf Found forward in NC_001136 between 309589 and 309750 with 100% identity. See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251
5882_at 1345.0 P
non-annotated SAGE orf Found forward in NC_001136 between 681671 and 681811 with 100% identity. See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251
5883_i_at 65.1 P
non-annotated SAGE orf Found forward in NC_001136 between 871688 and 871912 with 100% identity. See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251
5884_r_at -68.4 A
non-annotated SAGE orf Found forward in NC_001136 between 871688 and 871912 with 100% identity. See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251
5885_at 3970.1 P
non-annotated SAGE orf Found forward in NC_001136 between 937524 and 937712 with 100% identity. See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251
5886_at 545.5 P
non-annotated SAGE orf Found forward in NC_001136 between 1022638 and 1022775 with 100% identity. See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251
5841_at 607.5 P
non-annotated SAGE orf Found forward in NC_001136 between 1022913 and 1023059 with 100% identity. See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251
5842_at 21.8 A
non-annotated SAGE orf Found reverse in NC_001136 between 1045240 and 1045398 with 100% identity. See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251
5843_at -11.7 A
non-annotated SAGE orf Found forward in NC_001136 between 1095473 and 1095631 with 100% identity. See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251
5844_at 10.9 A
non-annotated SAGE orf Found reverse in NC_001136 between 1164717 and 1164953 with 100% identity. See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251
5845_at 444.8 A
non-annotated SAGE orf Found reverse in NC_001136 between 1204280 and 1204438 with 100% identity. See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251
5846_at 568.1 A
non-annotated SAGE orf Found forward in NC_001136 between 1480287 and 1480421 with 100% identity. See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251
5847_at 21.4 A
non-annotated SAGE orf Found reverse in NC_001136 between 48402 and 48554 with 100% identity. See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251
5848_at -5.5 A
non-annotated SAGE orf Found reverse in NC_001136 between 48561 and 48719 with 100% identity. See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251
5849_at 1699.1 P

non-annotated SAGE orf Found reverse in NC_001136 between 169367 and 169609 with 100% identity. See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251
5850_at 126.2 P
non-annotated SAGE orf Found forward in NC_001136 between 362352 and 362528 with 100% identity. See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251
5851_at 65.2 A
non-annotated SAGE orf Found reverse in NC_001136 between 366186 and 366452 with 100% identity. See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251
5852_at 286.8 A
non-annotated SAGE orf Found reverse in NC_001136 between 369351 and 369551 with 100% identity. See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251
5853_at 301.2 A
non-annotated SAGE orf Found reverse in NC_001136 between 386539 and 386772 with 100% identity. See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251
5854_at 1118.1 P
non-annotated SAGE orf Found reverse in NC_001136 between 471227 and 471388 with 100% identity. See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251
5855_at -197.7 A
non-annotated SAGE orf Found forward in NC_001136 between 542286 and 542432 with 100% identity. See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251
5856_at 185.2 P
non-annotated SAGE orf Found reverse in NC_001136 between 545720 and 545920 with 100% identity. See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251
5857_g_at 16.8 A
non-annotated SAGE orf Found reverse in NC_001136 between 545720 and 545920 with 100% identity. See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251
5858_at 101.5 A
non-annotated SAGE orf Found reverse in NC_001136 between 545791 and 545997 with 100% identity. See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251
5859_at -750.7 A
non-annotated SAGE orf Found reverse in NC_001136 between 721872 and 722042 with 100% identity. See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251
5860_g_at 130.6 A
non-annotated SAGE orf Found reverse in NC_001136 between 721872 and 722042 with 100% identity. See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251
5861_at 205.7 A
non-annotated SAGE orf Found reverse in NC_001136 between 721952 and 722089 with 100% identity. See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251
5862_at 554.0 P
non-annotated SAGE orf Found reverse in NC_001136 between 909885 and 910028 with 100% identity. See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251
5863_at 340.7 P
non-annotated SAGE orf Found reverse in NC_001136 between 1182750 and 1182914 with 100% identity. See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251
5817_at 574.1 P
non-annotated SAGE orf Found reverse in NC_001136 between 1251950 and 1252093 with 100% identity. See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251
5818_at -3.3 A
non-annotated SAGE orf Found reverse in NC_001136 between 1258336 and 1258488 with 100% identity. See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251
5819_at 3349.4 P
non-annotated SAGE orf Found reverse in NC_001136 between 1353218 and 1353430 with 100% identity. See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell

8:243-251

5820_at 787.3 P

non-annotated SAGE orf Found reverse in NC_001136 between 1385513 and 1385758 with 100% identity. See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251

5821_at -85.8 A

non-annotated SAGE orf Found reverse in NC_001136 between 1394780 and 1394965 with 100% identity. See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251

5822_at -11.6 A

non-annotated SAGE orf Found reverse in NC_001136 between 1518910 and 1519074 with 100% identity. See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251

5823_at -5.7 A

non-annotated SAGE orf Found reverse in NC_001136 between 1519095 and 1519325 with 100% identity. See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251

5824_i_at 212.9 A

non-annotated SAGE orf Found forward in NC_001136 between 174671 and 174826 with 100% identity. See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251

5825_r_at -5.4 A

non-annotated SAGE orf Found forward in NC_001136 between 174671 and 174826 with 100% identity. See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251

5826_at 850.1 P

non-annotated SAGE orf Found reverse in NC_001136 between 235889 and 236071 with 100% identity. See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251

5827_at -527.2 A

non-annotated SAGE orf Found reverse in NC_001136 between 286761 and 286994 with 100% identity. See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251

5828_at 3671.9 P

non-annotated SAGE orf Found forward in NC_001136 between 371892 and 372080 with 100% identity. See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251

5829_at 401.8 A

non-annotated SAGE orf Found reverse in NC_001136 between 423540 and 423701 with 100% identity. See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251

5830_at 82.6 A

non-annotated SAGE orf Found reverse in NC_001136 between 428438 and 428608 with 100% identity. See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251

5831_at 252.8 P

non-annotated SAGE orf Found reverse in NC_001136 between 463178 and 463426 with 100% identity. See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251

5832_i_at 113.1 P

non-annotated SAGE orf Found reverse in NC_001136 between 541225 and 541422 with 100% identity. See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251

5833_r_at 85.3 P

non-annotated SAGE orf Found reverse in NC_001136 between 541225 and 541422 with 100% identity. See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251

5834_s_at 371.2 P

non-annotated SAGE orf Found reverse in NC_001136 between 541225 and 541422 with 100% identity. See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251

5835_i_at 106.1 A

non-annotated SAGE orf Found reverse in NC_001136 between 541283 and 541441 with 100% identity. See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251

5836_at -28.5 A

non-annotated SAGE orf Found reverse in NC_001136 between 558081 and 558245 with 100% identity. See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251

5837_at -301.7 A

non-annotated SAGE orf Found reverse in NC_001136 between 664944 and 665141 with 100% identity. See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251

5838_at 1725.3 P

non-annotated SAGE orf Found reverse in NC_001136 between 678003 and 678185 with 100% identity. See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251

5839_at 2277.4 P

non-annotated SAGE orf Found forward in NC_001136 between 733117 and 733251 with 100% identity. See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251

5840_at 2674.1 P

non-annotated SAGE orf Found reverse in NC_001136 between 792041 and 792292 with 100% identity. See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251

5792_at 1736.7 P

non-annotated SAGE orf Found reverse in NC_001136 between 812871 and 813017 with 100% identity. See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251

5793_at 471.3 A

non-annotated SAGE orf Found forward in NC_001136 between 909701 and 909844 with 100% identity. See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251

5794_i_at 6112.7 P

non-annotated SAGE orf Found forward in NC_001136 between 945505 and 945678 with 100% identity. See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251

5795_at 52.9 A

non-annotated SAGE orf Found reverse in NC_001136 between 976132 and 976302 with 100% identity. See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251

5796_at 118.0 A

non-annotated SAGE orf Found forward in NC_001136 between 979658 and 979807 with 100% identity. See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251

5797_at 9.3 A

non-annotated SAGE orf Found forward in NC_001136 between 1013666 and 1013818 with 100% identity. See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251

5798_at 761.3 P

non-annotated SAGE orf Found forward in NC_001136 between 1013978 and 1014130 with 100% identity. See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251

5799_at 1566.5 P

non-annotated SAGE orf Found forward in NC_001136 between 1108476 and 1108613 with 100% identity. See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251

5800_at 3921.3 P

non-annotated SAGE orf Found reverse in NC_001136 between 1233267 and 1233506 with 100% identity. See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251

5801_at -281.9 A

non-annotated SAGE orf Found forward in NC_001136 between 1359610 and 1359834 with 100% identity. See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251

5802_at 9.9 A

non-annotated SAGE orf Found forward in NC_001136 between 1362215 and 1362352 with 100% identity. See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251

5803_at 6.3 M

non-annotated SAGE orf Found reverse in NC_001136 between 1500930 and 1501154 with 100% identity. See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251

5804_at 2772.6 P

snRNA
5805_i_at -70.3 A
Centromere
5806_i_at 661.3 P
snRNA
5807_at 9631.7 P
snRNA
5808_i_at -32.6 A
questionable ORF
5809_i_at 425.4 P
similarity to subtelomeric encoded proteins
5810_s_at 2563.6 P
similarity to subtelomeric encoded proteins
5811_at 133.2 P
similarity to YJR108w
5812_at 98.8 A
hypothetical protein
5813_at 6036.8 P
strong similarity to Aip2p
5814_at 374.0 P
hypothetical protein
5815_at -54.2 A
weak similarity to YKL083w
5816_at 5132.9 P
Histone and other Protein Acetyltransferase\; Has sequence homology to known HATs and NATs
5769_at 1002.9 P
probably multidrug resistance protein
5770_at 476.0 P
similarity to YBL089w
5771_at 5376.5 P
arginine permease
5772_at 310.5 P
Non-membrane-embedded, PEST sequence-containing protein
5773_at 761.9 P
Kinesin-related protein involved in establishment and maintenance of mitotic spindle
5774_at 4240.6 P
vacuolar protease B
5775_at 3120.9 P
high copy suppressor of imp1 mutation, may be required for the function of the Imp1 peptidase and\/or the protein sorting machinery
5776_at 900.7 P
hypothetical protein
5777_at 9830.5 P
Phosphoacetylglucosamine Mutase
5778_at 46.9 A
hypothetical protein
5779_at 4814.4 P
subunit of a cytoplasmic histone acetyltransferase
5780_at 3448.0 P
DNA polymerase V that has motifs typical of DNA polymerase family
5781_i_at 11403.6 P
Ribosomal protein L12A (L15A) (YL23)
5782_at 1556.4 P
glucose-repressible protein
5783_at 3640.1 P
ATPase family gene

5784_at 6560.2 P
Vacuolar H-ATPase D subunit of the V1 catalytic sector
5785_at 4194.5 P
Mitochondrial ribosomal protein L2 of the large subunit
5786_f_at 383.7 A
member of the seripauperin protein\/gene family (see Gene_class PAU)
5787_at 106.0 P
hypothetical protein
5788_at 7922.9 P
strong similarity to Osm1p
5789_at 8553.8 P
Threonine Aldolase
5790_at 275.6 P
weak similarity to cytochrome c oxidase III of T.brucei kinetoplast
5791_at 2503.8 P
hypothetical protein
5747_at 4892.7 P
weak similarity to Mad1p
5748_at 9246.8 P
Guanosine diphosphatase of Golgi membrane
5749_at 166.6 A
strong similarity to Utr1p
5750_at 12446.8 P
weak similarity to Bacillus 1,3-1,4-beta-glucanase
5751_at 581.1 P
iso-2-cytochrome c
5752_at 4275.3 P
similarity to K.oxytoca enolase-phosphatase E-1
5753_at 8039.9 P
ubiquitin-like protein
5754_at 6046.1 P
Mannan 8\; Protein of the endoplasmic reticulum with a role in retention of glycosyltransferases in the Golgi, also involved in osmotic sensitivity and resistance to aminonitrophenyl propanediol
5755_at -155.9 A
protein of unknown function
5756_at 8748.2 P
Translation initiation factor eIF-5A
5757_at 3570.4 P
weak similarity to Sauroleishmania mitochondrial hypothetical ORF-5 protein
5758_at 4726.5 P
Member of complex that acts at ARS s to initiate replication
5759_at 8954.4 P
P-type ATPase
5760_at 270.6 A
ExtraCellular Mutant
5761_at 1508.2 P
similarity to hypothetical protein YNR027w
5762_at 224.0 P
hypothetical protein
5763_at 10868.3 P
Vacuolar ATP synthase 17-kDa proteolipid C subunit of VO sector\; dicyclohexylcarbodiimide binding subunit
5764_at 14581.9 P
strong similarity to high mobility group-like protein Nhp2p
5765_at 784.5 P
hypothetical protein

5766_at	11195.3	P	Rieske iron-sulfur protein of the mitochondrial cytochrome bc1 complex
5767_at	285.7	P	hypothetical protein
5768_at	1603.8	P	ARF GTP\/GDP exchange factor
5724_at	311.1	P	orotidine-5 -phosphate decarboxylase
5725_at	1209.6	P	similarity to O.formigenes oxalyl-CoA decarboxylase
5726_at	118.2	P	Protein involved in DNA repair
5727_at	2138.4	P	weak similarity to Rad50p
5728_i_at	15813.8	P	Proteolipid associated with plasma membrane H(+)-ATPase (Pma1p)
5729_f_at	11753.4	P	Proteolipid associated with plasma membrane H(+)-ATPase (Pma1p)
5730_at	6240.6	P	hypothetical protein
5731_at	647.2	P	similarity to human nucleotide pyrophosphatase
5732_at	3131.6	P	weak similarity to Spa2p
5733_at	467.7	P	hypothetical protein
5734_at	2577.4	P	An armadillo repeat-containing protein localized on the vacuolar membrane
5735_at	402.8	P	1,4-glucan-6-(1,4-glucano)-transferase
5736_at	-144.6	A	hypothetical protein
5737_at	10249.5	P	transcriptional activator of amino acid biosynthetic genes
5738_at	41.9	A	hypothetical protein
5739_at	4282.5	P	similarity to S.pombe pac2 protein
5740_at	2448.4	P	similarity to peroxisomal membrane and mitochondrial carrier proteins
5741_at	532.7	P	hypothetical protein
5742_at	730.5	P	Shows sequence similarity to GOG5, a gene involved in vanadate resistance
5743_at	3636.9	P	Putative homolog of subunit 2 of bovine prefoldin, a chaperone comprised of six subunits
5744_at	11501.2	P	oligosaccharyl transferase glycoprotein complex, beta subunit
5745_at	11807.6	P	hypothetical protein
5746_at	7845.4	P	Alpha-1,3-mannosyltransferase
5701_at	3294.4	P	weak similarity to chicken microfibril-associated protein
5702_at	10220.6	P	mannose-6-phosphate isomerase

5703_at 8502.0 P
similarity to hypothetical E.coli and C.elegans proteins
5704_at 1265.2 P
similarity to Gda1p
5705_at 7689.6 P
similarity to P.polycephalum myosin-related protein mlpA
5706_at 1168.4 P
Required for viability in the absence of the kinesin-related mitotic motor Cin8p\; required for normal microtubule stability
5707_at 9544.5 P
putattive ORF identified by SAGE
5708_at 3486.7 P
SEC3 encodes the 144 kD and 91 kD components of the Exocyst complex\; the 91 kD component is a C-terminal proteolytic breakdown product of full length Sec3p
5709_at 9801.0 P
May coordinate the Ran-dependent (GSP1\/GSP2) association and disassociation reactions of nuclear import\; human homologue complements yeast mutants
5710_at 3625.8 P
similarity to L.pneumophila dlpA protein
5711_at 2665.7 P
Cold-shock induced protein of the Srp1p\/Tip1p family of serine-alanine-rich proteins
5712_at 7956.4 P
22.6 kDa proteasome subunit
5713_at 1236.9 P
helicase-like protein
5714_at 1621.4 P
protoporphyrinogen oxidase
5715_at 116.3 P
Acyl-CoA synthetase (fatty acid activator 2)
5716_at 525.7 P
BInding to Microtubules
5717_at 6245.0 P
ATP-dependent metalloprotease
5718_at 1460.6 P
component of spindle pole
5719_at 4567.1 P
putative neutral sphingomyelinase
5720_at 9430.1 P
homologous to Sbh1p
5721_at 3618.2 P
nucleotide binding regulatory protein
5722_at 3213.3 P
component of the regulatory module of the 26S proteasome, homologous to human p58 subunit
5723_at 647.8 P
subunit of RNA polymerase II holoenzyme\/mediator complex
5678_at 9731.7 P
delta 1-pyrroline-5-carboxylate reductase
5679_at 644.7 P
similarity to carnitine O-acetyltransferase Yat1p
5680_at 11259.9 P
gamma subunit of translational initiation factor eIF-2
5681_at 7524.9 P
phosphatidylserine synthase
5682_at 2588.9 P
glucose repression protein
5683_at 852.5 P

similarity to Mig1p

5684_at	3574.8	P

Associated with U1 snRNP as part of the Sm-core that is common to all spliceosomal snRNPs

5685_at	4655.4	P

similarity to mouse nucleolin

5686_at	4602.0	P

ras-like GTPase, highly homologous to YPT32

5687_at	1004.9	P

Putative participant in 3 mRNA processing

5688_at	932.9	P

weak similarity to Nmd2p, Kex1p and hamster nucleolin

5689_at	906.7	P

hypothetical protein

5690_at	1800.7	P

hypothetical protein

5691_at	11910.9	P

strong similarity to members of the ABC transporter family

5692_at	183.4	P

strong similarity to hypothetical protein YGL224c

5693_at	166.3	P

hypothetical protein

5694_at	523.8	P

Homologous to VRG4

5695_at	935.2	P

positive nitrogen regulatory protein

5696_at	1025.8	P

weak similarity to DNA repair protein Rad2p and Dsh1p

5697_at	1744.8	P

responsible for the reduction of methionine sulfoxide

5698_at	9110.1	P

putative S-adenosyl-L-homocysteine hydrolase

5699_at	8896.6	P

hypothetical protein

5700_at	180.6	M

Required for full sporulation. Dispensable for axial cores but required for full chromosome pairing seen by in situ hybridization, heteroduplex DNA, synaptonemal complexes, meiotic intra- and interchromosomal gene conversion, reciprocal recombination and viable spores. mei4 has near wild-type chromosome condensation, executes both divisions with a delay in meiosis II, is rescued by spo13 and is epiststic to rad52, and is classified and an early recombination function. mRNA is meiosis-specific and has 88 bp intron at 5 end spliced independently of MER1.

5655_n_at	-9.0	A

Required for full sporulation. Dispensable for axial cores but required for full chromosome pairing seen by in situ hybridization, heteroduplex DNA, synaptonemal complexes, meiotic intra- and interchromosomal gene conversion, reciprocal recombination and viable spores. mei4 has near wild-type chromosome condensation, executes both divisions with a delay in meiosis II, is rescued by spo13 and is epiststic to rad52, and is classified and an early recombination function. mRNA is meiosis-specific and has 88 bp intron at 5 end spliced independently of MER1.

5656_at	914.3	P

weak similarity to transcription factor Sko1p

5657_at	736.3	P

hypothetical protein

5658_at	938.2	P

member of the AAA ATPase family of proteins

5659_at	6646.5	P

Homologous to E. coli DnaJ\; contains leucine zipper-like motif

5660_at	1914.7	P

putative ORF identified by SAGE
5661_at 5329.2 P
strong similarity to hypothetical S.pombe protein YER049W
5662_at 2781.9 P
hypothetical protein
5663_at 230.5 P
similarity to C.elegans hypothetical protein
5664_at 6711.8 P
Aspartate kinase (L-aspartate 4-P-transferase) (EC 2.7.2.4)
5665_at 2094.9 P
strong similarity to mitochondrial phosphate carrier protein
5666_at 119.2 P
Glc7-interacting protein\; shares homology with PIG2\; contains conserved 25 residue motif, called the GVNK motif, also found in GAC1, PIG1, PIG2, and RGI, the mammalian type 1 phosphatase targeting subunit.
5667_at 11476.7 P
ATP phosphoribosyltransferase
5668_at 8768.7 P
purine-cytosine permease
5669_g_at 9176.2 P
purine-cytosine permease
5670_i_at 11864.1 P
Ribosomal protein L34A
5671_s_at 8711.8 P
Ribosomal protein L34A
5672_at 11210.5 P
Inhibitor of cell Growth\; heat shock inducible
5673_at 2923.8 P
cytochrome c oxidase assembly factor
5674_at 1075.3 P
PHO85 cyclin
5675_at 2623.7 P
purine-cytosine permease
5676_at 519.8 P
purine-cytosine permease
5677_at 1234.6 P
Protein homologous to beta-keto-acyl synthase
5633_at 2700.8 P
DL-glycerol-3-phosphatase
5634_at 5551.1 P
Suppressor of the Transcriptional (T) defect of Hpr1 (H) by Overexpression (O)
5635_at 6460.0 P
similarity to hypothetical protein YIL056w
5636_at 544.9 P
isocitrate lyase
5637_at 395.2 P
strong similarity to cell division control protein Cdc4p
5638_g_at 1919.0 P
strong similarity to cell division control protein Cdc4p
5639_at 761.3 P
hypothetical protein
5640_at 745.2 P
strong similarity to hypothetical protein YIL057c
5641_at 686.2 P
putative zinc finger protein
5642_at 6121.3 P
N-acetyl-gamma-glutamyl-phosphate reductase and acetylglutamate kinase

5643_at 8965.8 P
ribonucleotide reductase
5644_at 926.5 P
hypothetical protein
5645_at 14193.2 P
Homolog of S. pombe Nrf1 (97\% identical in predicted amino acid sequence), which was identified in a genetic screen by its ability to reverse the Cdc42p suppression of a cdc24-4ts mutant
5646_at 8806.8 P
aldehyde dehydrogenase (NAD+)
5647_s_at 13412.8 P
40S ribosomal protein S24A
5648_at 1224.6 P
Protein tyrosine phosphatase
5649_at 944.8 P
similarity to killer toxin Khr1p
5650_at 310.0 P
hypothetical protein
5651_at 1465.4 P
similarity to E.coli X-Pro aminopeptidase II
5652_at 3311.5 P
hypothetical protein
5653_at 3081.1 P
hypothetical protein
5654_at 624.9 P
strong similarity to phosphoglycerate dehydrogenases
5610_at 1353.1 P
similarity to M.sexta steroid regulated MNG10 protein
5611_at 10169.2 P
hypothetical protein
5612_at 1445.2 P
questionable ORF
5613_at 45.7 A
weak similarity to myosins
5614_at 9192.0 P
threonine deaminase
5615_at 1189.8 P
similarity to E.coli prolyl-tRNA synthetase
5616_at 6884.4 P
homologous to Sbh2p
5617_at 3464.1 P
Derepression Of Telomeric silencing
5618_at 6243.7 P
Protein phosphatase type 2C
5619_at 7994.2 P
anthranilate synthase Component I
5620_at 10846.3 P
vitamin B12-(cobalamin)-independent isozyme of methionine synthase (also called N5-methyltetrahydrofolate homocysteine methyltransferase or 5-methyltetrahydropteroyl triglutamate homocysteine methyltransferase)
5621_at 2555.1 P
hypothetical protein
5622_at 1018.6 P
weak similarity to S.epidermidis PepB protein
5623_at 1299.7 P
similarity to hypothetical protein YBL059w
5624_at 1535.3 P

similarity to hypothetical protein YBL059w
5625_at 8056.7 P
20S proteasome subunit (beta3)
5626_at 4818.3 P
RecA homolog\; Rad51p colocalizes to ~65 spots with Dmc1p prior to synapsis (independently of ZIP1 and DMC1), and interacts with Rad52p and Rad55p by two-hybrid analysis\; human Rad51p homolog interacts with Brca2 protein which has been implicated in causing breast cancer
5627_at 256.6 P
sporulation-specific homolog of csd4
5628_at -3.9 A
weak similarity to ribosomal S3 proteins
5629_at 243.6 P
ubiquitin carboxyl-terminal hydrolase
5630_at 2172.7 P
ribose-phosphate pyrophosphokinase 2
5631_at 1972.5 P
ubiquitin-conjugating enzyme
5632_at 1211.3 P
Protein involved in targeting of plasma membrane [H+]ATPase
5588_at 1324.5 P
member of 70 kDa heat shock protein family
5589_at 458.4 P
hypothetical protein
5590_at 5774.4 P
Nucleoporin similar to Nup157p and to mammalian Nup155p
5591_at 182.1 P
hypothetical protein
5592_at 3729.3 P
homologous to S. pombe RAE1 gene\; 2-hybrid analysis demonstrates an interaction with Srp1p and Rip1p\; copurifies with Nup116p
5593_at 716.9 P
putative transcriptional activator of FLO1
5594_at 202.6 P
putative transcriptional activator of FLO1
5595_at 7674.7 P
Karyopherin beta 4
5596_at 254.8 P
transcription factor
5597_at 2921.5 P
U6 snRNA associated protein
5598_at 1971.4 P
similarity to Emp70p
5599_at 3188.0 P
Protein which binds Bem1p and contains a proline-rich sequence, an SH3 domain, and a pleckstrin homology domain
5600_at 2812.3 P
sporulation-specific protein
5601_at 83.1 A
zinc-finger protein
5602_at 1540.0 P
Transmembrane osmosensor
5603_at 1033.1 P
weak similarity to E.herbicola tyrosine permease
5604_at -44.7 A
questionable ORF
5605_at 11391.7 P

Likely to be involved in regulating INO1 expression, suppressor of a dominant nuclear mutation that is inositol-dependent in the presence of choline
5606_at 202.8 A
hypothetical protein
5607_at 2937.8 P
Zinc-finger-containing protein with similarity to Gcs1p and Sps18p
5608_at 484.5 P
plasma membrane-bound casein kinase I homolog
5609_at 996.5 P
weak similarity to Dictyostelium WD40 repeat protein 2
5565_at 5593.4 P
Rsp5p encodes a hect (homologous to E6-AP C terminus) and encodes a ubiquitin-protein ligase (E3 enzyme)
5566_at 9102.9 P
weak similarity to E.coli colicin N
5567_at 1801.1 P
Lethal with conditional pap1 allele
5568_at 944.8 P
hypothetical protein
5569_at 613.1 P
DNA polymerase alpha suppressing protein kinase
5570_at 1037.6 P
similarity to Msn2p and weak similarity to Msn4p
5571_at 6856.7 P
Ribosomal protein S26B
5572_at 1931.9 P
Paralog of MDS3
5573_at 1264.2 P
protein phosphatase type I
5574_at 7425.7 P
protein phosphatase type I
5575_at 1366.8 P
weak similarity to S.pombe SPBC13G1 and C.elegans F26F2.d hypothetical proteins
5576_at -145.4 A
hypothetical protein
5577_at 7448.9 P
GDP dissociation inhibitor
5578_at 733.9 P
weak similarity to Mycoplasma hominis P120 protein
5579_at 392.2 P
similarity to hypothetical protein YDR066c
5580_at 876.6 P
hypothetical protein
5581_at 11018.8 P
cytochrome oxidase assembly factor
5582_at 512.9 P
3-methyladenine DNA glycosylase
5583_at 2133.7 P
DNA Damage Inducible
5584_at 1758.2 P
Putative Ubiquitin-specific protease
5585_at 6494.4 P
Iron permease
5586_at 6992.7 P
Sm-like protein
5587_at 1260.1 P

weak similarity to mouse NAD(P)H dehydrogenase (quinone)
5542_at 9074.5 P
TATA-binding protein (tfIId)
5543_at 876.9 P
Protein with coiled-coil domain
5544_at 890.3 P
strong similarity to putative cell surface glycoprotein Sed1p
5545_at 1216.2 P
Ubiquitin-specific protease
5546_at 6055.1 P
weak similarity to E.coli hypothetical protein f470
5547_at 0.1 A
translational activator of cytochrome c oxidase subunit III
5548_at 7463.2 P
Required for correct assembly of the cytochrome c oxidase and the ATP synthase complex
5549_at 4537.1 P
Rho-type GTPase activating protein (GAP)
5550_at 7548.5 P
similarity to hypothetical C. elegans protein C27H6.5
5551_at 612.3 P
hypothetical protein
5552_at 1090.7 P
weak similarity to Afr1p
5553_at 2814.2 P
Transcriptional regulator which functions in modulating the activity of the general transcription machinery in vivo
5554_at 1010.4 P
non-specific DNA binding protein (sin1)
5555_at 361.1 P
Nucleotide excision repair protein
5556_at 2277.5 P
weak similarity to E.coli cation transport protein
5557_at 1692.0 P
transcriptional regulator
5558_at 9735.0 P
Poly(A) binding protein, cytoplasmic and nuclear
5559_at 5074.0 P
similarity to ATPase P.falciparum ATPase 2
5560_at 842.5 P
Serine\/threonine protein kinase
5561_at 864.1 P
tRNA nucleotidyltransferase (tRNA CCA-pyrophosphorylase)
5562_at 1359.2 P
Repressor of PHR1 transcription\; binds to PHR1 URS
5563_at 644.0 P
Adenylate kinase (mitochondrial GTP:AMP phosphotransferase)
5564_at 1558.8 P
DNA repair helicase component of transcription factor b
5520_at 1512.1 P
putative ATP-dependent RNA helicase
5521_at 491.4 P
checkpoint protein
5522_at 2296.1 P
similarity to Legionella glutaredoxin-like protein
5523_at 295.2 A
similarity to hypothetical protein YHR209w

5524_at	3285.3	P	DNA Helicase I
5525_at	12716.7	P	Ribosomal protein L23B (L17aB) (YL32)
5526_at	9590.4	P	alpha subunit of pyruvate dehydrogenase (E1 alpha)
5527_at	60.4	A	meiosis-specific protein related to RecA and Rad51p. Dmc1p colocalizes with Rad51p to discrete subnuclear sites in nuclear spreads during mid prophase, briefly colocalizes with Zip1p, and then disappears by pachytene
5528_at	158.6	P	meiosis-specific protein related to RecA and Rad51p. Dmc1p colocalizes with Rad51p to discrete subnuclear sites in nuclear spreads during mid prophase, briefly colocalizes with Zip1p, and then disappears by pachytene
5529_at	871.6	P	Meiosis-specific protein required for spore formation
5530_at	98.5	P	questionable ORF
5531_at	1004.3	P	hypothetical protein
5532_at	4477.0	P	similarity to human 5,10-methenyltetrahydrofolate synthetase
5533_at	512.3	A	similarity to multidrug resistance proteins Pdr3p and Pdr1p
5534_at	228.5	P	strong similarity to Rtm1p
5535_at	2591.2	P	weak similarity to hypothetical protein YMR316w
5536_at	324.8	P	similarity to killer toxin KHS precursor
5537_at	310.7	P	hypothetical protein
5538_at	4176.8	P	Translocase in inner membrane of mitochondria involved in mitochondrial protein import
5539_at	156.5	A	hypothetical protein
5540_at	-277.4	A	hypothetical protein identified by SAGE
5541_at	1202.7	M	questionable ORF
5497_at	329.0	P	questionable ORF
5498_at	75.3	A	questionable ORF
5499_at	414.8	A	questionable ORF
5500_at	197.4	P	questionable ORF
5501_at	24.9	A	questionable ORF
5502_at	561.6	P	questionable ORF
5503_at	8.4	A	questionable ORF
5504_at	158.2	P	questionable ORF

5505_at 9.8 A
hypothetical protein
5506_s_at 850.8 P
ubiquitin-conjugating enzyme\; ubiquitin-protein ligase
5507_at 602.0 P
non-annotated SAGE orf Found forward in NC_001137 between 67199 and 67363 with 100% identity. See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251
5508_at -744.1 A
non-annotated SAGE orf Found reverse in NC_001137 between 159380 and 159517 with 100% identity. See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251
5509_at 636.2 P
non-annotated SAGE orf Found reverse in NC_001137 between 187315 and 187524 with 100% identity. See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251
5510_at 372.0 P
non-annotated SAGE orf Found reverse in NC_001137 between 251194 and 251418 with 100% identity. See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251
5511_at 2366.8 P
non-annotated SAGE orf Found reverse in NC_001137 between 288425 and 288625 with 100% identity. See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251
5512_at 878.4 P
non-annotated SAGE orf Found reverse in NC_001137 between 550562 and 550699 with 100% identity. See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251
5513_at 14.1 A
non-annotated SAGE orf Found reverse in NC_001137 between 90086 and 90226 with 100% identity. See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251
5514_at 5878.2 P
non-annotated SAGE orf Found reverse in NC_001137 between 31419 and 31562 with 100% identity. See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251
5515_at 845.9 P
non-annotated SAGE orf Found reverse in NC_001137 between 64206 and 64373 with 100% identity. See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251
5516_at 9613.3 P
non-annotated SAGE orf Found reverse in NC_001137 between 67364 and 67504 with 100% identity. See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251
5517_at 10781.3 P
non-annotated SAGE orf Found reverse in NC_001137 between 122338 and 122532 with 100% identity. See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251
5518_at 372.5 P
non-annotated SAGE orf Found forward in NC_001137 between 251443 and 251697 with 100% identity. See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251
5519_at 119.4 P
non-annotated SAGE orf Found reverse in NC_001137 between 258517 and 258651 with 100% identity. See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251
5473_at 1122.4 P
non-annotated SAGE orf Found reverse in NC_001137 between 308191 and 308394 with 100% identity. See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251
5474_at 128.6 P
non-annotated SAGE orf Found reverse in NC_001137 between 314164 and 314310 with 100% identity. See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251
5475_at 1136.7 P
non-annotated SAGE orf Found forward in NC_001137 between 401911 and 402066 with 100% identity. See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251
5476_at 5984.4 P
non-annotated SAGE orf Found reverse in NC_001137 between 407032 and 407214 with 100% identity. See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251
5477_at 7573.4 P

non-annotated SAGE orf Found reverse in NC_001137 between 499172 and 499306 with 100% identity.
See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251
5478_i_at 1445.7 P
non-annotated SAGE orf Found reverse in NC_001137 between 561482 and 561634 with 100% identity.
See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251
5479_r_at 937.9 P
non-annotated SAGE orf Found reverse in NC_001137 between 561482 and 561634 with 100% identity.
See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251
5480_f_at 13.1 M
non-annotated SAGE orf Found reverse in NC_001137 between 561482 and 561634 with 100% identity.
See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251
5481_at 507.0 A
non-annotated SAGE orf Found reverse in NC_001137 between 84843 and 84983 with 100% identity.
See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251
5482_at 2354.9 P
non-annotated SAGE orf Found reverse in NC_001137 between 118455 and 118607 with 100% identity.
See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251
5483_at 4861.1 P
non-annotated SAGE orf Found forward in NC_001137 between 251078 and 251278 with 100% identity.
See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251
5484_at 27.2 A
non-annotated SAGE orf Found forward in NC_001137 between 303311 and 303496 with 100% identity.
See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251
5485_at -1749.1 A
non-annotated SAGE orf Found reverse in NC_001137 between 545280 and 545498 with 100% identity.
See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251
5486_at 309.2 P
non-annotated SAGE orf Found reverse in NC_001137 between 15653 and 15832 with 100% identity.
See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251
5487_at 868.9 A
non-annotated SAGE orf Found reverse in NC_001137 between 46025 and 46180 with 100% identity.
See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251
5488_at -25.5 A
non-annotated SAGE orf Found reverse in NC_001137 between 117014 and 117220 with 100% identity.
See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251
5489_at 240.0 P
non-annotated SAGE orf Found reverse in NC_001137 between 117183 and 117380 with 100% identity.
See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251
5490_at -22.0 A
non-annotated SAGE orf Found reverse in NC_001137 between 135405 and 135575 with 100% identity.
See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251
5491_at -27.4 A
non-annotated SAGE orf Found reverse in NC_001137 between 137782 and 137961 with 100% identity.
See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251
5492_at 41.0 A
non-annotated SAGE orf Found reverse in NC_001137 between 144048 and 144257 with 100% identity.
See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251
5493_at 57.7 A
non-annotated SAGE orf Found forward in NC_001137 between 167407 and 167559 with 100% identity.
See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251
5494_at 197.5 P
non-annotated SAGE orf Found reverse in NC_001137 between 177402 and 177560 with 100% identity.
See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251
5495_at 127.7 A
non-annotated SAGE orf Found forward in NC_001137 between 194842 and 194988 with 100% identity.
See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251

5496_g_at 397.8 M
non-annotated SAGE orf Found forward in NC_001137 between 194842 and 194988 with 100% identity.
See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251
5449_at 60.1 M
non-annotated SAGE orf Found reverse in NC_001137 between 225472 and 225738 with 100% identity.
See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251
5450_g_at 170.7 A
non-annotated SAGE orf Found reverse in NC_001137 between 225472 and 225738 with 100% identity.
See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251
5451_at -44.9 A
non-annotated SAGE orf Found forward in NC_001137 between 249314 and 249451 with 100% identity.
See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251
5452_at -49.4 A
non-annotated SAGE orf Found forward in NC_001137 between 284319 and 284474 with 100% identity.
See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251
5453_at 99.0 A
non-annotated SAGE orf Found forward in NC_001137 between 284585 and 284719 with 100% identity.
See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251
5454_at 591.7 P
non-annotated SAGE orf Found forward in NC_001137 between 289637 and 289906 with 100% identity.
See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251
5455_at 873.9 A
non-annotated SAGE orf Found reverse in NC_001137 between 311731 and 311907 with 100% identity.
See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251
5456_at -79.7 A
non-annotated SAGE orf Found reverse in NC_001137 between 312162 and 312425 with 100% identity.
See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251
5457_at 1259.7 P
non-annotated SAGE orf Found forward in NC_001137 between 382263 and 382427 with 100% identity.
See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251
5458_at -15.3 A
non-annotated SAGE orf Found forward in NC_001137 between 434581 and 434727 with 100% identity.
See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251
5459_at 149.2 A
non-annotated SAGE orf Found forward in NC_001137 between 434925 and 435077 with 100% identity.
See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251
5460_at 1139.8 A
non-annotated SAGE orf Found reverse in NC_001137 between 467935 and 468081 with 100% identity.
See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251
5461_at 47.8 A
non-annotated SAGE orf Found reverse in NC_001137 between 504589 and 504738 with 100% identity.
See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251
5462_at 244.9 P
non-annotated SAGE orf Found forward in NC_001137 between 564706 and 564843 with 100% identity.
See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251
5463_r_at 2096.6 P
non-annotated SAGE orf Found reverse in NC_001137 between 52351 and 52515 with 100% identity.
See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251
5464_i_at 5615.5 P
non-annotated SAGE orf Found reverse in NC_001137 between 52351 and 52515 with 100% identity.
See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251
5465_f_at 5466.9 P
non-annotated SAGE orf Found reverse in NC_001137 between 52351 and 52515 with 100% identity.
See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251
5466_i_at 99.5 P
non-annotated SAGE orf Found reverse in NC_001137 between 52391 and 52549 with 100% identity.

See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251
5467_f_at 9738.5 P
non-annotated SAGE orf Found reverse in NC_001137 between 52391 and 52549 with 100% identity.
See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251
5468_at 66.9 M
non-annotated SAGE orf Found forward in NC_001137 between 77473 and 77622 with 100% identity.
See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251
5469_at 114.4 P
non-annotated SAGE orf Found forward in NC_001137 between 84901 and 85035 with 100% identity.
See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251
5470_at 982.5 P
non-annotated SAGE orf Found forward in NC_001137 between 89863 and 90009 with 100% identity.
See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251
5471_at 2015.9 P
non-annotated SAGE orf Found forward in NC_001137 between 122467 and 122670 with 100% identity.
See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251
5472_at 43.1 A
non-annotated SAGE orf Found reverse in NC_001137 between 212096 and 212341 with 100% identity.
See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251
5436_i_at -25.4 A
non-annotated SAGE orf Found reverse in NC_001137 between 212169 and 212351 with 100% identity.
See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251
5437_s_at 12.3 A
non-annotated SAGE orf Found reverse in NC_001137 between 212169 and 212351 with 100% identity.
See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251
5438_at 114.5 A
non-annotated SAGE orf Found reverse in NC_001137 between 250626 and 250775 with 100% identity.
See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251
5439_at -61.0 A
non-annotated SAGE orf Found forward in NC_001137 between 272216 and 272383 with 100% identity.
See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251
5440_at 632.9 P
non-annotated SAGE orf Found forward in NC_001137 between 367587 and 367721 with 100% identity.
See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251
5441_at 2168.8 P
non-annotated SAGE orf Found forward in NC_001137 between 412758 and 412901 with 100% identity.
See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251
5442_at 442.6 A
non-annotated SAGE orf Found forward in NC_001137 between 422493 and 422669 with 100% identity.
See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251
5443_g_at -267.5 A
non-annotated SAGE orf Found forward in NC_001137 between 422493 and 422669 with 100% identity.
See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251
5444_at 498.1 A
non-annotated SAGE orf Found forward in NC_001137 between 422560 and 422781 with 100% identity.
See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251
5445_i_at 2275.1 P
non-annotated SAGE orf Found reverse in NC_001137 between 441063 and 441299 with 100% identity.
See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251
5446_r_at 235.0 A
non-annotated SAGE orf Found reverse in NC_001137 between 441063 and 441299 with 100% identity.
See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251
5447_at 4286.0 P
non-annotated SAGE orf Found forward in NC_001137 between 546517 and 546675 with 100% identity.
See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251
5448_at 3409.1 P

snRNA		
5412_at	187.2	P
snRNA		
5413_at	2822.9	P
RNase P RNA		
5414_i_at	-43.4	A
Centromere		
5415_r_at	-3.3	A
Centromere		
5416_at	1090.2	P
snRNA R14		
5417_at	5545.1	P
snRNA U4		
5418_at	324.1	P
snRNA		
5419_at	3408.9	P
small cytoplasmic RNA		
5420_s_at	485.3	P
weak similarity to hypothetical E.coli protein		
5421_i_at	-37.4	A
similarity to mouse period clock protein		
5422_s_at	1424.5	A
similarity to mouse period clock protein		
5423_s_at	1141.6	P
strong similarity to aryl-alcohol dehydrogenases		
5424_at	28.3	A
Hypothetical aryl-alcohol dehydrogenase (AAD)		
5425_at	181.7	A
Amino acid permease		
5426_at	668.2	P
similarity to channel proteins		
5427_at	494.6	A
dihydroxyacetone kinase		
5428_at	47.8	A
strong similarity to Mal63p, YPR196w and Mal13p		
5429_at	215.6	A
putative pseudogene		
5430_at	157.6	P
ALuminium Resistance 2		
5431_at	835.2	P
weak similarity to Npl6p		
5432_at	2459.2	P
47 kDa type I transmembrane protein localized to the Golgi		
5433_at	2539.0	P
similarity to S.pombe hypothetical protein SPAC2F7.18c		
5434_at	1034.9	P
weak similarity to middle part of C.elegans myosin heavy chain A		
5435_at	11466.7	P
phosphomannomutase		
5389_at	2661.9	P
weak similarity to human dystrophin		
5390_at	2429.7	P
multicopper oxidase, type 1 integral membrane protein		
5391_at	-103.9	A
similarity to yeast glucose transport proteins		
5392_at	8065.3	P

Actin
5393_at 12039.1 P
Ras-like GTP-binding protein\; most similar to mammalian Rab1A protein
5394_at 10390.2 P
beta-tubulin
5395_at 3085.3 P
mitochondrial RNA polymerase II
5396_at 7755.4 P
Ribosomal protein L22B (L1c) (rp4) (YL31)
5397_at 292.2 P
similarity to hypothetical S. pombe protein and to C.elegans F35D11 protein
5398_at 1305.0 P
Trehalose-associated protein kinase related to S. pombe cek1+
5399_at -46.8 A
questionable ORF
5400_at 436.4 P
similarity to several transaminases
5401_at 1681.0 P
Cyclin-dependent kinase-activating kinase
5402_at 1487.0 P
ABC ATPase
5403_at 1312.7 P
weak similarity to P.falciparum Pfmdr2 protein
5404_at 101.4 A
alpha-factor pheromone receptor\; seven-transmembrane domain protein
5405_at 2353.7 P
Negatively regulates COPII vesicle formation
5406_at 489.8 P
Probable chromatin protein because of homology to Drosophila Enahncer of Polycomb
5407_at 1755.2 P
similarity to repeat structures in a Plasmodium falciparum protein (MESA) that binds human erythrocyte protein 4.1.
5408_at 9807.3 P
Phenylalanyl-tRNA synthetase, beta subunit, cytoplasmic
5409_at 363.7 P
transcriptional activator with GATA-1-type Zn finger DNA-binding motif
5410_f_at 793.0 P
member of the seripauperin protein\/gene family (see Gene_class PAU)
5411_at 1.0 A
hypothetical protein
5367_at 12651.4 P
dihydrolipoamide dehydrogenase precursor (mature protein is the E3 component of alpha-ketoacid dehydrogenase complexes)
5368_at 2419.3 P
snRNP G protein (the homologue of the human Sm-G)
5369_at 2392.3 P
similarity to hypothetical S. pombe protein and to hypothetical C.elegans B0024.12 protein
5370_at 2621.1 P
DnaJ homolog involved in mitochondrial biogenesis and protein folding
5371_at 344.2 A
weak similarity to YDR504c
5372_at 1610.8 P
12 kDa heat shock protein
5373_at 669.9 P
weak similarity to Dictyostelium protein kinase
5374_at -42.9 A

questionable ORF
5375_at 59.4 A
hypothetical protein
5376_at 50.1 A
High-affinity hexose transporter
5377_at 414.1 P
Involved in ammonia regulation of GAP1 activity
5378_at 7797.7 P
questionable ORF
5379_at 995.2 P
beta subunit of large (heterotrimeric) G-proteins (beta-transducin)
5380_at 2244.8 P
omosome segregation protein
5381_at 5989.1 P
weak similarity to Mms19p
5382_at 2980.2 P
hypothetical protein
5383_at 6978.2 P
Ras-like small GTP-binding protein
5384_at 7524.0 P
strong similarity to hypothetical protein YPL019c
5385_at 283.7 P
meiosis specific protein, E.coli MutS protein, localizes to discrete sites on meiotic chromosomes
5386_at 3122.0 P
ATP-dependent RNA helicase
5387_at 1687.0 P
Depressed growth-rate protein
5388_at 6076.1 P
weak similarity to rabbit triadin Spp41p
5344_at 2477.9 P
96 kDa nucleoporin-interacting component
5345_at 2051.9 P
hypothetical protein
5346_at 4906.8 P
Similar to S. pombe PAD1 gene product
5347_at 1357.4 P
similarity to hypothetical A. thaliana proteins
5348_at 4884.5 P
similarity to X-Pro dipeptidases
5349_at 898.2 P
weak similarity to YER176w
5350_at 167.9 P
weak similarity to human centromere protein E
5351_at 8525.1 P
Member of ATP-binding cassette (ABC) family of proteins
5352_at 7821.5 P
encodes putative deubiquitinating enzyme
5353_at 1551.8 P
ochre suppressor tyr-tRNA
5354_at 348.1 P
similarity to hypothetical protein YOL019w
5355_at 850.4 P
similarity to YOL017w
5356_at 262.9 P
Calmodulin-dependent protein kinase
5357_at 426.9 P

Glycogen synthase (UDP-gluocse--starch glucosyltransferase)
5358_at 1730.0 P
similarity to mammalian neurofilament proteins and to Dictyostelium protein kinase
5359_at 324.3 P
hypothetical protein
5360_at 5811.2 P
similarity to human glutaminyl-peptide cyclotransferase
5361_at 3207.9 P
type II PI(4)P5-kinase (PIP4,5 kinase) similar to human PIP5K-II
5362_at 2233.5 P
hypothetical protein
5363_at 1764.3 P
similarity to hypothetical protein YPL100w
5364_at 157.5 A
similarity to Rod1p
5365_at -4.9 A
poly(A) binding protein\; related to PES4 protein homolog YHR015w
5366_s_at 3231.4 P
similarity to Acanthamoeba myosin heavy chain IC and weak similarity to other myosin class I heavy chains
5322_at 771.0 P
Histidinolphosphatase
5323_at 232.2 P
hypothetical protein
5324_at 339.6 P
hypothetical protein
5325_at 1805.0 P
soluble tyrosine-specific protein phosphatase
5326_at 526.3 P
Regulator of expression of the PTR2, GAP1, and BAP2 genes\; involved in the the control of peptide transport
5327_at 937.4 P
subunit of assimilatory sulfite reductase
5328_at 1844.9 P
nuclear protein related to ScII (chicken), XCAPE (xenopus), and cut14 (S. pombe)\; involved in chromosome segregation and condensation, interacts with Smc1p and Trf4p
5329_s_at 4215.7 A
Ribosomal protein L2A (L5A) (rp8) (YL6)
5330_at 1256.9 P
weak similarity to S.pombe polyadenylate-binding protein, YPR112c and Sbp1p
5331_at 9718.2 P
Ribosomal protein L29 (YL43)
5332_at 10058.1 P
ubiquinol-cytochrome c oxidoreductase subunit 6 (17 kDa)
5333_at 1400.2 P
myc-type helix-loop-helix transcription factor
5334_at 299.0 P
hypothetical protein
5335_at 1490.4 P
cell division control protein
5336_at 3089.7 P
Rsc8 is the eighth largest subunit of RSC, a fifteen-protein chromatin remodeling complex and related to the Swi\/snf Complex.
5337_at 858.0 P
strong similarity to mouse lymphocyte specific helicase
5338_at 1435.3 P

similarity to hypothetical protein YGL228w

5339_at	1254.7	P	155 kDa SIT4 protein phosphatase-associated protein
5340_at	971.2	P	weak similarity to dnaJ-like heat shock proteins
5341_at	2246.5	P	hypothetical protein
5342_at	900.7	P	hypothetical protein
5343_at	14850.0	P	similarity to hypothetical protein YBR281c
5299_at	700.7	P	similarity to mitochondrial citrate transport proteins
5300_at	1140.6	P	hypothetical protein
5301_at	6193.5	P	strong similarity to human quinolinate phosphoribosyltransferase
5302_at	868.1	P	similarity to hypothetical S.pombe protein SPAC12G12.14 and to YDL001w and YDR282c
5303_at	4494.6	P	mitochondrial ribosomal protein (precursor)
5304_at	10868.5	P	proteasome subunit necessary for peptidyl glutamyl peptide hydrolyzing activity
5305_at	8406.2	P	Coatomer (COPI) complex delta subunit
5306_at	3706.9	P	cytoplasmic 32 - 34 kDa protein
5307_at	1405.1	P	Hexokinase I (PI) (also called Hexokinase A)
5308_at	46.4	A	hypothetical protein
5309_at	-69.7	A	questionable ORF
5310_at	4841.6	P	strong similarity to beta-cystathionases
5311_at	110.3	A	weak similarity to Cha4p
5312_s_at	584.6	P	hypothetical protein
5313_s_at	2818.2	P	Mob1p-like protein
5314_at	-342.4	A	hypothetical protein
5315_at	212.6	A	questionable ORF
5316_at	772.7	P	questionable ORF
5317_s_at	546.2	P	similarity to hypothetical protein YLR072w
5318_s_at	7434.8	P	bZIP (basic-leucine zipper) protein
5319_at	2865.1	P	non-annotated SAGE orf Found reverse in NC_001138 between 76336 and 76470 with 100% identity. See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251
5320_at	52.6	P	non-annotated SAGE orf Found forward in NC_001138 between 101436 and 101573 with 100% identity.

See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251

5321_at 1283.3 P

non-annotated SAGE orf Found forward in NC_001138 between 234229 and 234471 with 100% identity. See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251

5274_at 1533.3 P

non-annotated SAGE orf Found reverse in NC_001138 between 44407 and 44547 with 100% identity. See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251

5275_i_at 71.5 A

non-annotated SAGE orf Found reverse in NC_001138 between 101326 and 101529 with 100% identity. See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251

5276_r_at 6.8 A

non-annotated SAGE orf Found reverse in NC_001138 between 101326 and 101529 with 100% identity. See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251

5277_at 9154.3 P

non-annotated SAGE orf Found reverse in NC_001138 between 224760 and 224996 with 100% identity. See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251

5278_at 657.1 P

non-annotated SAGE orf Found forward in NC_001138 between 226566 and 226700 with 100% identity. See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251

5279_at -95.6 A

non-annotated SAGE orf Found reverse in NC_001138 between 184330 and 184470 with 100% identity. See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251

5280_i_at -31.6 A

non-annotated SAGE orf Found reverse in NC_001138 between 5806 and 6033 with 100% identity. See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251

5281_f_at 93.9 A

non-annotated SAGE orf Found reverse in NC_001138 between 5806 and 6033 with 100% identity. See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251

5282_at 704.6 P

non-annotated SAGE orf Found reverse in NC_001138 between 48096 and 48248 with 100% identity. See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251

5283_at 104.5 P

non-annotated SAGE orf Found forward in NC_001138 between 48548 and 48715 with 100% identity. See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251

5284_at 1093.8 P

non-annotated SAGE orf Found forward in NC_001138 between 48735 and 48926 with 100% identity. See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251

5285_at 1081.4 P

non-annotated SAGE orf Found reverse in NC_001138 between 111442 and 111588 with 100% identity. See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251

5286_at 545.5 A

non-annotated SAGE orf Found forward in NC_001138 between 119115 and 119252 with 100% identity. See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251

5287_at 311.2 P

non-annotated SAGE orf Found forward in NC_001138 between 184290 and 184454 with 100% identity. See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251

5288_at -440.0 A

non-annotated SAGE orf Found forward in NC_001138 between 265809 and 265952 with 100% identity. See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251

5289_at 185.6 A

non-annotated SAGE orf Found forward in NC_001138 between 27951 and 28130 with 100% identity. See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251

5290_at 9.8 A

non-annotated SAGE orf Found forward in NC_001138 between 97531 and 97710 with 100% identity. See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251

5291_at 365.8 P

non-annotated SAGE orf Found forward in NC_001138 between 161226 and 161405 with 100% identity. See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251

5292_at	553.1	P

non-annotated SAGE orf Found reverse in NC_001138 between 181991 and 182221 with 100% identity. See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251

5293_g_at	-137.8	A

non-annotated SAGE orf Found reverse in NC_001138 between 181991 and 182221 with 100% identity. See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251

5294_at	113.5	P

ARS605 Found forward in NC_001138 between 135973 and 136029 with 100% identity.

5295_f_at	-35.2	A

ARS607 Found forward in NC_001138 between 199390 and 199446 with 100% identity.

5296_i_at	-41.4	A

ARS608 Found forward in NC_001138 between 216458 and 216508 with 100% identity.

5297_at	-51.0	A

Protein with strong similarity to subtelomerically-encoded proteins including Cos2p, Cos4p, Cos8p, YIR040c, Cos5p, Cos9p, and Cos6p

5298_at	-42.5	A

similarity to hypothetical protein YER187w

5251_f_at	1796.6	P

strong similarity to members of the Srp1/Tip1 family

5252_at	168.3	M

GPI-anchored aspartic protease

5253_g_at	343.3	P

GPI-anchored aspartic protease

5254_i_at	-1.5	A

strong similarity to hypothetical protein YOR387c

5255_s_at	127.5	A

strong similarity to hypothetical protein YOR387c

5256_at	2719.8	P

similarity to Mnn1p

5257_at	5558.2	P

alcohol dehydrogenase isoenzyme IV

5258_at	3781.9	P

high-affinity zinc transport protein

5259_at	2075.6	P

putative transcription factor, has five zinc fingers

5260_at	11847.3	P

Hexokinase II (PII) (also called Hexokinase B)

5261_at	2397.5	P

Protein involved in interorganelle communication between mitochondria, peroxisomes, and nucleus

5262_at	345.8	P

C4 zinc finger DNA-binding protein of low sequence specificity in vitro\; Probable 119 kD DNA\/RNA helicase family member

5263_at	146.2	P

hypothetical protein

5264_at	23.6	A

Required for ZIPpering up meiotic chromosomes during chromosome synapsis

5265_at	2153.4	P

3 ,5 -Cyclic-nucleotide phosphodiesterase, low affinity

5266_at	2178.8	P

similarity to hypothetical protein YHR036w

5267_at	966.1	P

weak similarity to C.elegans dom-3 protein

5268_at	11011.4	P

strong similarity to glutamine--tRNA ligase

5269_at	893.5	P	Nuclear protein
5270_at	860.0	P	tRNA-specific adenosine deaminase 1 (TAD1)\; Tad1p\/scADAT1
5271_at	4300.1	P	weak similarity to Drosophila ANK protein
5272_at	1606.5	P	similarity to Cse1p
5273_at	166.6	A	Doc1p and Cdc26p are associated with the anaphase-promoting complex and are involved in the degradation of Clb2p
5229_at	136.4	A	questionable ORF
5230_at	5202.5	P	Protein required for accurate mitotic chromosome segregation
5231_at	372.7	P	transcriptional activator protein of CYC1
5232_at	1505.7	P	strong similarity to gidA E.coli protein
5233_at	-865.9	A	questionable ORF
5234_at	8694.6	P	glycinamide ribotide synthetase and aminoimidazole ribotide synthetase
5235_at	891.7	P	113kD component of the Exocyst complex, which contains the gene products encoded by SEC3, SEC5, SEC6, SEC8, SEC10, SEC15 and EXO70.
5236_n_at	523.5	P	weak similarity to P.falciparum dihydropteroate synthase
5237_at	1021.1	P	weak similarity to P.falciparum dihydropteroate synthase
5238_at	4545.7	P	hypothetical protein
5239_at	34.2	A	hypothetical protein
5240_at	633.0	P	SAP4 is related to SAP155, SAP185, and SAP190, all of which associate with the SIT4 protein phosphatase
5241_at	6264.7	P	mRNA (identified by a library screen) that causes growth arrest when overexpressed
5242_at	645.3	P	TOR inhibitor
5243_at	7915.5	P	9.5-kDa zeta subunit of oligosaccharyltransferase complex
5244_at	1207.2	P	similarity to N.crassa cytochrome-c oxidase chain V
5245_at	9949.1	P	May regulate Golgi function and glycosylation in Golgi
5246_at	2071.8	P	strong similarity to hypothetical protein YER037w
5247_at	1770.4	P	weak similarity to Clostridium regulatory protein
5248_at	-178.2	A	hypothetical protein
5249_at	1078.2	P	Ngg1p-interacting factor 3
5250_at	6659.7	P	

weak similarity to V.alginolyticus bolA protein
5206_at 751.0 P
hypothetical protein
5207_at 57.2 A
questionable ORF
5208_at 217.0 A
questionable ORF
5209_at 1099.9 P
Kinesin-related protein
5210_at 2211.9 P
Cyclin-like protein that interacts with Pho85p in affinity chromatography
5211_at -62.7 A
questionable ORF
5212_at 2503.7 P
antiviral protein, mRNA is induced early in meiosis
5213_at 396.1 P
hydrophilic protein, heptad repeat motif
5214_at 2283.4 P
similarity to M.jannaschii hypothetical proteins MJ1157 and MJ1478
5215_at 2988.4 P
ras-like GTPase, highly homologous to YPT31
5216_at 3736.2 P
Protein containing zinc fingers very similar to zinc fingers in Mig1p
5217_at 470.7 P
Member of a family of proteins, including Sip1p and Gal83p, that interact with Snf1p and Snf4p and are involved in the response to glucose starvation
5218_at 7209.6 P
transcription factor
5219_at 6867.6 P
presumed vesicle coat protein
5220_at 3.4 A
fatty-acyl coenzyme A oxidase
5221_at 3444.2 P
questionable ORF
5222_at 854.5 P
carboxypeptidase B-like processing protease
5223_at 11040.6 P
aromatic amino acid aminotransferase
5224_at 444.0 P
Member of the MCM\/P1 family of proteins involved in DNA replication
5225_at 12887.3 P
type I transmemebrane protein, component of COPII-coated, ER-derived transport vesicles
5226_at 186.9 P
questionable ORF
5227_at 6443.1 P
weak similarity to Yip1p
5228_at 1879.5 P
Mck1 Dosage Suppressor 3\; negative regulator of early meiotic gene expression
5183_at 4025.2 P
hypothetical protein
5184_at 5331.5 P
translational activator of GCN4 through activation of GCN2 in response to starvation
5185_at 199.2 P
Protein with similarity to Hda1p, Rpd3p, Hos1p, and Hos3p
5186_at 1137.0 P
questionable ORF

5187_at 27.4 A
IME4 appears to activate IME1 in response to cell-type and nutritional signals and thereby regulate meiosis
5188_at 6464.2 P
subunit VIa of cytochrome c oxidase, may specifically interact with ATP
5189_at 1240.6 P
Protein phosphatase 2A regulatory subunit B
5190_i_at 1029.3 A
Ribosomal protein S26A
5191_f_at 10080.3 P
Ribosomal protein S26A
5192_at 191.9 P
hypothetical protein
5193_at 6660.0 P
subunit IV of cytochrome c oxidase
5194_at 3905.9 P
similarity to hypothetical protein Fcy21p and weak similarity to FCY2 protein
5195_at 2780.8 P
weak similarity to dehydrogenases
5196_at 462.1 P
strong similarity to Emericella nidulans cystathionine beta-lyase
5197_at -83.4 A
hypothetical protein
5198_at 136.2 A
questionable ORF
5199_at 972.4 P
Glycine-threonine-serine repeat protein
5200_at 521.2 P
Protein kinase
5201_at 566.2 P
ser/thr protein kinase
5202_at 840.2 P
questionable ORF
5203_at 7406.9 P
multicopy suppressor of POP2
5204_at 1173.0 P
weak similarity to Oryctolagus calcium channel BIII
5205_at 65.7 A
involved in meiotic recombination and chromosome metabolism
5161_at 833.0 P
weak similarity to C.elegans hypothetical protein R08D7.1
5162_at 6998.9 P
DNA strand-transfer protein exoribonuclease I\; catalyzes the formation of hybrid DNA in vitro\; has 5 -to-3 exonuclease activity on DNA and RNA\; binds to G4 tetraplex DNA and cuts in a single-stranded region 5 to the G4 structure\; protein increases several-fold in meiotic cells
5163_at 4730.2 P
nuclear pore complex protein with GLFG repetitive sequence motif
5164_at 6263.3 P
Contains domains found in the DEAD protein family of ATP-dependent RNA helicases\; high-copy suppressor of kem1 null mutant
5165_at 66.1 A
hypothetical protein
5166_at 848.6 P
Protein involved in translation initiation
5167_at 386.6 A
questionable ORF

5168_at 3046.4 P
Ca++-Pump, ATPase
5169_at 1736.6 P
Activator of transcription
5170_at 510.7 P
questionable ORF
5171_at 1364.4 P
similarity to S.pombe hypothetical protein SPAC31A2.10
5172_at 1104.1 P
Required for X-ray damage repair, mitotic recombination, and full meiotic recombination. mRNA increases in meiosis.
5173_at 1625.9 P
Involved in sterol uptake
5174_at 4577.0 P
hypothetical protein
5175_at 446.6 P
similarity to hypothetical protein YLR047c and Fre2p
5176_at 2306.5 P
hypothetical protein
5177_at -49.2 A
Serine\/threonine protein kinase
5178_at 3277.6 P
similarity to V.vinifera dihydroflavonol 4-reductase
5179_at 299.6 P
vacuolar alpha mannosidase
5180_at 1625.8 P
polypeptide subunit of a yeast type 1 protein geranylgeranyltransferase
5181_at 2481.0 P
aminoadipate-semialdehyde dehydrogenase small subunit (alpha-aminoadipate reductase)
5182_at 248.2 A
questionable ORF
5137_at 1773.3 P
Peroxisomal peripheral membrane protein (peroxin) involved in import of peroxisomal matrix proteins
5138_at 678.6 P
negative regulator of URS2 of the HO promoter
5139_at 2932.0 P
Shows similarity to the Snf2p family of DNA-dependent ATPases
5140_at 308.3 M
questionable ORF
5141_at 9843.9 P
Chorismate synthase
5142_i_at 5668.7 P
Ribosomal protein L9A (L8A) (rp24) (YL11)
5143_at 163.5 P
hypothetical protein
5144_at 558.3 P
transport protein that interacts with Sec20p\; required for protein transport from the endoplasmic reticulum to the golgi apparatus
5145_at 505.0 P
strong similarity to hypothetical protein YDL109c
5146_at 841.2 P
Mitochondrial polypeptide chain release factor
5147_at 929.7 P
Most likely an alpha 1,2 mannosyltransferase utilized for the addition of the third mannose onto the GPI core structure.
5148_at 2564.1 P
similarity to human human E6-associated protein

5149_at 2345.2 P
weak similarity to Lactobacillus putative histidine protein kinase SppK
5150_at 1217.3 P
strong similarity to hypothetical protein YPL221w
5151_at -36.2 A
hypothetical protein
5152_at 7136.5 P
encodes beta -subunit of yeast coatomer
5153_at 770.1 P
weak similarity to E.coli ftsJ protein
5154_at 678.1 P
PHO85 cyclin
5155_at 763.3 P
similarity to hypothetical protein YPL216w
5156_at 43.6 A
questionable ORF
5157_at 780.7 P
weak similarity to S.pombe hypothetical protein C3H1.12C
5158_at 1912.6 P
mRNA guanylyltransferase (mRNA capping enzyme), alpha subunit
5159_at 527.4 P
hypothetical protein
5160_at 917.6 P
weak similarity to rat cysteine string protein
5115_at 1377.3 P
SOH1 encodes a novel 14-kD protein with limited sequence similarity to RNA polymerases. The Soh1 protein interacts with a DNA repair protein, Rad5p, in a two-hybrid system assay.
5116_at 6424.3 P
required for inositol prototrophy
5117_at 2297.7 P
putative methylenetetrahydrofolate reductase (mthfr)
5118_at 585.8 P
similarity to S.pombe hypothetical protein
5119_at 9001.8 P
Ribosomal protein S2 (S4) (rp12) (YS5)
5120_at 7662.6 P
nuclear polyadenylated RNA binding protein
5121_at 454.8 P
hypothetical protein
5122_at 9637.7 P
pre-mRNA processing factor involved in disassembly of spliceosomes after the release of mature mRNA
5123_at 1289.3 P
multicopy suppressor of a cytochrome b mRNA translation defect, essential for the electron transfer in the bc1 complex
5124_at 84.3 P
questionable ORF
5125_at 731.2 P
hypothetical protein
5126_at 1569.9 P
beta-transducin homolog
5127_at 2212.3 P
associates with Snf1p
5128_at 2315.0 P
weak similarity to H.influenzae permease
5129_at 1583.7 P
weak similarity to YOR165w

5130_at	3320.0	P	TATA-binding protein-associated-factor
5131_at	5095.2	P	hypothetical protein
5132_at	943.6	P	hypothetical protein
5133_at	-450.6	A	questionable ORF
5134_at	1411.8	P	weak similarity to hypotetical S.pombe protein
5135_at	2824.8	P	strong similarity to hypothetical protein YBR238c
5136_at	9212.1	P	light chain for myosin Myo2p
5092_at	10377.7	P	Associated with tRNA and amino acyl-tRNA synthetases\; has affinity for quadruplex nucleic acids
5093_at	230.7	P	similarity to glucose transport proteins
5094_at	14244.0	P	Ribosomal protein L28 (L29) (rp44) (YL24)
5095_at	876.9	P	questionable ORF
5096_at	2324.2	P	strong similarity to hypothetical protein YBR242w
5097_at	3593.1	P	nuclear pore protein, homologous to sec13
5098_at	4218.4	P	similarity to putative human GTP-binding protein MMR1
5099_at	821.1	P	hypothetical protein
5100_at	7217.4	P	pheromone response pathway suppressor
5101_at	638.5	P	similarity to copper homeostasis protein Cup9p
5102_at	595.5	P	cytosolic and peripheral membrane protein
5103_at	890.8	P	135-kDa protein that is subunit of poly(A) ribonuclease
5104_at	2396.1	P	component of spindle pole
5105_at	3288.8	P	Nuclear pore complex protein with GLFG motif
5106_at	1289.8	P	35 kDa nucleotide binding protein
5107_at	196.2	P	Ligase Interacting Factor 1\; physically interacts with DNA ligase 4 protein (Lig4p)
5108_at	11365.9	P	alpha mating factor
5109_at	4200.6	P	questionable ORF
5110_at	3722.3	P	Similar to ubiquitin conjugating protein family
5111_at	824.7	P	Coiled-coil protein involved in spindle-assembly checkpoint
5112_at	880.1	P	weak similarity to Staphylococcus aureus nuclease (SNase)

5113_at	3022.2	P	strong similarity to hypothetical protein YPL189w
5114_at	1399.9	P	suppressor of GTPase mutant
5069_at	5382.8	P	strong similarity to hypothetical protein YPL191c
5070_at	344.3	M	hypothetical protein
5071_at	3941.2	P	strong similarity to C.elegans R07E5.13 protein
5072_at	1486.4	P	hypothetical protein
5073_at	7920.5	P	ATP-dependent RNA helicase CA3 of the DEAD\/DEAH box family
5074_at	7646.3	P	Transporter (permease) for choline and nitrogen mustard\; share homology with UGA4
5075_i_at	10362.3	P	Ribosomal protein L7A (L6A) (rp11) (YL8)
5076_f_at	9464.3	P	Ribosomal protein L7A (L6A) (rp11) (YL8)
5077_at	275.6	P	Mitotic Membrane Component
5078_at	22.9	A	questionable ORF
5079_at	1917.3	P	heat shock transcription factor
5080_at	739.2	P	questionable ORF
5081_at	1624.3	P	Putative transcription factor that binds the consensus site PyPuCACCCPu
5082_at	6671.4	P	RNA polymerase II subunit
5083_at	-230.3	A	questionable ORF
5084_at	3473.3	P	probable ribosomal protein L12
5085_at	3721.0	P	weak similarity to H.influenzae hypothetical protein
5086_at	1630.9	P	hypothetical protein
5087_at	2481.0	P	glycosyltransferase
5088_at	1005.8	P	similarity to YLR276c and YKR024c
5089_at	609.6	P	pseudouridine synthase 2
5090_at	7784.7	P	pyruvate carboxylase
5091_at	-466.9	A	Death Upon Overexpression
5047_at	2023.5	P	strong similarity to hypothetical protein YBR216c
5048_at	85.6	A	similarity to rat branched-chain alpha-ketoacid dehydrogenase kinase
5049_at	3377.1	P	ubiquitin conjugating (E2) enzyme, separate domains of Rad6p interact with Ubr1 (an E3 ubiquitin ligase

needed for multiubiquitination), and Rad18p (a single-stranded DNA-binding protein). The C-terminal 23 residues are critical for sporulation and histone polyubiquitinating activity, but not UV repair or induced mutagenesis.

5050_at 689.5 P
hypothetical protein
5051_at 2360.9 P
homologue of pombe SDS23\; localizes to spindle pole body
5052_at 11609.0 P
delta-9-fatty acid desaturase
5053_at 4254.2 P
strong similarity to D.melagonaster cni protein
5054_at 1843.5 P
strong similarity to hypothetical proteins YAR031w, YGL051w, YAR028w, YAR033w and YCR007c
5055_at 187.0 P
questionable ORF
5056_at 637.1 P
strong similarity to YAR033w protein
5057_at 1452.9 P
hypothetical protein
5058_at 942.9 P
mRNA cap-binding protein (eIF-4F), 130K subunit
5059_at 11248.5 P
ATPase
5060_at 859.0 P
similarity to hypothetical S. pombe protein
5061_at 273.5 P
hypothetical protein
5062_at 491.4 P
hypothetical protein
5063_at 1685.6 P
component of the cleavage and polyadenylation factor CF I involved in pre-mRNA 3 -end processing
5064_at 1494.1 P
RNA polymerase II elongation factor
5065_at 908.4 P
questionable ORF
5066_at 183.5 A
weak similarity to YJL109c
5067_at 7376.7 P
delta-aminolevulinate dehydratase (porphobilinogen synthase)
5068_at 3370.5 P
similarity to V. vinifera dihydroflavonol reductase
5024_at 1897.2 P
membrane-bound mannosyltransferase
5025_at 5078.4 P
similarity to E.coli hypothetical 23K protein
5026_at 1415.5 P
Mtf1 Two Hybrid Clone 2
5027_at 845.1 P
C2H2 zinc finger protein which resembles the mammalian Egr and Wilms tumour proteins
5028_at 73.1 A
questionable ORF
5029_at 63.2 A
Meiosis-specific gene required for the pairing of homologous chromosomes
5030_at 59.4 A
adhesion subunit of a-agglutinin
5031_at 11380.2 P

Ribosomal protein L24A (rp29) (YL21) (L30A)
5032_at 13316.4 P
Large ribosomal subunit protein L30 (L32) (rp73) (YL38)
5033_at 4969.1 P
weak similarity to human chromatin assembly factor I p150 chain
5034_at 6225.1 P
glucanase gene family member
5035_at 3718.5 P
glucosidase I
5036_at 13288.0 P
tryptophan synthetase
5037_at 780.9 P
Probable transcription factor, polyglutamine domain protein
5038_at 594.6 A
questionable ORF
5039_at 4138.1 P
weak similarity to Vsp27p
5040_at 8869.2 P
required for protein glycosylation
5041_at 818.0 P
DNA damage-responsive protein
5042_at 6369.4 P
hypothetical protein
5043_at 5001.9 P
beta (38kDa) subunit of casein kinase II (CKII)
5044_at 655.2 P
Homolog of E. coli Hsc20 co-chaperone protein
5045_at 844.4 P
arginyl-tRNA-protein transferase
5046_at 1938.0 P
pleiotropic drug resistance regulatory protein
5002_at 264.5 P
hypothetical protein
5003_at 3006.7 P
similarity to Drosophila pumilio protein and Mpt5p protein
5004_at 2772.5 P
zinc-finger transcription factor of the Zn(2)-Cys(6) binuclear cluster domain type
5005_at 11059.4 P
Sterol C-24 reductase
5006_at 7374.1 P
Proteasome subunit YC7alpha\/Y8 (protease yscE subunit 7)
5007_at 1178.3 P
similarity to hypothetical S. pombe protein
5008_at 9084.7 P
isopropylmalate isomerase
5009_at 8737.2 P
plasma membrane H+-ATPase
5010_at 122.7 A
questionable ORF
5011_at 2760.2 P
putative vacuolar Ca2+ ATPase
5012_at 374.5 P
weak similarity to Xenopus kinesin-related protein Eg5
5013_at 1313.9 P
weak similarity to Tup1p
5014_at 794.4 P

protein required for Clb2 and Ase1 degradation
5015_at 1894.6 P
p24 protein involved in membrane trafficking
5016_at 9178.7 P
putative 3-beta-hydroxysteroid dehydrogenase
5017_at 1656.9 P
similarity to C.elegans hypothetical M142.5 protein
5018_at 2130.2 P
similarity to C.elegans hypothetical M142.5 protein
5019_at 1291.9 P
similarity to hypothetical S. pombe protein
5020_at 891.4 P
similarity to D.melanogaster lin19 protein
5021_at 1263.1 P
strong similarity to hypothetical protein YLR324w
5022_at 1515.6 P
transcription initiation factor TFIIF middle subunit
5023_at 293.5 P
RNA splicing factor associated with U5 snRNP
4979_at 5967.2 P
choline phosphate cytidylyltransferase (also called phosphoethanolamine cytidylyltransferase or phosphocholine cytidylyltransferase)
4980_at 2701.6 P
ATPase stabilizing factor
4981_at 2307.5 P
Putative t-SNARE of the plasma membrane
4982_at 890.0 P
strong similarity to hypothetical protein YLR328w
4983_g_at 1504.5 P
strong similarity to hypothetical protein YLR328w
4984_at 1663.7 P
questionable ORF
4985_at 1407.8 P
similarity to E.nidulans cysteine synthase
4986_at 1248.9 P
Associated with U1 snRNP (no counterpart in mammalian U1 snRNP. Contains few SR-, RE- and RD-dipeptides.
4987_at 6207.4 P
putative integral membrane protein
4988_at 405.0 P
similarity to hypothetical protein YGR031w
4989_at 425.6 P
weak similarity to M.jannaschii hypothetical protein MJ1317
4990_at 1322.5 P
hypothetical protein
4991_at 358.4 P
questionable ORF
4992_at 2415.2 P
gamma-aminobutyrate (GABA) transaminase (4-aminobutyrate aminotransferase)
4993_at 8933.4 P
Vacuolar H-ATPase 14 kDa subunit (subunit F) of the catalytic (V1) sector
4994_at 976.2 P
similarity to M.leprae yfcA protein
4995_at 220.0 A
questionable ORF
4996_at 318.8 P

acts in concert with Mid2p to transduce cell wall stress signals
4997_at 3661.4 P
weak similarity to Methanobacterium thermoautotrophicum hypothetical protein MTH972
4998_at 486.2 P
questionable ORF
4999_at 4490.3 P
hypothetical protein
5000_i_at 7958.0 P
Ribosomal protein S25A (S31A) (rp45) (YS23)
5001_f_at 8155.6 P
Ribosomal protein S25A (S31A) (rp45) (YS23)
4956_at 4105.5 P
40 kDa putative membrane-spanning ATPase
4957_at 2078.2 P
integral subunit of RNase P and apparent subunit of RNase MRP
4958_at 2497.9 P
similarity to hypothetical protein YGR015c and weak similarity H.influenzae dihydrolipoamide acetyltransferase
4959_at 2548.9 P
catalytic component of 1,3-beta-D-glucan synthase
4960_at 2977.8 P
hypothetical protein
4961_at 94.2 M
hypothetical protein
4962_at 455.1 P
Cwh8p contains 3 short stretches of amino acids that are characteristic for a wide variety of phosphatases, including lipid phosphatases and a protein phosphatase.
4963_at 15839.0 P
Acyl-CoA-binding protein (ACBP)\/Diazepam binding inhibitor (DBI)\/endozepine (EP)
4964_at 6597.4 P
strong similarity to hypothetical protein YLR350w
4965_at 225.6 P
questionable ORF
4966_at 424.2 P
MAP protein kinase homolog involved in pheromone signal transduction
4967_at 2264.9 P
Among a group of genes whose products are necessary for bud-site selection\; likely involvement in positioning the proximal pole signal
4968_at 543.9 P
hypothetical protein
4969_at 327.5 P
strong similarity to transaldolase
4970_at 1912.2 P
zinc finger protein\; negative regulator of meiosis\; directly repressed by a1-a2 regulator
4971_at 268.4 P
questionable ORF
4972_at 334.6 P
hypothetical protein
4973_at 2282.7 P
transcription factor tau (TFIIIC) subunit 131
4974_at 1676.2 P
ubiquitin fusion degradation protein
4975_at 7730.0 P
Protein that suppresses ts allele of CDC4 when overexpressed
4976_at 1435.2 P
questionable ORF

4977_at	154.2	A	questionable ORF
4978_at	147.6	A	similarity to ser/thr protein kinases
4934_at	42.1	A	hypothetical protein
4935_at	5552.0	P	similarity to C.elegans E04D5.1 protein
4936_at	7469.5	P	high affinity methionine permease
4937_at	2389.5	P	Member of RSC complex
4938_at	801.1	P	Required for amino acid permease transport from the Golgi to the cell surface
4939_at	733.8	P	similarity to mouse calcium-binding protein
4940_at	167.9	P	a sporulation-specific homologue of the yeast CDC3\/10\/11\/12 family of bud neck microfilament genes and is regulated by ABFI
4941_at	12835.5	P	C-4 sterol methyl oxidase
4942_at	9633.7	P	5-phosphoribosylformyl glycinamidine synthetase
4943_at	3178.5	P	Cytochrome OXidase gene 18
4944_at	5459.7	P	Zn-finger protein, transcriptional regulator
4945_at	652.3	P	questionable ORF
4946_at	2445.1	P	similarity to P.putida phthalate transporter
4947_at	59.7	P	similarity to hypothetical protein YBR105c
4948_at	617.1	A	weak similarity to transcription factors
4949_at	1273.9	P	weak similarity to Rod1p
4950_at	-46.7	A	questionable ORF
4951_at	688.8	P	GDP-GTP Exchange Protein (GEP) for the Rho1p Small GTP-binding Protein
4952_at	527.6	P	similarity to hypothetical protein YLR373c
4953_at	650.1	P	factor stimulating decay of mRNAs containing premature stop codons\; acts with Nmd2p and Nam7p
4954_at	620.5	P	questionable ORF
4955_at	1003.6	P	Homolog of human core snRNP protein D1, involved in snRNA maturation
4911_at	702.3	P	RNA splicing factor
4912_at	2534.8	P	Mitochondrial ribosomal protein MRPL25 (YmL25)
4913_at	4790.7	P	peroxisome associated protein containing a PTS1 signal
4914_at	4350.7	P	

Polypeptide 3 of a Yeast Non-native Actin Binding Complex, homolog of a component of the bovine NABC complex
4915_at 4913.3 P
hypothetical protein
4916_at 3640.3 P
Twinfilin A, an actin monomer sequestering protein
4917_at 1781.0 P
weak similarity to mammalian myosin heavy chain
4918_at 8048.4 P
20 kDa mitochondrial outer membrane protein import receptor
4919_at 1770.8 P
translation initiation factor eIF2B, 71 kDa (delta) subunit\; translational repressor of GCN4 protein
4920_at 2007.1 P
35 kDa mitochondrial ribosomal small subunit protein
4921_i_at 14625.4 P
60S ribosomal protein L11B (L16B) (rp39B) (YL22)
4922_at 8369.8 P
strong similarity to hypothetical protein YPL004c
4923_at 34.7 A
Third, minor isozyme of pyruvate decarboxylase
4924_at 164.3 A
cytoplasmic catalase T
4925_at 371.7 P
weak similarity to rat tropomyosin
4926_at 5501.7 P
hypothetical protein
4927_at 871.2 P
pre-mRNA splicing protein
4928_at 1425.9 P
Serine\/threonine protein kinase
4929_at 2468.7 P
similarity to hypothetical S.pombe protein
4930_at 11871.2 P
mitochondrial and cytoplasmic valyl-tRNA synthetase
4931_at 6993.8 P
Putative 3 ->5 exoribonuclease\; component of exosome complex of 3 ->5 exonucleases
4932_at 407.7 P
similarity to bovine Graves disease carrier protein
4933_at 4580.1 P
transcriptional activator of the SKN7 mediated two-component regulatory system
4888_at 1591.1 P
Esp1 promotes sister chromatid separation by mediating dissociation from the chromatin of the cohesin Scc1. The anaphase-promoting complex promotes anaphase by mediating destruction of Pds1 which binds to Esp1 and inhibits its activity
4889_at 1449.8 P
involved in controlling telomere length
4890_at 842.5 P
Mac1-dependent regulator
4891_at 1929.8 P
weak similarity to B.subtilis YqgP
4892_at 1092.2 P
hypothetical protein
4893_at 5005.9 P
similarity to zebrafish essential for embryonic development gene pescadillo
4894_at 708.2 P
subunit of RNA polymerase II holoenzyme\/mediator complex

4895_at	3968.9	P	Protein involved in vacuolar H-ATPase assembly or function
4896_at	10499.2	P	hypothetical protein
4897_at	17.4	A	questionable ORF
4898_at	1875.9	P	G(sub)2-specific B-type cyclin
4899_at	562.2	P	B-type cyclin
4900_at	238.9	P	weak similarity to YLR099c and YDR125c
4901_at	987.9	P	weak similarity to mosquito carboxylesterase
4902_at	627.6	P	mitochondrial protein with homology to the mammalian SURF-1 gene
4903_at	621.1	P	Duo1 And Mps1 interacting
4904_at	164.0	A	questionable ORF
4905_g_at	1677.7	P	questionable ORF
4906_at	67.5	A	questionable ORF
4907_at	1252.8	P	transcriptional regulator, interacts with histones, primarily histone H3, possesses nucleosome assembly activity
4908_at	2535.5	P	hypothetical protein
4909_f_at	17375.6	P	Ribosomal protein S23A (S28A) (rp37) (YS14)
4910_at	1101.6	P	Contains GLFG repeats in N-terminal half and heptad repeats in C-terminal half
4865_at	1020.0	P	required for ER to golgi vesicle docking
4866_at	1075.8	P	ammonia permease
4867_at	911.0	P	hypothetical protein
4868_at	2102.8	P	serine\/threonine phosphatase
4869_at	11956.5	P	asparagine synthetase
4870_at	3011.0	P	similarity to S.pombe hypothetical protein SPAC24H6.11c
4871_at	76.6	A	weak similarity to hypothetical protein YPR156c
4872_at	910.6	P	weak similarity to mouse T10 protein
4873_at	4068.0	P	hypothetical protein
4874_at	530.4	P	SYnthetic lethal with cdcForty
4875_at	622.5	P	weak similarity to myosin heavy chain proteins
4876_at	289.6	P	

strong similarity to Nce2p
4877_at 3571.6 P
mitochondrial protein, prohibitin homolog\; similar to S. cerevisiae Phb2p
4878_at 199.0 A
Member of ubiquitin-conjugating protein family
4879_at 1676.4 P
hypothetical protein
4880_at 6935.2 P
proteasome component Y13
4881_at 7111.2 P
weak similarity to chicken growth factor receptor-binding protein GRB2 homolog
4882_g_at 3480.4 P
weak similarity to chicken growth factor receptor-binding protein GRB2 homolog
4883_at 801.2 P
questionable ORF
4884_i_at 8541.8 P
similarity to multidrug resistance proteins
4885_at 59.7 A
questionable ORF
4886_at 718.2 P
110 kDa subunit of the centromere binding factor CBF3
4887_at 826.3 P
strong similarity to hypothetical protein YPR157w
4842_at 2062.1 P
similarity to hypothetical protein YPR158w
4843_at 3652.2 P
encodes a predicted type II membrane protein highly homologous to Kre6p
4844_at 684.7 P
component of the biosynthetic pathway producing the thiazole precursor of thiamine
4845_at 4554.5 P
similarity to C.elegans hypothetical protein
4846_at 3652.7 P
hypothetical protein
4847_at 1672.7 P N
alpha-acetyltransferase that acts on methionine termini
4848_at 8047.3 P
Ribosomal protein L24B (rp29) (YL21) (L30B)
4849_at 1757.4 P
hypothetical protein
4850_at 440.3 P
hypothetical protein
4851_i_at 7775.9 P
questionable ORF
4852_s_at 2805.1 P
questionable ORF
4853_at 876.7 P
GTP-binding protein of the ras superfamily involved in bud site selection
4854_at 315.6 A
hypothetical protein
4855_at 270.1 P
strong similarity to hypothetical proteins YKR076w and YMR251w
4856_at 12969.2 P
Cystathionine beta-synthase
4857_at 1060.2 P
hypothetical protein
4858_at 6132.2 P

Phosphatidyl-ethanolamine N-methyltransferase
4859_at 1458.7 P
involved in mRNA transport
4860_at 11108.8 P
nuclear localization sequence binding protein
4861_at 385.1 P
questionable ORF
4862_at 636.9 P
hypothetical protein
4863_at 3474.3 P
mRNA cap-binding protein (eIF-4F), 150K subunit , highly homologous to Tif4632p, homologs of mammalian p220
4864_at 1117.6 P
GTP-binding protein
4819_at -37.4 A
questionable ORF
4820_at 2115.9 P
hypothetical protein
4821_at 1440.7 P
Involved in biosynthetic pathway for cell wall beta-glucans
4822_at 4702.8 P
Clathrin light chain
4823_at 670.9 P
hypothetical protein
4824_at 2722.4 P
similarity to Rib2p
4825_at 1355.6 P
phosphatidylserine decarboxylase located in vacuole or Golgi
4826_at 1901.9 P
mitochondrial methionyl-tRNA synthetase
4827_at 4134.8 P
Golgi membrane protein
4828_at 5719.3 P
strong similarity to human GTP-binding protein
4829_at 685.2 P
Essential for the expression and activity of ubiquinol-cytochrome c reductase
4830_at 7008.1 P
Squalene monooxygenase
4831_at -22.5 A
questionable ORF
4832_at 2639.5 P
Alcohol acetyltransferase
4833_at 7258.5 P
Poly(A)-binding protein binding protein
4834_at 825.4 P
hypothetical protein
4835_at 11759.8 P
Ribonucleotide Reductase
4836_at 7185.9 P
similarity to YHR004c-a
4837_at 5411.8 P
questionable ORF
4838_at 7571.8 P
7.3 kDa subunit 9 of the ubiquinol cytochrome c oxidoreductase complex
4839_at 2512.0 P
Ubiquitin-protein ligase

4840_at 8727.7 P
tyrosyl-tRNA synthetase, cytoplasmic
4841_at 3430.4 P
Transcription factor TFIIF large subunit
4797_at 6733.3 P
HMG1\/2 homolog
4798_at 172.5 P
Serine\/threonine protein kinase required for cell cycle arrest in response to loss of microtubule function
4799_at 8883.7 P
similarity to Aspergillus fumigatus rAsp
4800_at 80.7 A
questionable ORF
4801_at 4638.9 P
histidine permease
4802_i_at 115.9 A
Glyceraldehyde-3-phosphate dehydrogenase 3
4803_at 1678.3 P
Protein X component of mitochondrial pyruvate dehydrogenase complex
4804_at 699.9 P
xylulokinase
4805_at 5487.0 P
homolog of RNAse PH
4806_at 972.5 P
weak similarity to Tetrahymena acidic repetitive protein arp1
4807_at 2234.0 P
involved in nitrosoguanidine resistance
4808_at 3950.4 P
hypothetical protein
4809_at 3313.5 P
dolichyl phosphate-D-mannose:protein O-D-mannosyltransferase
4810_at 2809.3 P
weak similarity to rape guanine nucleotide regulatory protein
4811_at 759.8 P
strong similarity to translation elongation factor eEF1 alpha chain Cam1p
4812_at 1418.5 P
phosphorylcholine transferase\; or cholinephosphate cytidylyltransferase
4813_at 2919.4 P
weak similarity to X.laevis protein-tyrosin-phosphatase cdc homolog 2 and to hypothetical protein YPR200c
4814_at 11953.4 P
encodes the cytoplasmic trifunctional enzyme C1-tetrahydrofolate synthase
4815_at 155.5 P
similarity to S.pombe hypothetical protein D89234
4816_at 1369.5 P
similarity to Xenopus transcription factor Oct-1.17
4817_at 560.4 P
electron-transferring flavoprotein, beta chain
4818_at 4013.4 P
phosphoserine phosphatase
4774_at 9033.3 P
thioredoxin
4775_at 5306.0 P
similarity to M.jannaschii GTP-binding protein and to M.capricolum hypothetical protein SGC3
4776_at 5967.6 P
zinc finger protein
4777_at 188.3 P

weak similarity to S.pombe hypothetical protein SPAC18B11.03c
4778_at 263.7 P
involved in 7-aminocholesterol resistance
4779_f_at 13512.3 P
Ribosomal protein S0A
4780_at 12259.1 P
Ribosomal protein S0A
4781_at 1315.8 P
strong similarity to hypothetical S. pombe protein
4782_at 1462.6 P
Participates in synthesis of N-acetylglucoaminylphosphatidylinositol, the first intermediate in synthesis of glycosylphosphatidylinositol (GPI) anchors
4783_at 1431.3 P
putative calcium channel
4784_at 890.6 P
omosome region maintenance protein
4785_at 299.2 P
questionable ORF
4786_at 4595.1 P
Mitochondrial ribosomal protein MRPL9 (YmL9) (E. coli L3) (human MRL3)
4787_at 586.8 P
similarity to hypothetical protein YHR149c
4788_at 3493.0 P
translational activator of cytochrome c oxidase subunit III
4789_at 1192.3 P
weak similarity to hypothetical protein YFR021w
4790_at 581.1 P
strong similarity to drug resistance protein SGE1
4791_at 103.2 A
weak similarity to human p55CDC and Cdc20p
4792_at -40.8 A
hypothetical protein
4793_at 2846.2 P
De-repression of ITR1 Expression
4794_at 1300.5 P
questionable ORF
4795_at 3001.1 P
57 kDa nuclear protein
4796_at 369.4 P
questionable ORF
4751_at 7837.1 P
mitochondrial protein, prohibitin homolog\; homolog of mammalian BAP37 and S. cerevisiae Phb1p
4752_at 3856.5 P
possible homolog of human 26S proteasome regulatory subunit p28
4753_at 5448.5 P
Positive regulatory protein of phosphate pathway
4754_at 10502.6 P
Flavohemoglobin
4755_at 3757.5 P
hypothetical protein
4756_at 111.0 A
questionable ORF
4757_at 1208.5 P
weak similarity to YOR019w
4758_at 1003.8 P
protein containing kelch repeats, similar to YHR158c and YPL263c

4759_at	517.1	P	weak similarity to hypothetical protein YHR160c
4760_at	9116.3	P	phosphofructokinase alpha subunit
4761_at	2003.9	P	Yeast Assembly Polypeptide, member of AP180 protein family, binds Pan1p and clathrin
4762_at	-96.7	A	questionable ORF
4763_at	148.5	A	strong similarity to hypothetical protein YHR162w
4764_at	5610.9	P	Succinate-CoA Ligase (ADP-Forming)
4765_at	4657.9	P	similarity to hypothetical S.pombe protein
4766_at	2344.5	P	RNA polymerase III transcription factor with homology to TFIIB
4767_at	298.0	M	hypothetical protein
4768_at	500.7	P	similar to SOL3
4769_at	238.0	P	Mga1p shows similarity to heat shock transcription factor
4770_at	537.4	P	weak similarity to human cleavage stimulation factor 64K chain
4771_at	2863.2	P	hypothetical protein
4772_at	1306.4	P	histone acetyltransferase
4773_at	8547.5	P	Proteasome subunit
4729_i_at	10107.7	P	enolase I
4730_s_at	7410.1	P	enolase I
4731_at	4425.1	P	COQ6 monooxygenase
4732_at	227.1	A	6-phosphogluconate dehydrogenase
4733_at	3215.7	P	similarity to C.elegans C16C10.1
4734_at	1289.8	P	homolog of xeroderma pigmentosum group G (XPG) protein, copufurifies with transcription factor, TFIIH, mRNA is cell cycle regulated and induced by DNA damage and by meiosis (different cis-sites utilized in damage and meiotic induction
4735_at	397.7	P	questionable ORF
4736_at	10223.0	P	similarity to allantoate transport protein
4737_at	2703.0	P	putative beta adaptin component of the membrane-associate clathrin assembly complex
4738_at	3110.9	P	ser/thr protein kinase
4739_at	1223.9	P	weak similarity to E.coli lipase like enzyme
4740_at	9921.0	P	methionyl tRNA synthetase

4741_at	-6.8	A	questionable ORF
4742_at	2638.1	P	hypothetical protein
4743_at	3759.5	P	GTP-cyclohydrolase I
4744_at	2428.0	P	weak similarity to S.pombe hypothetical protein SPAC17A5
4745_at	121.6	P	questionable ORF
4746_at	2584.2	P	Member of CDC48\/PAS1\/SEC18 family of ATPases
4747_at	572.5	P	strong similarity to S.pombe RNA helicase
4748_at	3324.2	P	similarity to hypothetical S.pombe protein SPAC12G12.02
4749_at	-79.0	A	similarity to hypothetical protein YMR295c
4750_at	3180.4	P	Component of the TAFII complex required for activated transcription
4705_at	2456.6	P	hypothetical protein
4706_at	3125.5	P	ribonuclease H
4707_at	3092.1	P	similarity to hypothetical S.pombe protein
4708_at	353.1	P	similarity to C.elegans LET-858
4709_at	11314.2	P	glucanase gene family member
4710_at	9509.9	P	weak similarity to Cbf5p
4711_at	2911.8	P	ABC transporter
4712_at	13265.6	P	Cell wall endo-beta-1,3-glucanase
4713_at	2902.3	P	similarity to hypothetical protein YMR310c
4714_at	5549.3	P	similarity to mouse Surf-4 protein
4715_at	11408.3	P	Zuotin, putative Z-DNA binding protein
4716_at	4486.8	P	Biotin synthase
4717_at	112.2	P	strong similarity to maltase
4718_at	444.3	P	maltose pathway regulatory protein
4719_at	223.5	P	alpha-glucoside transporter
4720_at	350.1	A	hypothetical protein
4721_at	-259.4	A	hypothetical protein
4722_s_at	167.4	P	strong similarity to hypothetical protein YBR300c

4723_f_at 1124.7 P
strong similarity to members of the Srp1p/Tip1p family
4724_i_at 4884.8 P
hypothetical protein
4725_f_at 374.4 P
hypothetical protein
4726_at 118.4 A
identified by SAGE
4727_s_at 4165.9 P
Protein essential for mitochondrial biogenesis and cell viability
4728_at 196.4 A
non-annotated SAGE orf Found reverse in NC_001139 between 110655 and 110840 with 100% identity. See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251
4681_at 3251.2 P
non-annotated SAGE orf Found reverse in NC_001139 between 323513 and 323677 with 100% identity. See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251
4682_at 6513.6 P
non-annotated SAGE orf Found reverse in NC_001139 between 836149 and 836340 with 100% identity. See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251
4683_at 3057.9 P
non-annotated SAGE orf Found reverse in NC_001139 between 836381 and 836659 with 100% identity. See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251
4684_at 622.0 P
non-annotated SAGE orf Found reverse in NC_001139 between 904806 and 904952 with 100% identity. See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251
4685_at 3121.1 P
non-annotated SAGE orf Found reverse in NC_001139 between 905006 and 905158 with 100% identity. See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251
4686_s_at 3324.1 P
non-annotated SAGE orf Found reverse in NC_001139 between 939417 and 939581 with 100% identity. See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251
4687_at 799.1 P
non-annotated SAGE orf Found reverse in NC_001139 between 225922 and 226092 with 100% identity. See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251
4688_at -37.8 A
non-annotated SAGE orf Found forward in NC_001139 between 323656 and 323817 with 100% identity. See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251
4689_at 423.5 P
non-annotated SAGE orf Found reverse in NC_001139 between 324866 and 325024 with 100% identity. See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251
4690_at 337.3 P
non-annotated SAGE orf Found forward in NC_001139 between 363944 and 364078 with 100% identity. See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251
4691_at -16.9 A
non-annotated SAGE orf Found forward in NC_001139 between 437993 and 438127 with 100% identity. See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251
4692_f_at 206.0 P
non-annotated SAGE orf Found reverse in NC_001139 between 536199 and 536372 with 100% identity. See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251
4693_i_at 42.6 A
non-annotated SAGE orf Found reverse in NC_001139 between 931768 and 932025 with 100% identity. See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251
4694_at 177.6 P
non-annotated SAGE orf Found reverse in NC_001139 between 974228 and 974395 with 100% identity. See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251
4695_at 541.5 A

non-annotated SAGE orf Found forward in NC_001139 between 299797 and 299946 with 100% identity.
See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251
4696_at 9400.4 P
non-annotated SAGE orf Found forward in NC_001139 between 312929 and 313105 with 100% identity.
See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251
4697_at 782.8 P
non-annotated SAGE orf Found forward in NC_001139 between 326361 and 326609 with 100% identity.
See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251
4698_at 2092.1 P
non-annotated SAGE orf Found reverse in NC_001139 between 366397 and 366531 with 100% identity.
See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251
4699_at 505.4 P
non-annotated SAGE orf Found forward in NC_001139 between 393563 and 393697 with 100% identity.
See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251
4700_at 360.6 P
non-annotated SAGE orf Found forward in NC_001139 between 400350 and 400547 with 100% identity.
See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251
4701_at 7104.5 P
non-annotated SAGE orf Found reverse in NC_001139 between 554044 and 554199 with 100% identity.
See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251
4702_at 3575.7 P
non-annotated SAGE orf Found forward in NC_001139 between 669960 and 670145 with 100% identity.
See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251
4703_at 129.4 P
non-annotated SAGE orf Found forward in NC_001139 between 670145 and 670321 with 100% identity.
See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251
4704_at 211.7 P
non-annotated SAGE orf Found reverse in NC_001139 between 736379 and 736513 with 100% identity.
See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251
4658_at 1190.4 P
non-annotated SAGE orf Found forward in NC_001139 between 772010 and 772228 with 100% identity.
See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251
4659_at 853.6 P
non-annotated SAGE orf Found forward in NC_001139 between 777630 and 777860 with 100% identity.
See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251
4660_i_at 381.0 A
non-annotated SAGE orf Found forward in NC_001139 between 783944 and 784078 with 100% identity.
See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251
4661_r_at -2.2 A
non-annotated SAGE orf Found forward in NC_001139 between 783944 and 784078 with 100% identity.
See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251
4662_at 10509.9 P
non-annotated SAGE orf Found forward in NC_001139 between 827159 and 827320 with 100% identity.
See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251
4663_at 1970.8 P
non-annotated SAGE orf Found forward in NC_001139 between 836328 and 836597 with 100% identity.
See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251
4664_at 304.6 P
non-annotated SAGE orf Found reverse in NC_001139 between 853388 and 853528 with 100% identity.
See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251
4665_at -18.2 A
non-annotated SAGE orf Found reverse in NC_001139 between 949043 and 949216 with 100% identity.
See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251
4666_r_at 2841.8 P
non-annotated SAGE orf Found reverse in NC_001139 between 970567 and 970722 with 100% identity.
See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251

4667_at 104.3 P
non-annotated SAGE orf Found forward in NC_001139 between 973737 and 973922 with 100% identity. See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251
4668_at 221.5 A
non-annotated SAGE orf Found forward in NC_001139 between 974544 and 974699 with 100% identity. See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251
4669_i_at -13.3 A
non-annotated SAGE orf Found reverse in NC_001139 between 1037741 and 1037887 with 100% identity. See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251
4670_f_at 8399.8 P
non-annotated SAGE orf Found reverse in NC_001139 between 1037741 and 1037887 with 100% identity. See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251
4671_at 967.0 P
non-annotated SAGE orf Found reverse in NC_001139 between 1037796 and 1037987 with 100% identity. See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251
4672_at 8.8 A
non-annotated SAGE orf Found forward in NC_001139 between 110756 and 110950 with 100% identity. See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251
4673_at 269.6 P
non-annotated SAGE orf Found reverse in NC_001139 between 255333 and 255473 with 100% identity. See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251
4674_at 324.9 P
non-annotated SAGE orf Found forward in NC_001139 between 255355 and 255549 with 100% identity. See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251
4675_at 1013.6 P
non-annotated SAGE orf Found forward in NC_001139 between 384772 and 384945 with 100% identity. See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251
4676_at 17.3 A
non-annotated SAGE orf Found reverse in NC_001139 between 394718 and 394915 with 100% identity. See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251
4677_at 0.5 A
non-annotated SAGE orf Found forward in NC_001139 between 773986 and 774189 with 100% identity. See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251
4678_at -105.7 A
non-annotated SAGE orf Found forward in NC_001139 between 1069513 and 1069650 with 100% identity. See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251
4679_at 74.9 P
non-annotated SAGE orf Found forward in NC_001139 between 1083045 and 1083293 with 100% identity. See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251
4680_at -69.3 A
non-annotated SAGE orf Found reverse in NC_001139 between 10114 and 10350 with 100% identity. See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251
4631_at -88.4 A
non-annotated SAGE orf Found reverse in NC_001139 between 74536 and 74757 with 100% identity. See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251
4632_g_at 176.8 A
non-annotated SAGE orf Found reverse in NC_001139 between 74536 and 74757 with 100% identity. See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251
4633_at 422.1 A
non-annotated SAGE orf Found reverse in NC_001139 between 74628 and 74810 with 100% identity. See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251

4634_at 192.1 A
non-annotated SAGE orf Found reverse in NC_001139 between 93374 and 93667 with 100% identity.
See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251
4635_g_at 19.0 A
non-annotated SAGE orf Found reverse in NC_001139 between 93374 and 93667 with 100% identity.
See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251
4636_i_at 152.6 A
non-annotated SAGE orf Found reverse in NC_001139 between 93459 and 93722 with 100% identity.
See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251
4637_r_at 78.4 A
non-annotated SAGE orf Found reverse in NC_001139 between 93459 and 93722 with 100% identity.
See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251
4638_i_at 5.9 A
non-annotated SAGE orf Found reverse in NC_001139 between 148828 and 148968 with 100% identity.
See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251
4639_f_at 122.7 P
non-annotated SAGE orf Found reverse in NC_001139 between 148828 and 148968 with 100% identity.
See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251
4640_at 138.7 P
non-annotated SAGE orf Found forward in NC_001139 between 319819 and 320073 with 100% identity.
See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251
4641_s_at 2542.4 A
non-annotated SAGE orf Found forward in NC_001139 between 319845 and 319982 with 100% identity.
See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251
4642_i_at 5.8 A
non-annotated SAGE orf Found reverse in NC_001139 between 401513 and 401656 with 100% identity.
See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251
4643_f_at -95.6 A
non-annotated SAGE orf Found reverse in NC_001139 between 401513 and 401656 with 100% identity.
See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251
4644_i_at -3.1 M
non-annotated SAGE orf Found forward in NC_001139 between 405114 and 405266 with 100% identity.
See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251
4645_at 67.4 A
non-annotated SAGE orf Found reverse in NC_001139 between 544488 and 544628 with 100% identity.
See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251
4646_at 111.6 A
non-annotated SAGE orf Found forward in NC_001139 between 619977 and 620162 with 100% identity.
See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251
4647_at 190.7 A
non-annotated SAGE orf Found forward in NC_001139 between 700362 and 700583 with 100% identity.
See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251
4648_i_at -8.5 A
non-annotated SAGE orf Found reverse in NC_001139 between 701262 and 701477 with 100% identity.
See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251
4649_r_at 307.5 P
non-annotated SAGE orf Found reverse in NC_001139 between 701262 and 701477 with 100% identity.
See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251
4650_f_at 64.2 P
non-annotated SAGE orf Found reverse in NC_001139 between 701262 and 701477 with 100% identity.
See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251
4651_at 1153.3 P
non-annotated SAGE orf Found reverse in NC_001139 between 707583 and 707720 with 100% identity.
See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251
4652_at 1435.8 P
non-annotated SAGE orf Found reverse in NC_001139 between 707915 and 708058 with 100% identity.

See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251
4653_at 769.5 P
non-annotated SAGE orf Found reverse in NC_001139 between 708217 and 708372 with 100% identity.
See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251
4654_at 111.6 A
non-annotated SAGE orf Found reverse in NC_001139 between 711888 and 712022 with 100% identity.
See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251
4655_at -125.1 A
non-annotated SAGE orf Found reverse in NC_001139 between 801856 and 801993 with 100% identity.
See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251
4656_f_at -141.0 A
non-annotated SAGE orf Found forward in NC_001139 between 818376 and 818591 with 100% identity.
See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251
4657_at 137.2 P
non-annotated SAGE orf Found reverse in NC_001139 between 823398 and 823550 with 100% identity.
See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251
4608_g_at 212.4 A
non-annotated SAGE orf Found reverse in NC_001139 between 823398 and 823550 with 100% identity.
See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251
4609_at 189.2 A
non-annotated SAGE orf Found reverse in NC_001139 between 919562 and 919735 with 100% identity.
See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251
4610_at -108.1 A
non-annotated SAGE orf Found reverse in NC_001139 between 994368 and 994517 with 100% identity.
See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251
4611_at 11.6 A
non-annotated SAGE orf Found reverse in NC_001139 between 994531 and 994671 with 100% identity.
See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251
4612_at -16.9 A
non-annotated SAGE orf Found reverse in NC_001139 between 994842 and 994976 with 100% identity.
See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251
4613_at 384.7 P
non-annotated SAGE orf Found forward in NC_001139 between 23385 and 23675 with 100% identity.
See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251
4614_at 1262.2 P
non-annotated SAGE orf Found reverse in NC_001139 between 52581 and 52715 with 100% identity.
See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251
4615_at 3928.9 P
non-annotated SAGE orf Found forward in NC_001139 between 94489 and 94638 with 100% identity.
See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251
4616_at 507.1 P
non-annotated SAGE orf Found forward in NC_001139 between 129257 and 129394 with 100% identity.
See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251
4617_at 1636.0 P
non-annotated SAGE orf Found reverse in NC_001139 between 139723 and 139965 with 100% identity.
See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251
4618_at 3828.6 A
non-annotated SAGE orf Found reverse in NC_001139 between 163077 and 163232 with 100% identity.
See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251
4619_at 600.6 P
non-annotated SAGE orf Found reverse in NC_001139 between 199054 and 199209 with 100% identity.
See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251
4620_at 276.9 A
non-annotated SAGE orf Found reverse in NC_001139 between 249627 and 249773 with 100% identity.
See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251
4621_at 568.9 P

non-annotated SAGE orf Found forward in NC_001139 between 274428 and 274583 with 100% identity.
See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251
4622_at 1734.6 P
non-annotated SAGE orf Found forward in NC_001139 between 318551 and 318691 with 100% identity.
See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251
4623_at 6241.9 P
non-annotated SAGE orf Found reverse in NC_001139 between 474298 and 474432 with 100% identity.
See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251
4624_at 253.3 P
non-annotated SAGE orf Found forward in NC_001139 between 512819 and 513070 with 100% identity.
See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251
4625_at 9756.8 P
non-annotated SAGE orf Found reverse in NC_001139 between 533928 and 534068 with 100% identity.
See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251
4626_at 3698.2 P
non-annotated SAGE orf Found forward in NC_001139 between 576609 and 576782 with 100% identity.
See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251
4627_at 1405.6 P
non-annotated SAGE orf Found reverse in NC_001139 between 604571 and 604726 with 100% identity.
See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251
4628_at 331.7 P
non-annotated SAGE orf Found forward in NC_001139 between 682320 and 682556 with 100% identity.
See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251
4629_at 154.3 P
non-annotated SAGE orf Found reverse in NC_001139 between 727849 and 728022 with 100% identity.
See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251
4630_at 2113.7 P
non-annotated SAGE orf Found forward in NC_001139 between 733406 and 733621 with 100% identity.
See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251
4585_at 1068.5 P
non-annotated SAGE orf Found forward in NC_001139 between 757467 and 757625 with 100% identity.
See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251
4586_at 147.1 A
non-annotated SAGE orf Found forward in NC_001139 between 787843 and 788070 with 100% identity.
See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251
4587_at 733.3 A
non-annotated SAGE orf Found forward in NC_001139 between 788087 and 788224 with 100% identity.
See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251
4588_at 224.4 P
non-annotated SAGE orf Found forward in NC_001139 between 810111 and 810293 with 100% identity.
See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251
4589_g_at 282.7 P
non-annotated SAGE orf Found forward in NC_001139 between 810111 and 810293 with 100% identity.
See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251
4590_at 1320.5 P
non-annotated SAGE orf Found forward in NC_001139 between 810221 and 810499 with 100% identity.
See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251
4591_at 1167.6 P
non-annotated SAGE orf Found forward in NC_001139 between 810507 and 810659 with 100% identity.
See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251
4592_at -182.4 A
non-annotated SAGE orf Found forward in NC_001139 between 867541 and 867681 with 100% identity.
See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251
4593_at -11.3 A
non-annotated SAGE orf Found reverse in NC_001139 between 878323 and 878487 with 100% identity.
See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251

4594_at	39.4	A	non-annotated SAGE orf Found forward in NC_001139 between 965707 and 965874 with 100% identity. See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251
4595_at	325.1	P	non-annotated SAGE orf Found reverse in NC_001139 between 974572 and 974772 with 100% identity. See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251
4596_at	-11.8	A	non-annotated SAGE orf Found forward in NC_001139 between 1007443 and 1007601 with 100% identity. See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251
4597_at	251.6	P	non-annotated SAGE orf Found forward in NC_001139 between 1011451 and 1011660 with 100% identity. See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251
4598_g_at	96.3	A	non-annotated SAGE orf Found forward in NC_001139 between 1011451 and 1011660 with 100% identity. See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251
4599_i_at	271.4	P	non-annotated SAGE orf Found forward in NC_001139 between 1011506 and 1011688 with 100% identity. See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251
4600_at	2018.9	P	non-annotated SAGE orf Found forward in NC_001139 between 1012179 and 1012379 with 100% identity. See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251
4601_at	1112.4	A	non-annotated SAGE orf Found forward in NC_001139 between 1057363 and 1057593 with 100% identity. See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251
4602_at	2471.1	P	non-annotated SAGE orf Found reverse in NC_001139 between 1058818 and 1058976 with 100% identity. See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251
4603_at	1789.7	P	snRNA
4604_i_at	763.4	P	snRNA
4605_s_at	1639.0	P	snRNA
4606_at	1725.3	P	snRNA
4607_at	1202.2	P	snRNA
4561_s_at	1049.0	P	snRNA
4562_at	141.6	A	similarity to C.carbonum toxin pump
4563_f_at	2220.8	P	strong similarity to members of the Srp1p/Tip1p family
4564_at	121.3	P	similarity to subtelomeric encoded proteins
4565_at	129.5	P	ExtraCellular Mutant
4566_at	-67.4	A	similarity to subtelomeric encoded proteins

4567_at 257.5 A
weak similarity to Drosophila hypothetical protein 6
4568_at 1216.0 P
similarity to C.carbonum toxin pump
4569_at 3099.0 P
weak similarity to YPL208w
4570_at 242.5 P
Cytochrome B pre-mRNA processing protein
4571_at 372.2 A
hypothetical protein
4572_at 692.5 P
very low affinity methionine permease
4573_at 684.4 P
ABC transporter
4574_at 8309.8 P
Single-strand nucleic acid binding protein
4575_i_at 16163.7 P
Ribosomal protein L8A (rp6) (YL5) (L4A)
4576_at 731.7 P
glyerol kinase (converts glycerol to glycerol-3-phosphate
4577_at 5276.9 P
SNARE protein with a C-terminal membrane anchor
4578_at 2018.3 P
ExtraCellular Mutant
4579_at 3242.7 P
hypothetical protein
4580_at 1398.2 P
Putative integral membrane protein containing novel cysteine motif. Similarity to SLG1 (WSC1), WSC2 and WSC3
4581_at 8435.0 P
Meiotic regulatory protein\; Cys-His zinc fingers
4582_at 1968.3 P
hypothetical protein
4583_at 3297.5 P
transcriptional regulator
4584_at 246.3 P
RNA binding domain (N-term) with asparagine rich region?
4539_at 802.8 P
hypothetical protein
4540_at -97.1 A
Encodes one of the earliest meiosis-specific recombination functions.
4541_at 1003.3 P
weak similarity to Pseudomonas gamma-butyrobetaine hydroxylase
4542_at 5454.1 P
negative regulator of phospholipid biosynthesis
4543_at 604.4 P
Similiar to clathrin coat proteins
4544_at 92.4 P
Dimerization cofactor of homeodomian protein NF1-alpha
4545_at 1149.8 P
Probable transmembrane protein PTM1
4546_at 482.3 P
Urea transporter
4547_at 12818.4 P
Ribosomal protein S20
4548_at 268.2 P

GTP-binding protein and glycogen phosphorylase (weak)
4549_at 3894.8 P
similarity to C.elegans hypothetical protein F21D5.2
4550_at -51.2 A
UDP Glucose pyrophosphorylase
4551_at 7829.6 P
ribose-phosphate pyrophosphokinase 3
4552_at 191.9 P
similarity to C.elegans hypothetical protein
4553_at 350.5 P
bZip DNA binding proteins
4554_at 3494.1 P
Potential formate transporter nirC
4555_at 2141.8 P
serine\/threonine protein kinase
4556_at 697.6 P
hypothetical protein
4557_at -36.7 A
hypothetical protein
4558_at 1337.6 P
mitochondrial ribosomal protein, homologous to E. coli ribosomal protein S2, component of the 37 S subunit of mitochondrial ribosomes
4559_at 2487.8 P
YKL008c
4560_at 1767.7 P
SH3 domain
4515_i_at 11511.8 P
Ribosomal protein L14B
4516_f_at 10479.3 P
Ribosomal protein L14B
4517_at 3398.5 P
60kD chaperonin (weak)
4518_at 6302.5 P
8.5 kDa subunit of the ubiqunol-cytochrome c oxidoreductase complex
4519_at 710.7 P
Mitochondrial carrier protein\/Grave s disease carrier protein
4520_at 2044.4 P
thiF, moeB, ubiquitin activating enzyme (all weak)
4521_at 611.9 P
similarity to YLL010c, YLR019w
4522_at 2306.6 P
alpha subunit of G protein coupled to mating factor receptors
4523_at 8001.9 P
May act cooperatively with Mrs5p in mitochondrial protein import or other related essential mitochondrial processes
4524_at 1108.1 P
Zinc finger (Cys(2)-His(2))
4525_at 17525.8 P
cytochrome P450 lanosterol 14a-demethylase
4526_at 4469.5 P
Manganese-containing superoxide dismutase
4527_at 5605.2 P
similarity to S.pombe hypothetical protein
4528_i_at 7949.8 P
Ribosomal protein L27A
4529_f_at 8841.8 P

Ribosomal protein L27A
4530_at 635.7 P
Seryl-tRNA synthetase
4531_at 2678.8 P
Vacuolar protein sorting
4532_at 3051.7 P
subunit of the major N alpha-acetyltransferase, complexes with the catalytic subunit of N-a-acetyltransferase (Nat1)
4533_at 93.5 A
Encodes a 33.4 kDa basic protein that localizes to the nucleus. Thought to be a meiosis-specific negative regulator of M-phase during meiosis I, coordinating sister-chromatid\/centromere cohesion with nuclear division. Spo13p has transcriptional activation activity in one-hybrid analysis.
4534_at 261.4 P
PolyA-binding protein
4535_at 1140.8 P
SH3 domain in C-terminus
4536_at 1099.6 P
strong similarity to S.douglasii YSD83
4537_at 5749.8 P
argininosuccinate lyase
4538_at 11547.9 P
Asparaginyl-tRNA synthetase
4493_at 10634.9 P
Aminoacyl tRNA-synthetase
4494_at 11228.0 P
40S Ribosomal protein S27B (rp61) (YS20)
4495_at 11.4 A
ExtraCellular Mutant
4496_at 73.8 P
RAS-related protein
4497_at 523.3 P
Class II Myosin
4498_at 1613.6 P
53 kDa subunit of the mitochondrial processing protease
4499_at 13064.4 P
homoserine kinase
4500_at 9733.6 P
proteolipid protein of the proton ATPase
4501_at 8299.1 P
Subunit of 26S Proteasome (PA700 subunit)
4502_at 3098.3 P
Dipeptidyl aminopeptidase B (DPAP B)
4503_at 1630.8 P
Thymidylate synthase (putative\; weak)
4504_at 4261.8 P
putative protein kinase
4505_at 1581.3 P
Pif1p, mitochondrial DNA repair and recombination protein
4506_at 3771.7 P
ethionine resistance protein
4507_at 1119.3 P
Pro1p (Gamma-glutamyl kinase)
4508_at 812.2 P
hypothetical protein
4509_at 274.2 A
Sec23p (weak)

4510_at	416.8	P	similarity to hypothetical protein YGL247w
4511_at	2919.0	P	delta-1-pyrroline-5-carboxylate dehydrogenase
4512_at	591.9	A	Killed in Mutagen, sensitive to Diepoxybutane and\/or Mitomycin C
4513_at	6797.0	P	Aldehyde dehydrogenases
4514_at	14111.4	P	13-kDa vacuolar H-ATPase subunit
4469_at	1532.6	P	weak similarity to Hit1p
4470_at	4738.3	P	RNA polymerase II holoenzyme\/mediator subunit
4471_at	9810.1	P	NADP-cytochrome P450 reductase
4472_s_at	2860.8	P	2-deoxyglucose-6-phosphate phosphatase
4473_i_at	2.3	A	2-deoxyglucose-6-phosphate phosphatase
4474_at	3632.9	P	hypothetical protein
4475_at	2642.7	P	Inositol monophosphatase
4476_at	7207.7	P	arginine\/alanine aminopeptidase
4477_at	480.4	P	similarity to multidrug resistance proteins
4478_at	6350.3	P	similarity to S.pombe dihydrofolate reductase and YOR280c
4479_at	380.5	P	questionable ORF
4480_at	2570.8	P	localized to mitochondrial membrane
4481_at	8283.0	P	subunit VI of cytochrome c oxidase
4482_at	3951.6	P	weak similarity to P.yoelii rhoptry protein
4483_s_at	10034.3	P	copper-binding metallothionein
4484_s_at	4813.4	P	weak similarity to YOR262w
4485_at	3949.8	P	Peptidylprolyl isomerase (cyclophilin) ER or secreted
4486_at	1239.8	P	RNA polymerase II transcriptional regulation mediator
4487_at	658.6	P	weak similarity to Ustilago hordei B east mating protein 2
4488_at	1945.6	P	required for V-ATPase activity
4489_at	1944.7	P	GTPase-interacting component 1
4490_at	2658.3	P	Protein subunit of nuclear ribonuclease P (RNase P)
4491_at	4525.5	P	weak similarity to translational activator CBS2

4492_at 12418.1 P
Hsp70 Protein
4446_at 3849.0 P
RRP3 is a DEAD box gene homologous to eIF-4a which encodes an RNA-dependent ATPase possessing helicase activity which is not specific for RNA
4447_at 1309.1 P
homologous to Ssf2p
4448_at 872.3 P
hypothetical protein
4449_at 11230.9 P
Deoxyhypusine synthase
4450_at 2338.4 P
3->5 exoribonuclease\; Component of the exosome 3->5 exonuclease complex with Rrp41p, Rrp42p, Rrp43p and Dis3p (Rrp44p).
4451_at 4008.6 P
strong similarity to N.crassa met-10+ protein
4452_at 3493.0 P
G1\/S cyclin (weak)
4453_at 6790.4 P
2,3-oxidosqualene-lanosterol cyclase
4454_at 416.7 P
Oxysterol-binding protein
4455_at 1999.7 P
weak similarity to B.subtilis spore outgrowth factor B
4456_at 454.8 P
ribosomal protein of the small subunit, mitochondrial
4457_at 1746.4 P
weak similarity to C.elegans hypothetical protein CEW09D10
4458_at 2450.2 P
hypothetical protein
4459_at 784.6 P
Ire1p is a transmembrane protein that has both serine-threonine kinase and endoribonuclease activities
4460_i_at 6.7 A
Ire1p is a transmembrane protein that has both serine-threonine kinase and endoribonuclease activities
4461_r_at 13.4 A
Ire1p is a transmembrane protein that has both serine-threonine kinase and endoribonuclease activities
4462_at 1469.4 P
similarity to hypothetical protein YDR326c, YFL042c and YLR072w
4463_at 1227.5 P
weak similarity to human C1D protein
4464_at 3440.6 P
Ser\/Thr protein kinase
4465_at 2682.2 P
hypothetical protein
4466_at 3177.9 P
Transcription factor
4467_at 3064.9 P
weak similarity to fruit fly brahma transcriptional activator
4468_at 2503.4 P
putative RNA binding protein, involved in meiosis-specific splicing of the REC107 transcripts in cooperation with the Mer1 protein
4423_at 665.3 P
hypothetical protein
4424_at 2980.0 P
similarity to hypothetical protein YNL075w
4425_at 10690.0 P

small nucleolar RNP proteins
4426_at 1934.6 P
NuBbiN
4427_at 2602.8 P
Arginyl-tRNA synthetase
4428_at 5504.5 P
High-affinity glucose transporter
4429_at 668.9 P
the AHT1 DNA sequence is upstream of HXT4 and contains an HXT4 regulatory element which is a multicopy suppressor of glucose transport defects\; probable non-functional ORF
4430_at 9354.6 P
High-affinity hexose (glucose) transporter
4431_at 110.8 A
hypothetical protein
4432_at 339.1 A
hexose transporter
4433_at 2089.8 P
strong similarity to hypothetical protein YDR348c
4434_at 984.0 P
strong similarity to hypothetical protein YDR348c
4435_at 5535.5 P
binds to Sed5p and Sec23p by distinct domains
4436_at 3598.6 P
ATM\/Mec1\/TOR1+2-related
4437_at 2275.1 P
hypothetical protein
4438_at 2058.5 P
Bad in glucose or big cells
4439_at 626.0 P
Bad in glucose or big cells
4440_at 991.6 P
Ser\/Thr protein kinase
4441_at 2275.7 P
functionally redundant and similar in structure to SBE2
4442_at 2768.0 P
Aldo-keto reductase
4443_at 101.4 P
weak similarity to Mvp1p
4444_at 1433.7 P
Thioredoxin reductase
4445_at 1887.3 P
Component of 10 nm filaments of mother-bud neck (septin)
4401_at 8043.7 P
strong similarity to hypothetical protein YDR358w
4402_at 246.9 P
hypothetical protein
4403_at 3363.4 P
p24 protein involved in membrane trafficking
4404_at 1514.3 P
moeB, thiF, UBA1
4405_at 2912.8 P
Cystathionine gamma-synthase
4406_at 3725.8 P
Vacuolar aminopeptidase
4407_at 1209.4 P
SH3 domain

4408_at 2709.6 P
strong similarity to hypothetical protein YNL116w
4409_at 651.0 P
hypothetical protein
4410_at 1741.3 P
71-kDa component of the protein translocase of the outer membrane of mitochondria
4411_at 130.0 P
50-kDa subunit of ORC
4412_at 1783.4 P
trithorax
4413_at 1169.9 P
mutS homolog involved in mitochondrial DNA repair
4414_at 2596.1 P
weak similarity to C.elegans hypothetical protein
4415_at 2215.2 P
similarity to hypothetical C. elegans protein F45G2.a
4416_at 2355.7 P
sn-1,2-diacylglycerol ethanolamine- and cholinephosphotranferase
4417_at 4323.9 P
sn-1,2-diacylglycerol ethanolamine- and cholinephosphotranferase
4418_at 227.2 P
meiosis-specific gene, mRNA is sporulation-specific
4419_at 12.9 A
questionable ORF
4420_at 96.8 A
hypothetical protein
4421_at 2898.0 P
(H)igh copy (S)uppressor of (N)34 dominant negative allele of SEC4. Suppression is very specific to this allele. It has no affect on the analogous YPT1 allele. No homology or known function.
4422_at 11669.9 P
UPRTase
4378_at 300.2 P
Centractin
4379_at 901.3 P
weak similarity to T.brucei H+-transporting ATP synthase
4380_at 971.7 P
Highly acidic C-terminus
4381_at 5661.4 P
Carboxypeptidase
4382_at 11845.9 P
similarity to hypothetical protein YNL156c
4383_at 274.6 P
hypothetical protein
4384_at 3767.8 P
membrane-bound casein kinase I homolog
4385_at 7867.9 P
17 kDa protein
4386_at 10536.8 P
aromatic amino acid aminotransferase II
4387_at 1609.4 P
hypothetical protein
4388_at 72.8 A
sporulation-specific wall maturation protein
4389_at 40.8 A
hypothetical protein
4390_at 93.4 M

hypothetical protein
4391_at 6393.8 P
weak similarity to cytochrome-c oxidases
4392_at 9794.4 P
Ser-Thr rich protein
4393_at 5666.8 P
subunit of RNA polymerase II
4394_at 3643.5 P
dCMP deaminase
4395_at -1.3 A
questionable ORF
4396_at 2411.5 P
similarity to pheromone-response G-protein Mdg1p
4397_at 2202.1 P
Mitochondrial ribosomal protein MRPL6 (YmL6)
4398_at 4319.0 P
ribosomal protein (weak similarity)
4399_at 994.9 P
similarity to hypothetical protein YGR221c
4400_at 362.9 P
weak similarity to YDR479c
4356_at 2865.2 P
hypothetical protein
4357_at 2903.3 P
20 kDa protein with negatively charged C-terminus required for function\; thought to be a positive regulator of exit from M-phase in mitosis and meiosis. Spo12p interacts with Dbf2p and Dbf20p protein kinases.
4358_at 100.4 P
sporulation protein
4359_at 1353.5 P
Establishes Silent omatin
4360_at 1178.7 P
Snf1-interacting protein Sip3p
4361_at 311.1 A
weak similarity to mouse kinesin KIF3B
4362_at 227.6 A
mRNA is induced early in meiosis
4363_at 1399.7 P
protein containing kelch repeats, similar to YGR238c
4364_at 25.8 A
hypothetical protein
4365_at 90.9 A
weak similarity to hypothetical protein YGR239c
4366_at 1382.1 P
Yeast Assembly Polypeptide, member of AP180 protein family, binds Pan1p and clathrin
4367_at 9280.4 P
strong similarity to hypothetical protein YGR243w
4368_at 7476.1 P
shows similarity to glucose-6-phosphate dehydrogenase non-catalytic domains\; homologous to Sol2p and Sol1p
4369_at 901.1 P
DNA replication helicase
4370_at 3262.9 P
RNA splicing factor
4371_at -9.6 A
Cell division cycle protein

4372_at	822.4	P	hypothetical protein
4373_at	671.8	P	GTP-binding protein
4374_at	4469.5	P	DEAD-box protein
4375_at	7370.8	P	putative Upf1p-interacting protein
4376_at	520.5	P	autophagy
4377_at	1285.7	P	spindle pole body component, associates in a complex with Spc98p and Tub4p perhaps as part of the microtubule attachment site of the SBP
4333_at	11.6	A	hypothetical protein
4334_i_at	9114.2	P	enolase
4335_at	7717.1	P	Putative low-affinity copper transport protein
4336_at	1119.7	P	Dimethylaniline monoxygenase
4337_at	599.2	P	weak similarity to Spombe pac2 protein
4338_at	799.4	P	Zinc finger (6-Cys)
4339_at	11745.3	P	NAPDH dehydrogenase (old yellow enzyme), isoform 2
4340_at	420.1	P	hypothetical protein
4341_at	5841.5	P	similarity to mouse TEG-261 protein
4342_at	940.0	P	hypothetical protein
4343_at	13956.9	P	Phosphogluconate Dehydrogenase (Decarboxylating)
4344_at	646.0	P	Involved in the control of meiotic nuclear divisions and spore formation
4345_at	81.1	P	hypothetical protein
4346_at	2503.3	P	similarity to C.elegans hypothetical protein C10C5.6
4347_at	400.0	P	confers sensitivity to killer toxin
4348_at	4945.3	P	similarity to hypothetical C. elegans proteins F17c11.7
4349_at	713.0	A	similarity to peptidyl-tRNA hydrolases
4350_at	9071.8	P	squalene synthetase
4351_at	1329.5	P	protein of unknown function
4352_at	1786.3	P	hypothetical protein
4353_at	9823.9	P	GAL4 enhancer protein, homolog of human alpha NAC subunit of the nascent-polypeptide-associated complex

4354_at 1905.4 P
similarity to hypothetical protein YOR147w
4355_at 2234.3 P
hypothetical protein
4310_at 3067.1 P
hypothetical protein
4311_at 7048.5 P
hypothetical protein
4312_at 740.1 P
strong similarity to hypothetical protein YHR199c
4313_at 3839.3 P
strong similarity to hypothetical protein YHR198c
4314_at 8651.9 P
homolog of the mammalian S5a protein, component of 26S proteasome
4315_at 3290.5 P
Cytosolic exopolyphosphatase
4316_at 1132.8 P
similarity to S.pombe hypothetical protein SPAC17G6
4317_at 4028.3 P
similarity to alpha-mannosidases
4318_at 2282.2 P
cAMP-dependent protein kinase homolog, suppressor of cdc25ts
4319_at 3066.8 P
Protein with similarity to DNA-binding region of heat shock transcription factors
4320_at 1497.6 P
weak similarity to YPL165c
4321_at 11647.7 P
branched-chain amino acid transaminase, highly similar to mammalian ECA39, which is regulated by the oncogene myc
4322_at 684.7 P
UDP-glucose-4-epimerase (GAL10, galE)
4323_f_at 9250.0 P
IMP dehydrogenase\; probable PUR5 gene
4324_s_at 4533.8 P
gene in Y repeat region
4325_at 18.3 A
questionable ORF
4326_at 723.6 P
questionable ORF
4327_at 120.4 A
questionable ORF
4328_at 469.7 A
questionable ORF
4329_at -330.5 A
questionable ORF
4330_at 628.4 P
questionable ORF
4331_at 14.6 A
questionable ORF
4332_at -125.0 A
questionable ORF
4286_s_at 1621.1 P
Highly acidic C-terminus
4287_s_at 225.2 P
similarity to hypothetical protein YER175c
4288_at 2743.5 P

non-annotated SAGE orf Found reverse in NC_001140 between 34593 and 34790 with 100% identity. See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251

4289_at -32.0 A

non-annotated SAGE orf Found reverse in NC_001140 between 518765 and 518938 with 100% identity. See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251

4290_at 214.2 A

non-annotated SAGE orf Found reverse in NC_001140 between 519037 and 519228 with 100% identity. See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251

4291_i_at -232.4 A

non-annotated SAGE orf Found reverse in NC_001140 between 91713 and 91919 with 100% identity. See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251

4292_at 423.6 P

non-annotated SAGE orf Found reverse in NC_001140 between 146614 and 146772 with 100% identity. See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251

4293_at 1968.8 P

non-annotated SAGE orf Found forward in NC_001140 between 370055 and 370342 with 100% identity. See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251

4294_at 274.6 A

non-annotated SAGE orf Found forward in NC_001140 between 56060 and 56263 with 100% identity. See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251

4295_at 191.0 P

non-annotated SAGE orf Found forward in NC_001140 between 80439 and 80615 with 100% identity. See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251

4296_at 553.2 A

non-annotated SAGE orf Found reverse in NC_001140 between 122543 and 122758 with 100% identity. See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251

4297_at 8.6 A

non-annotated SAGE orf Found forward in NC_001140 between 146159 and 146308 with 100% identity. See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251

4298_at 70.0 A

non-annotated SAGE orf Found reverse in NC_001140 between 167438 and 167620 with 100% identity. See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251

4299_at 497.7 P

non-annotated SAGE orf Found reverse in NC_001140 between 225199 and 225351 with 100% identity. See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251

4300_at 732.1 P

non-annotated SAGE orf Found reverse in NC_001140 between 374400 and 374564 with 100% identity. See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251

4301_at 40.9 A

non-annotated SAGE orf Found forward in NC_001140 between 508759 and 508923 with 100% identity. See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251

4302_at 1130.1 P

non-annotated SAGE orf Found forward in NC_001140 between 209467 and 209637 with 100% identity. See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251

4303_at 4736.2 P

non-annotated SAGE orf Found forward in NC_001140 between 467972 and 468148 with 100% identity. See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251

4304_f_at 453.0 P

non-annotated SAGE orf Found forward in NC_001140 between 528967 and 529113 with 100% identity. See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251

4305_at 1241.2 P

non-annotated SAGE orf Found reverse in NC_001140 between 5662 and 5796 with 100% identity. See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251

4306_i_at -505.0 A

non-annotated SAGE orf Found reverse in NC_001140 between 5778 and 5924 with 100% identity. See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251

4307_f_at -28.9 A

non-annotated SAGE orf Found reverse in NC_001140 between 5778 and 5924 with 100% identity. See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251

4308_at 127.9 P

non-annotated SAGE orf Found reverse in NC_001140 between 202505 and 202657 with 100% identity. See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251

4309_i_at 55.9 A

non-annotated SAGE orf Found forward in NC_001140 between 203161 and 203328 with 100% identity. See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251

4261_s_at -44.2 A

non-annotated SAGE orf Found forward in NC_001140 between 203161 and 203328 with 100% identity. See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251

4262_i_at 11.2 A

non-annotated SAGE orf Found forward in NC_001140 between 203174 and 203335 with 100% identity. See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251

4263_at -81.9 P

non-annotated SAGE orf Found reverse in NC_001140 between 204089 and 204277 with 100% identity. See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251

4264_at 289.5 P

non-annotated SAGE orf Found reverse in NC_001140 between 422491 and 422676 with 100% identity. See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251

4265_s_at 273.6 P

non-annotated SAGE orf Found reverse in NC_001140 between 422739 and 422921 with 100% identity. See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251

4266_at 1890.2 P

non-annotated SAGE orf Found reverse in NC_001140 between 422746 and 422961 with 100% identity. See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251

4267_at 124.2 A

non-annotated SAGE orf Found reverse in NC_001140 between 458162 and 458326 with 100% identity. See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251

4268_at -7.5 A

non-annotated SAGE orf Found reverse in NC_001140 between 522720 and 522872 with 100% identity. See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251

4269_f_at 2221.9 P

non-annotated SAGE orf Found forward in NC_001140 between 530130 and 530267 with 100% identity. See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251

4270_f_at 201.4 A

non-annotated SAGE orf Found reverse in NC_001140 between 530754 and 530897 with 100% identity. See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251

4271_at -3.8 A

non-annotated SAGE orf Found reverse in NC_001140 between 531037 and 531177 with 100% identity. See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251

4272_at 6270.5 P

non-annotated SAGE orf Found reverse in NC_001140 between 111584 and 111718 with 100% identity. See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251

4273_at 516.5 M

non-annotated SAGE orf Found forward in NC_001140 between 157505 and 157675 with 100% identity. See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251

4274_at 3401.7 P

non-annotated SAGE orf Found forward in NC_001140 between 175186 and 175365 with 100% identity. See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251

4275_at 62.8 A

non-annotated SAGE orf Found forward in NC_001140 between 198428 and 198592 with 100% identity. See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251

4276_at 113.5 A

non-annotated SAGE orf Found reverse in NC_001140 between 410821 and 411015 with 100% identity.

See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251

4277_i_at	9.5	A	Centromere
4278_at	1083.9	P	snRNA
4279_at	1078.7	P	snRNA
4280_f_at	1492.1	P	strong similarity to members of the Srp1p/Tip1p family
4281_i_at	1885.7	P	High-affinity hexose transporter
4282_f_at	102.0	A	High-affinity hexose transporter
4283_at	71.0	A	L-serine dehydratase
4284_at	-9.8	A	serine dehydratase
4285_at	617.0	P	similarity to allantoate permease Dal5p
4237_at	829.3	P	putative pseudogene
4238_at	1141.3	P	Nit1 nitrilase
4239_at	-16.7	A	questionable ORF
4240_at	2014.7	P	hypothetical protein
4241_at	184.5	P	peroxisomal 3-oxoacyl CoA thiolase
4242_at	197.5	P	Bni1p-related protein, helps regulate reorganization of the actin cytoskeleton, potential target of Rho4p
4243_at	2605.1	P	similarity to hypothetical protein YKR100c
4244_at	4624.3	P	hypothetical protein
4245_at	417.1	P	Ubiquitin-specific protease
4246_at	2094.6	P	glycerol-3-phosphate dehydrogenase, mitochondrial
4247_at	2852.9	P	transcription factor
4248_at	2837.6	P	Resistant to Rapamycin Deletion
4249_at	1128.1	P	hypothetical protein
4250_at	665.4	P	similarity to mitochondrial aldehyde dehydrogenase Ald1p
4251_at	370.6	P	Protein required for S-phase (DNA synthesis) initiation or completion
4252_at	1261.6	P	similarity to Mlp1p and myosin heavy chains
4253_i_at	13471.5	P	Ribosomal protein L40A
4254_at	3873.7	P	histidine kinase osmosensor that regulates an osmosensing MAP kinase cascade and is similar to bacterial two-component regulators

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4255_at     465.5       P
ExtraCellular Mutant
4256_at     1619.2      P
similarity to E.coli pantothenate synthetase
4257_at     144.2       P
Dmc1p interacting protein
4258_at     1455.2      P
DNA helicase homolog\; homolog of human XPBC, ERCC3
4259_at     9145.8      P
molecular chaperone
4260_at     1041.6      P
questionable ORF
4215_g_at   2200.0      P
questionable ORF
4216_at     1099.0      P
localizes to the plasma membrane
4217_at     211.8       P
subunit of DNA polymerase-zeta (Pol-zeta), an enzyme whose sole function appears to be translesion
synthesis
4218_at     2278.1      P
Tropomyosin isoform 2
4219_at     1948.1      P
similarity to M.musculus aminopeptidase
4220_at     -87.3       A
45-kDa mitochondrial outer membrane protein
4221_at     1186.9      P
similarity to Ymk1p
4222_at     1198.8      P
mitochondrial inner membrane carrier protein for FAD
4223_at     10277.8     P
Ribosomal protein L16A (L21A) (rp22) (YL15)
4224_at     385.4       P
hypothetical protein
4225_at     2030.0      P
similarity to Drosophila fork head protein
4226_at     1527.7      P
similarity to Put3p and to hypothetical protein YJL206c
4227_at     5079.5      P
similarity to hypothetical human protein
4228_at     1230.6      P
Involved in nucleotide excision repair and regulation of TFIIH
4229_at     2148.2      P
weak similarity to Smy2p
4230_at     3375.8      P
helicase related protein, snf2 homolog
4231_at     6501.9      P
alpha-ketoglutarate dehydrogenase
4232_at     5579.6      P
similarity to C.perfringens nanH protein
4233_at     9558.9      P
involved in cell cycle regulation and aging
4234_at     330.7       P
hypothetical protein
4235_at     706.6       P
similarity to antibiotic resistance proteins
4236_at     354.6       P
```

similarity to antibiotic resistance proteins
4192_at 913.5 P
inhibitor of ras
4193_at 2981.4 P
ras homolog--GTP binding protein
4194_at 1729.2 P
hydrophobic transmembrane domain
4195_at 3896.0 P
histidinol-phosphate aminotransferase
4196_at 3600.2 P
159-kDa nucleoporin with coiled-coil domain and repeated motifs typical of nucleoporins
4197_at 2297.1 P
voltage dependent anion channel (YVDAC2)
4198_at 38.3 A
strong similarity to dual-specificity phosphatase Msg5p
4199_at 350.4 P
similarity to ankyrin and coiled-coil proteins
4200_at 93.0 A
Cytochrome-c oxidase chain Vb
4201_at 1806.9 P
weak similarity to hypothetical C.elegans protein
4202_at 6132.8 P
The Sec23p-Sec24p complex is one of three cytoplamic COPII factors involved in ER to Golgi transport
4203_at 1925.0 P
similarity to hypothetical S. pombe protein

4204_at 105.7 P
6-Phosphofructose-2-kinase
4205_at 898.7 P
weak similarity to probable transcription factor Ask10p
4206_at 1007.6 P
similarity to hypothetical S. pombe protein
4207_at 3741.5 P
weak similarity to Dph2 protein
4208_at -58.1 A
strong similarity to YIL014c-a
4209_at -247.8 A
DNA-binding transcriptional repressor
4210_at -66.5 A
similarity to mouse Gcap1 protein and fruit fly Bkm-like sex-determining region hypothetical protein CS314
4211_at 789.6 P
intracellular glucoamylase
4212_g_at -79.9 A
intracellular glucoamylase
4213_at 1106.8 P
Formation of Mitochondrial Cytochromes 1
4214_at 404.9 P
hypothetical protein
4170_at 3652.5 P
hypothetical protein
4171_at 49.4 A
probable serine\/threonine-protein kinase
4172_at 7896.1 P
Homo-isocitrate dehydrogenase
4173_at 462.9 P

weak similarity to S.pombe hypothetical protein SPBC16A3
4174_at 420.1 P
hypothetical protein
4175_at 2552.3 P
weak similarity to spt5p
4176_at 3322.0 P
similarity to hypothetical S. pombe protein
4177_at 960.2 P
similarity to hypothetical protein YLR036c
4178_at 3483.6 P
weak similarity to A.thaliana aminoacid permease AAP4
4179_at 2759.2 P
hypothetical protein
4180_at 94.2 A
hypothetical protein
4181_at 939.0 P
Putative mannosyltransferase of the KRE2 family
4182_at 218.1 P
Functions are similar to those of SIN3 and RPD3
4183_at 4184.1 P
hypothetical protein
4184_s_at 2487.4 P
Ty3-2 orf C fragment
4185_at 1225.2 P
strong similarity to hypothetical protein YDL175c
4186_at 10128.0 P
Threonyl-tRNA synthetase, cytoplasmic
4187_at 455.6 P
hypothetical protein
4188_at 6060.9 P
epsilon-COP coatomer subunit Sec28p
4189_at 7478.7 P
RPN2p is a component of the 26S proteosome
4190_at 3504.4 P
strong similarity to E.coli phosphoglycerate dehydrogenase
4191_at 57.4 A
weak similarity to mouse polycystic kidney disease-related protein
4147_at 14.2 A
Meiosis-specific protein involved in homologous chromosome synapsis and chiasmata formation
4148_at 203.7 P
hypothetical protein
4149_at 7488.5 P
mitochondrial acidic matrix protein
4150_at 3152.5 P
88 kD component of the Exocyst complex, which contains the gene products encoded by SEC3, SEC5, SEC6, SEC8, SEC10, SEC15 and EXO70
4151_at 2459.0 P
hypothetical protein
4152_at 2705.8 P
similarity to C.elegans hypothetical protein
4153_at 1626.3 P
weak similarity to fowlpox virus major core protein
4154_at 1536.1 P
nuclear protein, interacts with Gsp1p and Crm1p
4155_at 8647.1 P
Arp Complex Subunit

4156_at 255.6 P
U1snRNP 70K protein homolog
4157_at 243.3 P
questionable ORF
4158_at 520.7 P
hypothetical protein
4159_at 295.7 A
hypothetical protein
4160_at 161.3 A
strong similarity to YER067w
4161_at 2001.1 P
similarity to YER064c
4162_at 301.3 P
hypothetical protein
4163_at 232.5 P
weak similarity to fruit fly NADH dehydrogenase
4164_at 7832.6 P
DL-glycerol-3-phosphatase
4165_i_at 15406.6 P
Ribosomal protein L34B
4166_at 10237.0 P
Maintenance of Mitochondrial DNA 1
4167_at 2943.9 P
PHO85 cyclin
4168_at 4138.2 P
Protein required for filamentous growth, cell polarity, and cellular elongation
4169_at 3160.3 P
ATPase that leads to neomycin-resistant protein when overexpressed
4124_at 7858.7 P
plasma membrane protein
4125_at 1492.6 P
Met30p contains five copies of WD40 motif and interacts with and regulates Met4p
4126_at 175.8 P
Protein with 30\%% identity to protein corresponding to YER054
4127_at 1770.8 P
weak similarity to zinc finger protein Gcs1p
4128_at 8847.8 P
cytochrome b reductase
4129_at 1290.2 P
similarity to rat branched-chain alpha-ketoacid dehydrogenase kinase
4130_at 9660.2 P
similarity to S.pombe hypothetical protein
4131_at 2954.9 P
weak similarity to T.brucei NADH dehydrogenase
4132_at 7494.7 P
hypothetical protein
4133_at 1820.3 P
General negative regulator of transcription\; may inhibit RNA polymerase II transcription machinery
4134_at -18.2 A
hypothetical protein
4135_at 1268.4 P
weak similarity to human cAMP responce element-binding protein
4136_at 3048.0 P
alpha subunit of casein kinase II
4137_at 3044.9 P
beta subunit of capping protein

4138_at 7540.5 P
regulatory subunit of cAMP-dependent protein kinase
4139_at 753.1 A
hypothetical protein
4140_at 786.2 P
Suppressor of Mif Two
4141_at 4076.8 P
integral nuclear membrane protein
4142_at 63.6 P
strong similarity to hypothetical protein YPR071w
4143_at 232.3 A
putative pseudogene
4144_at 7215.4 P
hypothetical protein
4145_at 422.1 P
Irregular
4146_at 18.2 A
weak similarity to E.gracilis RNA polymerase subunit
4101_at 428.5 P
hypothetical protein
4102_at 3616.3 P
similarity to mouse MHC H-2K/t-w5-linked ORF precursor
4103_at 6130.1 P
48.8 kDa protein involved in mitochondrial protein import
4104_at 2964.4 P
45 kDa subunit of RNA polymerase II
4105_at 1585.1 P
phosphoribosyl-5-amino-1-phosphoribosyl-4-imidazolecarboxiamide isomerase
4106_at 1096.4 P
weak similarity to S.pombe hypothetical protein SPAC3F10
4107_at 463.5 P
hypothetical protein
4108_at 1386.3 P
18.3 kD integral membrane protein
4109_at -31.9 A
encodes a-cell barrier activity on alpha factor
4110_at -80.5 A
strong similarity to hypothetical protein YIL102c
4111_at 1478.3 P
similarity to Mnn1p
4112_at 434.8 P
Putative member of the ABC family of membrane transporters
4113_at 172.5 A
hypothetical protein
4114_at 4956.3 P
strong similarity to members of the Srp1p/Tip1p family
4115_at 4868.4 P
Derepression Of Telomeric silencing
4116_at 2196.2 P
181aa protein - 20.5 kD
4117_at 1310.3 P
181aa protein - 20.5 kD
4118_at 4755.3 P
Acyl CoA synthase
4119_at 3971.2 P
hypothetical protein

4120_at 587.0 P
similarity to C.elegans hypothetical protein
4121_at 945.1 P
similarity to Flx1p
4122_at 3612.8 P
similarity to protein disulfide isomerases
4123_at 1475.8 P
Synaptobrevin (t-SNARE) homolog present on ER vesicles recycling from Golgi
4079_at 2832.3 P
strong similarity to Nbp35p and human nucleotide-binding protein
4080_at 1153.2 P
phosphatidylinositol 4,5-bisphosphate 5-phosphatase
4081_at 891.7 P
similarity to S.pombe hypothetical protein, weak similarity to human ankyrin
4082_at 948.1 P
similarity to D.melanogaster RNA binding protein
4083_at 1138.0 P
weak similarity to ATP-dependent RNA helicases
4084_at 3108.5 P
weak similarity to mammalian neurofilament triplet H proteins
4085_at 2668.2 P
DnaJ-like protein required for Peroxisome biogenesis\; Djp1p is located in the cytosol
4086_at 590.5 P
similarity to RNA-binding proteins
4087_at 9063.1 P
polyA-specific ribonuclease
4088_at 368.2 P
hypothetical protein
4089_at 2164.9 P
p48 polypeptide of DNA primase
4090_at 772.3 P
encodes YU2B, a component of yeast U2 snRNP
4091_at 1345.2 P
hypothetical protein
4092_at 3539.9 P
restores protein transport when overexpressed and rRNA stability to a sec23 mutation
4093_at 8624.7 P
contains multiple WD repeats and interacts with Qsr1p in two hybrid
4094_at 153.1 A
strong similarity to YLR013w, similarity to YMR136w
4095_at 539.3 P
hypothetical protein
4096_at 164.1 M
an integral subunit of RNase P but not RNase MRP
4097_at 1901.3 P
weak similarity to YOL036w
4098_at 527.2 P
Transcriptional activator of sulfur amino acid metabolism
4099_at 398.3 P
bZIP protein\; transcription factor
4100_at 3671.3 P
cell surface flocculin with structure similar to serine\/threonine-rich GPI-anchored cell wall proteins
4056_at 566.3 P
hypothetical protein
4057_at 2633.8 P
mitochondrial RNA splicing

4058_at 3542.8 P
signal peptidase subunit
4059_at 1156.4 P
Transcriptional activator for allantoin and GABA catabolic genes, contains a Zn[2]-Cys[6] fungal-type binuclear cluster domain in the N-terminal region
4060_at 807.8 P
G1 Factor needed for normal G1 phase
4061_at 337.1 P
hypothetical protein
4062_at 3137.5 P
nitrogen starvation-induced protein phosphatase
4063_at 84.2 A
allantoinase
4064_at 148.8 P
allantoin permease
4065_at -129.9 A
allantoicase
4066_at 826.9 P
involved in nitrogen-catabolite metabolism
4067_at 402.3 P
Malate synthase 2
4068_at -100.6 A
ureidoglycolate hydrolase
4069_at 805.9 P
may be involved in the remodeling chromatin structure
4070_at 1957.8 P
saccharopine dehydrogenase
4071_at 5420.3 P
similarity to human corticosteroid 11-beta-dehydrogenase
4072_at 3202.9 P
similarity to E.coli fabD
4073_at 9273.6 P
putative glutathione-peroxidase
4074_at 1608.7 P
Glutathione transferase
4075_at 260.4 P
GPI-anchored aspartic protease
4076_f_at 136.1 P
similarity to members of the Srp1p/Tip1p family
4077_at 640.2 P
weak similarity to B.licheniformi hypothetical protein P20
4078_i_at 131.7 P
putative pseudogene
4032_f_at 64.9 A
putative pseudogene
4033_f_at 7900.1 P
putative pseudogene
4034_at 26.8 A
hypothetical protein
4035_at 134.7 A
questionable ORF
4036_at -16.6 A
questionable ORF
4037_at 16.7 A
questionable ORF
4038_at 532.1 P

questionable ORF
4039_at 29.7 A
questionable ORF
4040_at 39.8 A
questionable ORF
4041_at 94.1 M
hypothetical protein
4042_at 494.2 P
questionable ORF
4043_s_at 238.1 A
invertase (sucrose hydrolyzing enzyme)
4044_s_at 1882.8 P
Mps One Binder
4045_s_at 91.3 A
Ribonucleotide reductase (ribonucleoside-diphosphate reductase) large subunit
4046_at -20.0 A
non-annotated SAGE orf Found forward in NC_001141 between 197558 and 197818 with 100% identity.
See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251
4047_at 300.8 P
non-annotated SAGE orf Found forward in NC_001141 between 268308 and 268472 with 100% identity.
See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251
4048_at -20.4 A
non-annotated SAGE orf Found forward in NC_001141 between 414832 and 414975 with 100% identity.
See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251
4049_at 1162.8 P
non-annotated SAGE orf Found forward in NC_001141 between 438483 and 438695 with 100% identity.
See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251
4050_at 884.7 P
non-annotated SAGE orf Found forward in NC_001141 between 144104 and 144268 with 100% identity.
See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251
4051_at 145.5 A
non-annotated SAGE orf Found forward in NC_001141 between 173167 and 173406 with 100% identity.
See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251
4052_i_at -31.0 A
non-annotated SAGE orf Found forward in NC_001141 between 324288 and 324437 with 100% identity.
See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251
4053_s_at 4341.8 P
non-annotated SAGE orf Found forward in NC_001141 between 324288 and 324437 with 100% identity.
See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251
4054_at 4768.7 P
non-annotated SAGE orf Found forward in NC_001141 between 350298 and 350507 with 100% identity.
See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251
4055_at -183.4 A
non-annotated SAGE orf Found forward in NC_001141 between 398511 and 398723 with 100% identity.
See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251
4009_at 7220.2 P
non-annotated SAGE orf Found forward in NC_001141 between 26990 and 27169 with 100% identity.
See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251
4010_at -4.1 A
non-annotated SAGE orf Found reverse in NC_001141 between 139370 and 139600 with 100% identity.
See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251
4011_at 1570.1 P
non-annotated SAGE orf Found reverse in NC_001141 between 139503 and 139682 with 100% identity.
See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251
4012_at 405.7 A
non-annotated SAGE orf Found forward in NC_001141 between 169709 and 169858 with 100% identity.

See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251
4013_i_at -35.9 A
non-annotated SAGE orf Found reverse in NC_001141 between 210545 and 210736 with 100% identity.
See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251
4014_at 563.6 P
non-annotated SAGE orf Found forward in NC_001141 between 230002 and 230175 with 100% identity.
See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251
4015_at 535.8 P
non-annotated SAGE orf Found forward in NC_001141 between 258363 and 258509 with 100% identity.
See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251
4016_at 553.5 A
non-annotated SAGE orf Found forward in NC_001141 between 258506 and 258640 with 100% identity.
See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251
4017_at 241.9 P
non-annotated SAGE orf Found reverse in NC_001141 between 324125 and 324358 with 100% identity.
See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251
4018_at 165.9 A
non-annotated SAGE orf Found reverse in NC_001141 between 385561 and 385698 with 100% identity.
See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251
4019_at 1103.0 P
non-annotated SAGE orf Found reverse in NC_001141 between 385816 and 385959 with 100% identity.
See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251
4020_at 1101.2 P
non-annotated SAGE orf Found reverse in NC_001141 between 386017 and 386157 with 100% identity.
See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251
4021_at 73.7 P
non-annotated SAGE orf Found forward in NC_001141 between 387799 and 388053 with 100% identity.
See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251
4022_at 137.3 P
non-annotated SAGE orf Found forward in NC_001141 between 425520 and 425678 with 100% identity.
See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251
4023_s_at 112.8 P
non-annotated SAGE orf Found forward in NC_001141 between 21392 and 21526 with 100% identity.
See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251
4024_at 335.6 P
non-annotated SAGE orf Found reverse in NC_001141 between 30695 and 30898 with 100% identity.
See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251
4025_i_at 1011.6 P
non-annotated SAGE orf Found reverse in NC_001141 between 51611 and 51751 with 100% identity.
See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251
4026_at 468.1 A
non-annotated SAGE orf Found forward in NC_001141 between 122286 and 122549 with 100% identity.
See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251
4027_at 1021.2 P
non-annotated SAGE orf Found forward in NC_001141 between 154868 and 155122 with 100% identity.
See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251
4028_at 625.4 P
non-annotated SAGE orf Found reverse in NC_001141 between 231169 and 231306 with 100% identity.
See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251
4029_at 1435.6 P
non-annotated SAGE orf Found reverse in NC_001141 between 355843 and 356004 with 100% identity.
See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251
4030_at 931.6 P
non-annotated SAGE orf Found forward in NC_001141 between 385618 and 385767 with 100% identity.
See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251
4031_at 1498.5 P

snRNA
3983_at 57.6 A
cytochrome-c oxidase subunit II
3984_r_at 24.5 A
questionable ORF Found forward in NC_001224 between 74495 and 74804 with 99.677419% identity.
3985_i_at 44.8 P
questionable ORF Found forward in NC_001224 between 74495 and 74804 with 99.677419% identity.
3986_f_at 154.2 P
questionable ORF Found forward in NC_001224 between 74495 and 74804 with 99.677419% identity.
3987_at 16.1 A
similarity to Podospora cytb intron 1a and coII intron protein 2 Found forward in NC_001224 between 74755 and 75949 with 97.154812% identity.
3988_at 70.7 A
cytochrome-c oxidase chain III
3989_at 0.3 A
strong similarity to maturase-related hypothetical protein RF2
3990_i_at -10.0 A
similarity to hypothetical protein Sgc2p Found forward in NC_001224 between 75041 and 75472 with 64.392324% identity.
3991_r_at -108.5 A
similarity to hypothetical protein Sgc2p Found forward in NC_001224 between 75041 and 75472 with 64.392324% identity.
3992_f_at -107.2 A
similarity to hypothetical protein Sgc2p Found forward in NC_001224 between 75041 and 75472 with 64.392324% identity.
3993_at -11.9 A
strong similarity to Yeast (S.uvarum) mitochondria RF2 gene and maturase-related hypothetical protein RF2
3994_at 749.1 P
similarity to Sauroleishmania NADH dehydrogenase (ubiquinone) chain 5 Found forward in NC_001224 between 3940 and 4167 with 99.122807% identity.
3995_i_at 67.8 A
RF2 protein Found forward in NC_001224 between 8526 and 8736 with 84.489796% identity.
3996_s_at 2050.1 P
cytochrome-c oxidase subunit I Found forward in NC_001224 between 13818 and 13988 with 100% identity.
3997_at 2914.8 P
questionable ORF Found reverse in NC_001224 between 13748 and 14122 with 100% identity.
3998_at 362.9 P
COX1 intron 1 protein Found forward in NC_001224 between 13818 and 16322 with 99.92016% identity.
3999_at 1378.6 P
COX1 intron 2 protein Found forward in NC_001224 between 16473 and 18830 with 99.872774% identity.
4000_at 1146.2 A
COX1 intron 3 protein Found forward in NC_001224 between 18992 and 19996 with 98.308458% identity.
4001_at 7622.9 P
cytochrome-c oxidase subunit I Found forward in NC_001224 between 20508 and 20984 with 99.790356% identity.
4002_at 133.3 P
DNA endonuclease I-SceII Found forward in NC_001224 between 20985 and 21935 with 99.684543% identity.
4003_s_at 1769.1 P
cytochrome-c oxidase subunit I Found forward in NC_001224 between 21995 and 22246 with 97.222222% identity.
4004_at 1287.9 P

probable mRNA maturase aI5-alpha Found forward in NC_001224 between 21995 and 23167 with 99.40324% identity.
4005_at 10005.0 P
cytochrome-c oxidase subunit I Found forward in NC_001224 between 23612 and 23746 with 100% identity.
4006_at 108.1 P
COX1 intron protein aI5-beta Found forward in NC_001224 between 24120 and 25151 with 96.317829% identity.
4007_at 932.7 P
cytochrome-c oxidase subunit I Found forward in NC_001224 between 26228 and 26530 with 99.339934% identity.
4008_at 271.2 P
cytochrome-c oxidase subunit I Found forward in NC_001224 between 26627 and 26701 with 100% identity.
3956_i_at 1552.2 P
F1F0-ATPase complex, F0 subunit 8 Found forward in NC_001224 between 27666 and 27812 with 99.319728% identity.
3957_r_at 802.6 P
F1F0-ATPase complex, F0 subunit 8 Found forward in NC_001224 between 27666 and 27812 with 99.319728% identity.
3958_r_at 163.9 A
similarity to mouse Gcap1 Found forward in NC_001224 between 28122 and 28444 with 88.588589% identity.
3959_at 264.7 P
F1F0-ATPase complex, FO A subunit Found forward in NC_001224 between 28487 and 29266 with 97.564103% identity.
3960_at -45.8 A
endonuclease SCEI, small subunit Found forward in NC_001224 between 46046 and 46361 with 69.393939% identity.
3961_i_at -50.6 A
endonuclease SCEI, small subunit Found forward in NC_001224 between 8238 and 8509 with 72.463768% identity.
3962_f_at 301.4 P
endonuclease SCEI, small subunit Found forward in NC_001224 between 8238 and 8509 with 72.463768% identity.
3963_at -18.1 A
endonuclease SCEI, small subunit Found forward in NC_001224 between 11057 and 11551 with 65.530303% identity.
3964_at -34.7 A
endonuclease SCEI, small subunit Found forward in NC_001224 between 77067 and 77606 with 61.663653% identity.
3965_i_at -153.6 A
ORF5 Found forward in NC_001224 between 30874 and 31014 with 100% identity.
3966_i_at -72.3 A
similarity to T.brucei mitochondrion protein SGC6 Found reverse in NC_001224 between 34032 and 34430 with 88.279302% identity.
3967_r_at -30.2 A
similarity to T.brucei mitochondrion protein SGC6 Found reverse in NC_001224 between 34032 and 34430 with 88.279302% identity.
3968_s_at 726.2 P
ubiquinol--cytochrome-c reductase subunit (cytochrome B) Found forward in NC_001224 between 36540 and 36954 with 100% identity.
3969_at 46.5 A
mRNA maturase bI2 Found forward in NC_001224 between 37723 and 38579 with 99.883314% identity.
3970_s_at 719.2 P
ubiquinol--cytochrome-c reductase subunit (cytochrome B) Found forward in NC_001224 between 39141

and 39217 with 100% identity.
3971_at -24.5 A
mRNA maturase bI3 Found forward in NC_001224 between 39141 and 40265 with 98.577778% identity.
3972_s_at 745.2 P
ubiquinol--cytochrome-c reductase subunit (cytochrome B) Found forward in NC_001224 between 40841 and 41093 with 100% identity.
3973_at 68.5 P
mRNA maturase bI4 Found forward in NC_001224 between 40815 and 42251 with 99.860821% identity.
3974_at 489.6 P
ubiquinol--cytochrome-c reductase subunit (cytochrome B) Found forward in NC_001224 between 42508 and 42561 with 100% identity.
3975_at 1685.7 P
ubiquinol--cytochrome-c reductase subunit (cytochrome B) Found forward in NC_001224 between 43297 and 43647 with 100% identity.
3976_at 11865.5 P
F1F0-ATPase complex, F0 subunit 9 Found forward in NC_001224 between 46723 and 46953 with 100% identity.
3977_i_at 353.7 A
similarity to honeybee mitochondrion NADH dehydrogenase chain 6 (SGC4) Found reverse in NC_001224 between 48858 and 49169 with 99.679487% identity.
3978_r_at -62.5 A
similarity to honeybee mitochondrion NADH dehydrogenase chain 6 (SGC4) Found reverse in NC_001224 between 48858 and 49169 with 99.679487% identity.
3979_i_at 438.8 P
mitochondrial ribosomal protein Found forward in NC_001224 between 48901 and 50097 with 98.436214% identity.
3980_r_at 23.5 A
mitochondrial ribosomal protein Found forward in NC_001224 between 48901 and 50097 with 98.436214% identity.
3981_at 22.4 A
probable mRNA maturase in 21S rRNA intron Found forward in NC_001224 between 61193 and 61729 with 100% identity.
3982_at -49.5 A
kanamycin resistance casette
3932_at -67.6 A
MAL-activator 23 (MAL23) gene
3933_s_at 1168.0 P
Required for the catabolism of melibiose and regulated by several GAL genes
3934_at 1201.4 P
Protein that confers resistance to molasses
3935_at -152.0 A
Tropomyosin-related protein with transmembrane domain and basic C-terminal
3936_at 464.0 P
invertase (sucrose hydrolyzing enzyme)
3937_g_at 2051.0 P
invertase (sucrose hydrolyzing enzyme)
3938_at 2297.5 P
Protein involved in targeting of plasma membrane [H+]ATPase
3939_at 386.0 P
Probable aldehyde dehydrogenase (EC 1.2.1.-)
3940_at 409.1 P
Degradation in the Endoplasmic Reticulum
3941_at 815.4 P
Ser\/Thr protein kinase
3942_at 5076.3 P
bZIP (basic-leucine zipper) protein

3943_i_at	9943.8	P		bZIP (basic-leucine zipper) protein
3944_f_at	4690.4	P		bZIP (basic-leucine zipper) protein
3945_at	1089.8	P		Protein essential for mitochondrial biogenesis and cell viability
3946_at	1939.5	P		Protein essential for mitochondrial biogenesis and cell viability
3947_at	7556.0	P		strong similarity to holacid-halidohydrolase
3948_s_at	1122.5	P		probable serine\/threonine-specific protein kinase (EC 2.7.1.-)
3949_i_at	3024.3	P		protein of unknown function
3950_at	2110.6	P		Rho family GTPase
3951_at	3267.8	P	2	micron plasmid recombinase
3952_at	5332.3	P	2	micron plasmid rep1 protein
3953_at	6278.3	P	2	micron plasmid D protein
3954_at	6342.6	P	2	micron plasmid rep2 protein
3955_at	418.7	P	2	micron plasmid recombinase
3907_f_at	1420.5	P		strong similarity to subtelomeric encoded proteins
3908_i_at	14.8	A		Ty1 LTR
3909_f_at	72.8	A		Ty1 LTR
3910_at	42.7	A		Ty1 LTR
3911_at	-13.5	A		Ty1 LTR
3912_f_at	9937.0	P		Ty1 LTR
3913_s_at	5824.5	A		Full length Ty1
3914_s_at	15116.6	P		Full length Ty1
3915_s_at	11748.3	P		Full length Ty1
3916_s_at	13614.1	P		Full length Ty1
3917_f_at	9381.3	P		Full length Ty1
3918_f_at	12836.9	P		Full length Ty1
3919_f_at	10983.5	P		Saccharomyces cerevisiae chromosome I, complete chromosome sequence. Found reverse in NC_001133 between 160593 and 164183 with 100% identity.
3920_f_at	12545.8	P		Saccharomyces cerevisiae chromosome I, complete chromosome sequence. Found reverse in NC_001133 between 160593 and 164183 with 100% identity.

3921_s_at	12273.2	P	Saccharomyces cerevisiae chromosome I, complete chromosome sequence. Found reverse in NC_001133 between 164540 and 165862 with 100% identity.
3922_f_at	9581.2	P	Ty1 LTR
3923_f_at	2590.1	P	tRNA-Ala
3924_f_at	3516.2	P	tRNA-Ser
3925_f_at	8445.0	P	Ty3 LTR Found forward in NC_001133 between 182610 and 182949 with 100% identity.
3926_f_at	3922.1	P	Ty1 LTR
3927_f_at	3689.5	P	Ty2 LTR
3928_f_at	37.2	A	Ty1 LTR
3929_s_at	757.3	P	tRNA-Thr
3930_i_at	90.1	P	Ty1 LTR
3931_f_at	726.8	P	Ty1 LTR
3884_f_at	2927.4	P	tRNA-Glu
3885_f_at	4826.9	P	tRNA-Ala
3886_f_at	158.6	P	Ty3 LTR
3887_f_at	1128.4	P	Ty4 LTR
3888_s_at	58.3	M	Saccharomyces cerevisiae chromosome X, complete chromosome sequence. Found forward in NC_001142 between 197614 and 198699 with 100% identity.
3889_s_at	364.3	P	Saccharomyces cerevisiae chromosome X, complete chromosome sequence. Found forward in NC_001142 between 197614 and 198699 with 100% identity.
3890_s_at	-916.9	A	Saccharomyces cerevisiae chromosome X, complete chromosome sequence. Found forward in NC_001142 between 197614 and 198858 with 100% identity.
3891_s_at	-11.9	A	Saccharomyces cerevisiae chromosome X, complete chromosome sequence. Found forward in NC_001142 between 198701 and 203026 with 100% identity.
3892_s_at	157.5	A	Saccharomyces cerevisiae chromosome X, complete chromosome sequence. Found forward in NC_001142 between 198701 and 203026 with 100% identity.
3893_s_at	-95.8	A	Saccharomyces cerevisiae chromosome X, complete chromosome sequence. Found forward in NC_001142 between 198701 and 203026 with 100% identity.
3894_s_at	-7.9	A	Saccharomyces cerevisiae chromosome X, complete chromosome sequence. Found forward in NC_001142 between 198701 and 203026 with 100% identity.
3895_s_at	426.5	P	Saccharomyces cerevisiae chromosome X, complete chromosome sequence. Found forward in NC_001142 between 198701 and 203026 with 100% identity.
3896_s_at	-71.5	A	

Full length Ty4	3897_s_at	36.2	A
Full length Ty4	3898_s_at	-7.1	A
Full length Ty4	3899_s_at	117.2	P
Full length Ty4	3900_f_at	2068.8	P
Full length Ty4	3901_f_at	1307.7	P
Ty4 LTR	3902_f_at	4177.3	P
Ty1 LTR	3903_i_at	9.7	A
Ty1 LTR	3904_f_at	1589.2	P
Ty1 LTR	3905_s_at	2223.0	P
tRNA-Asp	3906_f_at	3480.5	P
tRNA-Arg	3859_i_at	-95.5	A
Ty1 LTR	3860_f_at	7414.7	P
Ty1 LTR	3861_f_at	7346.4	P
Ty1 LTR	3862_f_at	1346.1	P
tRNA-Arg	3863_f_at	1427.5	P
tRNA-Arg	3864_i_at	187.3	A
Ty1 LTR	3865_f_at	-8.5	A
Ty1 LTR	3866_at	9.0	A
Ty1 LTR	3867_s_at	6827.4	P
tRNA-Val	3868_s_at	201.2	P
tRNA-Met	3869_f_at	-580.4	P
tRNA-Gly	3870_s_at	2608.6	P
tRNA-Lys	3871_at	-32.5	A
Ty4 LTR	3872_i_at	17.7	A
Ty1 LTR	3873_f_at	-22.1	A
Ty1 LTR	3874_i_at	-12.7	A
Ty1 LTR	3875_f_at	12.0	A
Ty1 LTR	3876_at	826.7	P

Ty4 LTR
3877_at 636.7 P
Ty1 LTR
3878_s_at 4731.0 P
tRNA-Leu
3879_f_at 9104.2 P
Ty1 LTR
3880_f_at 10303.9 P
Saccharomyces cerevisiae chromosome X, complete chromosome sequence. Found forward in NC_001142 between 473751 and 477716 with 100% identity.
3881_f_at 10700.3 P
Full length Ty1
3882_f_at 10873.4 P
Full length Ty1
3883_f_at 6069.3 P
Ty1 LTR
3835_s_at 17851.7 P
Saccharomyces cerevisiae chromosome X, complete chromosome sequence. Found forward in NC_001142 between 479334 and 483300 with 100% identity.
3836_f_at 8385.9 P
Full length Ty1
3837_f_at 10697.7 P
Ty1 LTR
3838_s_at 724.6 P
tRNA-Met
3839_at -36.7 A
Ty1 LTR
3840_f_at 3771.2 P
tRNA-Ser
3841_at 459.5 P
Ty1 LTR
3842_f_at 820.3 P
tRNA-Gly
3843_at 330.0 P
Ty1 LTR
3844_f_at 9188.1 P
Ty1 LTR
3845_i_at -217.6 A
tRNA-Arg
3846_f_at 24.5 A
tRNA-Arg
3847_i_at -390.5 A
Ty1 LTR
3848_f_at 4484.6 P
Ty1 LTR
3849_f_at 118.8 A
Ty1 LTR
3850_at 858.5 P
Ty1 LTR
3851_s_at 8579.2 P
Protein with similarity to members of the Ybr302p\/Ycr007p\/Cos8p\/Cos9p family, coded from subtelomeric region
3852_f_at 3703.3 P
Protein with similarity to members of the Ybr302p\/Ycr007p\/Cos8p\/Cos9p family, coded from subtelomeric region
3853_f_at 361.3 A

strong similarity to subtelomeric encoded proteins
3854_f_at 74.2 A
strong similarity to Gin11p, YKL225w and other subtelomeric encoded proteins
3855_s_at -2.0 A
strong similarity to subtelomeric encoded proteins
3856_at -52.8 A
tRNA-Thr
3857_at -54.9 A
Ty1 LTR
3858_s_at 411.6 P
tRNA-Asn
3812_at 45.8 A
Ty1 LTR
3813_f_at 2842.7 P
tRNA-Glu
3814_f_at 1362.8 P
tRNA-Arg
3815_i_at -91.8 A
Ty1 LTR
3816_f_at 31.8 A
Ty1 LTR
3817_f_at 8071.9 P
Ty3 LTR
3818_at 314.9 A
Ty1 LTR
3819_f_at 4257.9 P
tRNA-Ala
3820_f_at 1140.5 P
Ty1 LTR
3821_f_at 1887.7 P
tRNA-His
3822_f_at 2998.2 P
Ty1 LTR
3823_f_at 3130.2 P
Ty1 LTR
3824_f_at 9468.6 P
Ty1 LTR
3825_at -60.2 A
Ty1 LTR
3826_at -93.3 A
Ty1 LTR
3827_f_at 4725.3 P
tRNA-Arg
3828_f_at 1165.2 A
Ty1 LTR
3829_f_at 12043.4 P
Ty1 LTR
3830_f_at 5779.5 P
tRNA-Ala
3831_s_at 90.1 A
strong similarity to subtelomeric encoded proteins
3832_s_at 30.5 A
strong similarity to subtelomeric encoded proteins
3833_f_at -72.8 A
Ty5 LTR
3834_s_at 6666.5 P

strong similarity to subtelomeric encoded proteins
3789_s_at 8067.4 P
strong similarity to subtelomeric encoded proteins
3790_s_at 7638.9 P
strong similarity to subtelomeric encoded proteins
3791_s_at 874.7 P
strong similarity to subtelomeric encoded proteins
3792_s_at 9246.1 P
strong similarity to subtelomeric encoded proteins
3793_f_at 1082.2 P
Ty1 LTR
3794_f_at 3301.7 P
tRNA-Ser
3795_at -86.8 A
Ty3 LTR
3796_f_at 1971.9 P
tRNA-Ala
3797_f_at 8863.7 P
Ty1 LTR
3798_s_at 15212.0 P
Saccharomyces cerevisiae chromosome XII, complete chromosome sequence. Found reverse in NC_001144 between 215441 and 219403 with 100% identity.
3799_f_at 8095.1 P
Ty1 LTR
3800_at 36.7 A
Ty1 LTR
3801_f_at 703.4 P
Ty1 LTR
3802_f_at 3930.2 P
Ty3 LTR
3803_f_at 4401.2 P
tRNA-Arg
3804_f_at 6013.1 P
tRNA-Gln
3805_f_at 4458.4 P
Ty1 LTR
3806_s_at 8935.8 P
35S ribosomal RNA
3807_s_at 3504.6 P
35S ribosomal RNA
3808_s_at 10531.9 P
35S ribosomal RNA
3809_s_at 10664.9 P
35S ribosomal RNA
3810_s_at 1255.6 P
35S ribosomal RNA
3811_s_at 2259.7 P
35S ribosomal RNA
3764_s_at 1929.7 P
35S ribosomal RNA
3765_s_at 2499.9 P
25S ribosomal RNA
3766_s_at 10957.5 P
25S ribosomal RNA
3767_s_at 1050.6 P
18S ribosomal RNA

3768_i_at	1873.8	P	5S ribosomal RNA
3769_s_at	1680.2	P	5S ribosomal RNA
3770_i_at	1818.5	P	5S ribosomal RNA
3771_f_at	10610.3	P	Ty1 LTR
3772_f_at	9408.7	P	Full length Ty1
3773_f_at	12632.1	P	Full length Ty1
3774_f_at	10323.1	P	Saccharomyces cerevisiae chromosome XII, complete chromosome sequence. Found reverse in NC_001144 between 476334 and 480296 with 100% identity.
3775_f_at	9919.9	P	Ty1 LTR
3776_i_at	-140.8	A	Ty1 LTR
3777_f_at	448.7	A	Ty1 LTR
3778_f_at	7386.3	P	Ty1 LTR
3779_f_at	10127.0	P	Saccharomyces cerevisiae chromosome XII, complete chromosome sequence. Found forward in NC_001144 between 594749 and 598706 with 100% identity.
3780_f_at	7604.3	P	Full length Ty1
3781_f_at	10687.8	P	Full length Ty1
3782_f_at	8061.0	P	Ty1 LTR
3783_at	178.7	A	Ty1 LTR
3784_at	-15.7	A	Ty4 LTR
3785_f_at	8565.8	P	Ty1 LTR
3786_s_at	13605.6	P	TY1B protein Found forward in NC_001144 between 652918 and 653385 with 100% identity.
3787_f_at	9560.1	P	Saccharomyces cerevisiae chromosome XII, complete chromosome sequence. Found forward in NC_001144 between 654177 and 656387 with 100% identity.
3788_f_at	14081.5	P	Saccharomyces cerevisiae chromosome XII, complete chromosome sequence. Found forward in NC_001144 between 654177 and 656387 with 100% identity.
3740_f_at	7741.9	P	Full length Ty1
3741_f_at	9729.3	P	Full length Ty1
3742_f_at	6702.6	P	Ty1 LTR
3743_f_at	5233.6	P	tRNA-Ala
3744_i_at	3226.7	P	Ty3 LTR

3745_f_at	1867.4	P	Ty3 LTR
3746_at	404.7	P	Ty1 LTR
3747_at	-52.2	A	Ty1 LTR
3748_i_at	1.0	A	Ty1 LTR
3749_r_at	16.0	A	Ty1 LTR
3750_f_at	178.6	P	Ty1 LTR
3751_f_at	7704.2	P	Ty2 LTR
3752_f_at	1587.9	P	Ty1 LTR
3753_s_at	645.0	P	tRNA-Ile
3754_s_at	2478.2	P	tRNA-Ser
3755_f_at	244.4	M	Ty3 LTR
3756_i_at	-17.3	A	Ty1 LTR
3757_f_at	5941.6	P	Ty1 LTR
3758_f_at	3508.9	P	tRNA-Glu
3759_f_at	3348.5	P	Ty1 LTR
3760_at	892.1	P	tRNA-Arg
3761_f_at	8764.7	P	Ty2 LTR
3762_s_at	7772.0	P	Saccharomyces cerevisiae chromosome XII, complete chromosome sequence. Found forward in NC_001144 between 941478 and 942778 with 100% identity.
3763_s_at	3637.4	P	Saccharomyces cerevisiae chromosome XII, complete chromosome sequence. Found forward in NC_001144 between 941478 and 942778 with 100% identity.
3717_s_at	12251.6	P	Saccharomyces cerevisiae chromosome XII, complete chromosome sequence. Found forward in NC_001144 between 942777 and 946791 with 100% identity.
3718_s_at	15314.5	P	Saccharomyces cerevisiae chromosome XII, complete chromosome sequence. Found forward in NC_001144 between 942777 and 946791 with 100% identity.
3719_s_at	9185.0	P	Saccharomyces cerevisiae chromosome XII, complete chromosome sequence. Found forward in NC_001144 between 942777 and 946791 with 100% identity.
3720_f_at	12727.2	P	Saccharomyces cerevisiae chromosome XII, complete chromosome sequence. Found forward in NC_001144 between 942777 and 946791 with 100% identity.
3721_s_at	9659.1	P	Full length Ty2
3722_s_at	10969.1	P	Full length Ty2

3723_f_at 11688.1 P
Full length Ty2
3724_f_at 7795.1 P
Ty2 LTR
3725_at 1209.4 P
Ty1 LTR
3726_f_at 5599.0 P
Ty2 LTR
3727_f_at 5348.6 P
Full length Ty2
3728_f_at 8988.2 P
Saccharomyces cerevisiae chromosome XII, complete chromosome sequence. Found reverse in NC_001144 between 976606 and 980109 with 100% identity.
3729_f_at 4374.5 P
Ty2 LTR
3730_at 739.8 P
Ty1 LTR
3731_s_at 1024.4 P
strong similarity to subtelomeric encoded proteins
3732_s_at 642.6 P
strong similarity to subtelomeric encoded proteins
3733_s_at 1562.8 P
strong similarity to subtelomeric encoded proteins
3734_s_at 3223.9 P
strong similarity to subtelomeric encoded proteins
3735_f_at 10353.2 P
strong similarity to subtelomeric encoded proteins
3736_s_at 1836.2 P
strong similarity to subtelomeric encoded proteins
3737_s_at 1527.7 P
strong similarity to subtelomeric encoded proteins
3738_s_at 10033.7 P
Protein with strong similarity to subtelomerically-encoded proteins such as Cos5p, Ybr302p, Cos3p, Cos1p, Cos4p, Cos8p, Cos6p, Cos9p (COS3 and YBR302C code for identical proteins)
3739_f_at 9531.5 P
Protein with strong similarity to subtelomerically-encoded proteins such as Cos5p, Ybr302p, Cos3p, Cos1p, Cos4p, Cos8p, Cos6p, Cos9p (COS3 and YBR302C code for identical proteins)
3695_f_at 1578.8 P
tRNA-Arg
3696_at 63.1 P
Ty1 LTR
3697_f_at 7801.6 P
Ty2 LTR
3698_f_at 747.6 P
tRNA-Gly
3699_f_at 11471.1 P
Ty1 LTR
3700_f_at 7504.1 P
Full length Ty1
3701_f_at 11282.7 P
Ty1 LTR
3702_f_at 9901.5 P
Ty1 LTR
3703_f_at 10450.8 P
Saccharomyces cerevisiae chromosome XIII, complete chromosome sequence. Found forward in NC_001145 between 197939 and 201896 with 100% identity.

3704_f_at	9596.2	P	Full length Ty1
3705_f_at	10349.4	P	Full length Ty1
3706_f_at	8364.3	P	Ty1 LTR
3707_f_at	3481.3	P	tRNA-Ser
3708_at	-68.3	A	Ty4 LTR
3709_f_at	2813.4	P	tRNA-Glu
3710_f_at	4210.9	P	tRNA-Ala
3711_f_at	8054.9	P	Ty1 LTR
3712_s_at	7906.3	P	Full length Ty1
3713_s_at	8947.2	P	Full length Ty1
3714_f_at	8279.8	P	Full length Ty1
3715_f_at	9585.0	P	Ty1 LTR
3716_f_at	1815.9	P	tRNA-His
3671_f_at	9072.2	P	Ty1 LTR
3672_f_at	8743.8	P	Full length Ty1
3673_f_at	9206.0	P	Ty1 LTR
3674_i_at	638.8	A	Ty1 LTR
3675_r_at	111.9	A	Ty1 LTR
3676_f_at	164.7	A	Ty1 LTR
3677_f_at	199.7	P	Ty1 LTR
3678_at	-24.0	A	Ty1 LTR
3679_at	69.6	A	Ty1 LTR
3680_i_at	-37.1	A	Ty1 LTR
3681_s_at	7.9	A	Ty1 LTR
3682_i_at	-27.4	A	Ty1 LTR
3683_f_at	170.3	P	Ty1 LTR
3684_f_at	1250.0	P	Ty4 LTR
3685_f_at	2743.5	P	Ty1 LTR

3686_f_at	137.1	P
Ty1 LTR		
3687_f_at	1587.4	P
tRNA-Arg		
3688_f_at	5367.6	P
tRNA-Ala		
3689_f_at	6315.2	P
Ty2 LTR		
3690_f_at	2246.5	P
tRNA-Gln		
3691_f_at	1651.2	P
Ty4 LTR		
3692_at	37.6	A
Ty1 LTR		
3693_f_at	171.1	P
Ty1 LTR		
3694_at	52.9	A
strong similarity to subtelomeric encoded proteins		
3646_s_at	324.0	P
strong similarity to subtelomeric encoded proteins		
3647_f_at	847.5	P
strong similarity to subtelomeric encoded proteins		
3648_f_at	9806.6	P
Protein with similarity to subtelomerically-encoded proteins such as Cos5p, Ybr302p, Cos3p, Cos1p, Cos4p, Cos8p, Cos6p, Cos9p		
3649_f_at	361.5	A
tRNA-Gly		
3650_f_at	2061.5	P
Ty4 LTR		
3651_f_at	9727.2	P
Ty1 LTR		
3652_f_at	8918.3	P
Full length Ty1		
3653_f_at	10013.2	P
Ty1 LTR		
3654_i_at	42.4	A
Ty3 LTR		
3655_f_at	-7.6	A
Ty3 LTR		
3656_f_at	6645.0	P
Ty1 LTR		
3657_f_at	9013.8	P
Saccharomyces cerevisiae chromosome XIV, complete chromosome sequence. Found forward in NC_001146 between 520758 and 524702 with 100% identity.		
3658_f_at	8619.2	P
Full length Ty1		
3659_f_at	7659.0	P
Full length Ty1		
3660_f_at	6562.7	P
Ty1 LTR		
3661_at	2997.9	P
Ty3 LTR		
3662_f_at	7875.5	P
Ty3 LTR		
3663_f_at	1256.1	P
Ty4 LTR		

3664_f_at	7903.5	P	Ty2 LTR
3665_f_at	9039.0	P	Full length Ty2
3666_f_at	8793.4	P	Saccharomyces cerevisiae chromosome XIV, complete chromosome sequence. Found reverse in NC_001146 between 562383 and 566402 with 100% identity.
3667_f_at	8466.7	P	Ty2 LTR
3668_f_at	5144.4	P	tRNA-Pro
3669_f_at	5446.1	P	Ty1 LTR
3670_f_at	773.1	P	Ty4 LTR
3621_i_at	-37.1	A	Ty3 LTR
3622_f_at	8951.4	P	Ty3 LTR
3623_f_at	7678.0	P	Ty1 LTR
3624_at	1384.5	P	Ty1 LTR
3625_at	588.0	P	Protein with strong similarity to subtelomerically-encoded proteins such as Cos5p, Ybr302p, Cos3p, Cos1p, Cos4p, Cos8p, Cos6p, Cos9p
3626_i_at	988.9	P	Protein with strong similarity to subtelomerically-encoded proteins such as Cos5p, Ybr302p, Cos3p, Cos1p, Cos4p, Cos8p, Cos6p, Cos9p
3627_r_at	753.7	P	Protein with strong similarity to subtelomerically-encoded proteins such as Cos5p, Ybr302p, Cos3p, Cos1p, Cos4p, Cos8p, Cos6p, Cos9p
3628_f_at	80.4	A	Protein with strong similarity to subtelomerically-encoded proteins such as Cos5p, Ybr302p, Cos3p, Cos1p, Cos4p, Cos8p, Cos6p, Cos9p
3629_f_at	410.4	A	strong similarity to subtelomeric encoded proteins
3630_at	17.1	A	Ty1 LTR
3631_s_at	1256.3	P	Ty4 LTR
3632_at	-34.5	A	Ty1 LTR
3633_f_at	248.7	M	tRNA-Gly
3634_f_at	520.4	P	Ty1 LTR
3635_f_at	10017.7	P	Ty1 LTR
3636_f_at	10695.2	P	Saccharomyces cerevisiae chromosome XV, complete chromosome sequence. Found forward in NC_001147 between 119305 and 123267 with 100% identity.
3637_f_at	9078.4	P	Full length Ty1
3638_f_at	10354.5	P	Full length Ty1

3639_f_at	11639.9	P	Ty1 LTR
3640_f_at	557.5	P	tRNA-Gly
3641_f_at	50.5	A	Ty3 LTR
3642_at	-78.7	A	Ty1 LTR
3643_i_at	-851.2	A	Ty1 LTR
3644_f_at	1103.2	P	Ty1 LTR
3645_f_at	290.4	P	tRNA-Gly
3597_at	-17.6	A	Ty1 LTR
3598_f_at	4421.7	P	tRNA-Arg
3599_at	-92.6	A	Ty1 LTR
3600_i_at	-261.5	A	Ty3 LTR
3601_f_at	61.6	A	Ty3 LTR
3602_at	163.8	A	Ty1 LTR
3603_at	194.3	P	Ty1 LTR
3604_f_at	173.6	A	tRNA-Gly
3605_f_at	62.5	P	Ty1 LTR
3606_f_at	8613.6	P	Ty1 LTR
3607_f_at	6299.1	P	Full length Ty1
3608_f_at	9531.9	P	Ty1 LTR
3609_i_at	42.0	A	Ty1 LTR
3610_f_at	132.3	A	Ty1 LTR
3611_f_at	113.0	A	Ty1 LTR
3612_f_at	8338.3	P	Ty2 LTR
3613_i_at	165.8	A	Ty1 LTR
3614_f_at	121.0	A	Ty1 LTR
3615_i_at	-36.6	A	Ty1 LTR
3616_f_at	188.3	P	Ty1 LTR
3617_f_at	1433.8	P	Ty4 LTR

3618_f_at 6889.7 P
Ty2 LTR
3619_f_at 9171.8 P
Full length Ty2
3620_f_at 11433.0 P
Saccharomyces cerevisiae chromosome XV, complete chromosome sequence. Found reverse in NC_001147 between 704417 and 708436 with 100% identity.
3572_f_at 6652.0 P
Ty2 LTR
3573_f_at 1340.0 P
Ty4 LTR
3574_f_at 2391.0 P
tRNA-Ala
3575_f_at 6027.3 P
Ty3 LTR
3576_f_at 1223.3 A
Ty3 LTR
3577_at 143.3 P
Ty1 LTR
3578_f_at 5596.5 P
Ty2 LTR
3579_f_at 10784.4 P
Saccharomyces cerevisiae chromosome XV, complete chromosome sequence. Found forward in NC_001147 between 971863 and 975882 with 100% identity.
3580_f_at 10731.4 P
Full length Ty2
3581_f_at 5600.8 P
Ty2 LTR
3582_f_at 7062.3 P
Ty1 LTR
3583_i_at 382.2 P
Ty1 LTR
3584_f_at 88.5 P
Ty1 LTR
3585_f_at -5.7 A
Ty3 LTR
3586_f_at 8766.1 P
Ty1 LTR
3587_f_at 9770.2 P
Saccharomyces cerevisiae chromosome XVI, complete chromosome sequence. Found forward in NC_001148 between 58054 and 62016 with 100% identity.
3588_f_at 9409.6 P
Full length Ty1
3589_f_at 11363.2 P
Full length Ty1
3590_f_at 9021.3 P
Ty1 LTR
3591_f_at 5201.7 P
Ty2 LTR
3592_i_at -1031.3 A
Ty1 LTR
3593_f_at 2073.8 P
Ty1 LTR
3594_f_at 3295.6 P
tRNA-Glu
3595_at -20.1 A

Ty1 LTR
3596_f_at 5901.1 P
Ty2 LTR
3548_s_at 1728.9 P
tRNA-Cys
3549_f_at 44.2 A
Ty1 LTR
3550_i_at -58.9 A
Ty1 LTR
3551_f_at 1119.1 A
Ty1 LTR
3552_f_at -26.7 A
Ty1 LTR
3553_f_at 1423.6 P
Ty4 LTR
3554_f_at 1875.9 P
Full length Ty4
3555_s_at 287.3 P
Saccharomyces cerevisiae chromosome XVI, complete chromosome sequence. Found reverse in NC_001148 between 437328 and 439490 with 100% identity.
3556_s_at 244.5 A
Saccharomyces cerevisiae chromosome XVI, complete chromosome sequence. Found reverse in NC_001148 between 437328 and 439490 with 100% identity.
3557_s_at 19.9 A
Saccharomyces cerevisiae chromosome XVI, complete chromosome sequence. Found reverse in NC_001148 between 439423 and 442737 with 100% identity.
3558_f_at 1245.8 P
Ty4 LTR
3559_f_at 10391.7 P
Ty1 LTR
3560_at 244.0 P
Ty1 LTR
3561_f_at -157.8 P
tRNA-Gly
3562_f_at 2726.1 P
tRNA-Ser
3563_s_at 438.5 P
tRNA-Thr
3564_f_at 9704.1 P
Ty3 LTR
3565_at 187.5 A
Ty1 LTR
3566_i_at 50.7 A
Ty1 LTR
3567_r_at 13.5 A
Ty1 LTR
3568_f_at 1317.6 P
Ty1 LTR
3569_at 296.0 P
Ty1 LTR
3570_f_at 1039.5 P
Ty1 LTR
3571_f_at 6471.6 P
Ty1 LTR
3524_f_at 6454.7 P
Full length Ty1

3525_f_at 10461.3 P
Full length Ty1
3526_f_at 10111.0 P
Saccharomyces cerevisiae chromosome XVI, complete chromosome sequence. Found reverse in NC_001148 between 804996 and 808958 with 100% identity.
3527_f_at 7065.2 P
Ty1 LTR
3528_f_at 9140.7 P
Ty1 LTR
3529_f_at 10110.6 P
Full length Ty3
3530_f_at 9668.8 P
Ty1 LTR
3531_at 263.2 P
Ty1 LTR
3532_f_at 12466.7 P
Ty1 LTR
3533_f_at 10519.2 P
Full length Ty1
3534_f_at 10767.4 P
Ty1 LTR
3535_i_at 98.0 P
Ty3 LTR
3536_f_at 7229.8 P
Ty3 LTR
3537_f_at 6001.0 P
tRNA-Ala
3538_f_at 876.4 P
tRNA-Gly
3539_f_at 3186.5 P
Ty3 LTR
3540_at 62.7 P
Ty4 LTR
3541_at 418.0 A
Ty4 LTR
3542_f_at 7847.3 P
strong similarity to subtelomeric encoded proteins
3543_s_at 9480.8 P
strong similarity to subtelomeric encoded proteins
3544_at 41.3 A
strong similarity to subtelomeric encoded proteins
3545_i_at 73.1 P
Ty1 LTR
3546_f_at -51.5 A
Ty1 LTR
3547_f_at 3594.4 P
Ty2 LTR
3500_f_at -89.5 A
Ty1 LTR
3501_f_at 3855.3 P
Ty2 LTR
3502_f_at 10525.5 P
Saccharomyces cerevisiae chromosome II, complete chromosome sequence. Found forward in NC_001134 between 31221 and 35240 with 100% identity.
3503_f_at 4950.5 P
Full length Ty2

3504_f_at	3945.1	P
Ty2 LTR		
3505_s_at	1146.5	A
Ty1 LTR		
3506_s_at	1396.8	P
Ty4 LTR		
3507_at	53.0	A
Ty1 LTR		
3508_f_at	-375.0	P
tRNA-Gly		
3509_f_at	5434.9	P
Ty3 LTR		
3510_s_at	397.6	P
Ty1 LTR		
3511_f_at	8861.6	P
Ty1 LTR		
3512_f_at	8898.7	P
Full length Ty1		
3513_f_at	9844.1	P
Ty1 LTR		
3514_f_at	3543.9	P
tRNA-Ser		
3515_at	522.6	P
Ty1 LTR		
3516_f_at	8032.7	P
Ty1 LTR		
3517_f_at	6829.8	P
Full length Ty1		
3518_f_at	7751.2	P
Ty1 LTR		
3519_f_at	-9.0	A
Ty1 LTR		
3520_s_at	1829.9	P
tRNA-Val		
3521_i_at	7.9	A
Ty1 LTR		
3522_f_at	2039.5	P
Ty1 LTR		
3523_at	357.4	A
Ty1 LTR		
3477_at	-34.9	A
Ty1 LTR		
3478_f_at	8951.2	P
tRNA-Gln		
3479_f_at	1694.0	P
tRNA-Arg		
3480_at	-19.4	A
Ty1 LTR		
3481_at	236.9	P
Ty1 LTR		
3482_f_at	3002.1	P
tRNA-Glu		
3483_f_at	8822.3	P
Protein with similarity to members of the Cos3\/Cos5\/Cos1\/Cos4\/Cos8\/Cos6\/Cos9 family, coded from subtelomeric region		
3484_f_at	39.3	A

Ty5 LTR		
3485_at	-373.5	A
Full length Ty5		
3486_at	75.0	A
Full length Ty5		
3487_g_at	202.4	A
Full length Ty5		
3488_at	68.5	A
Full length Ty5		
3489_f_at	-53.7	A
Full length Ty5		
3490_f_at	-5.4	A
Ty5 LTR		
3491_f_at	2724.6	P
tRNA-Glu		
3492_f_at	1764.6	P
Ty1 LTR		
3493_f_at	3363.0	P
Ty1 LTR		
3494_f_at	6090.2	P
Ty1 LTR		
3495_f_at	1122.0	P
Ty1 LTR		
3496_f_at	7569.7	P
Ty2 LTR		
3497_f_at	10368.4	P
Saccharomyces cerevisiae chromosome III, complete chromosome sequence. Found forward in NC_001135 between 86005 and 90030 with 100% identity.		
3498_f_at	12074.9	P
Full length Ty2		
3499_f_at	7613.4	P
Ty2 LTR		
3451_f_at	4588.8	P
tRNA-Pro		
3452_f_at	7463.6	P
Ty1 LTR		
3453_at	216.1	P
strong similarity to subtelomeric encoded proteins		
3454_s_at	707.6	P
tRNA-Asn		
3455_f_at	390.0	P
tRNA-Gly		
3456_i_at	16.5	A
Ty1 LTR		
3457_f_at	4441.0	P
Ty1 LTR		
3458_f_at	689.9	P
Ty1 LTR		
3459_at	213.4	A
Ty1 LTR		
3460_at	61.7	A
Ty4 LTR		
3461_f_at	8424.3	P
Ty1 LTR		
3462_f_at	7205.3	P
tRNA-Gln		

3463_at	286.7	P	Ty1 LTR
3464_at	453.5	P	Ty1 LTR
3465_at	35.6	A	Ty5 LTR
3466_i_at	24.1	A	Ty1 LTR
3467_f_at	3912.7	P	Ty1 LTR
3468_i_at	-72.1	A	Ty1 LTR
3469_f_at	-11.5	A	Ty1 LTR
3470_i_at	1922.9	P	Protein with strong similarity to other subtelomerically-encoded proteins such as Cos5p, Ybr302p, Cos3p, Cos1p, Cos4p, Cos8p, Cos6p, Cos9p
3471_f_at	3673.5	P	Protein with strong similarity to other subtelomerically-encoded proteins such as Cos5p, Ybr302p, Cos3p, Cos1p, Cos4p, Cos8p, Cos6p, Cos9p
3472_f_at	444.3	P	tRNA-Gly
3473_f_at	4625.4	P	tRNA-Ala
3474_f_at	1665.3	P	Ty1 LTR
3475_f_at	1403.5	P	Ty4 LTR
3476_f_at	3282.6	P	tRNA-Ser
3427_at	131.3	M	Ty1 LTR
3428_f_at	3455.5	P	Ty1 LTR
3429_f_at	7561.1	P	Ty2 LTR
3430_f_at	11873.6	P	Full length Ty2
3431_f_at	10763.3	P	Saccharomyces cerevisiae chromosome IV, complete chromosome sequence. Found reverse in NC_001136 between 514037 and 518056 with 100% identity.
3432_f_at	6531.0	P	Ty2 LTR
3433_i_at	74.3	P	Ty1 LTR
3434_f_at	299.1	P	Ty1 LTR
3435_f_at	2562.7	P	Ty1 LTR
3436_f_at	5976.6	P	tRNA-Gln
3437_f_at	1393.0	P	tRNA-Arg
3438_f_at	4402.9	P	tRNA-Arg
3439_f_at	6360.8	P	

tRNA-Gln
3440_f_at 7049.4 P
Ty1 LTR
3441_f_at 8028.9 P
Full length Ty1
3442_f_at 10281.3 P
Full length Ty1
3443_f_at 11848.4 P
Saccharomyces cerevisiae chromosome IV, complete chromosome sequence. Found reverse in NC_001136 between 645851 and 649813 with 100% identity.
3444_f_at 7539.9 P
Ty1 LTR
3445_f_at 1700.1 P
Ty3 LTR
3446_i_at -108.7 A
Ty1 LTR
3447_f_at 448.8 A
Ty1 LTR
3448_s_at 2976.4 P
Ty3 LTR
3449_i_at 183.6 P
Ty1 LTR
3450_r_at 1.9 A
Ty1 LTR
3404_f_at 2608.7 P
Ty1 LTR
3405_f_at 7590.3 P
tRNA-Gln
3406_f_at 9339.9 P
Ty1 LTR
3407_at 469.0 P
Saccharomyces cerevisiae chromosome IV, complete chromosome sequence. Found forward in NC_001136 between 804494 and 805681 with 100% identity.
3408_f_at 5926.5 P
Ty1 LTR
3409_f_at 14410.6 P
Saccharomyces cerevisiae chromosome IV, complete chromosome sequence. Found forward in NC_001136 between 873398 and 877417 with 100% identity.
3410_f_at 4913.9 P
Full length Ty2
3411_f_at 5294.0 P
Ty1 LTR
3412_f_at 8605.8 P
Full length Ty1
3413_f_at 10674.3 P
Full length Ty1
3414_f_at 10202.5 P
Saccharomyces cerevisiae chromosome IV, complete chromosome sequence. Found reverse in NC_001136 between 878651 and 882613 with 100% identity.
3415_i_at 18.6 A
Ty1 LTR
3416_s_at 4654.9 P
Ty1 LTR
3417_f_at 5245.8 P
Ty3 LTR
3418_f_at 3370.3 P

tRNA-Ser
3419_f_at 4915.5 P
Ty1 LTR
3420_f_at 11823.8 P
Saccharomyces cerevisiae chromosome IV, complete chromosome sequence. Found forward in NC_001136 between 982747 and 986766 with 100% identity.
3421_f_at 8882.5 P
Full length Ty2
3422_f_at 7409.0 P
Ty1 LTR
3423_f_at 7107.1 P
Ty1 LTR
3424_f_at 7558.8 P
Full length Ty1
3425_f_at 8582.3 P
Full length Ty1
3426_f_at 7796.1 P
Saccharomyces cerevisiae chromosome IV, complete chromosome sequence. Found reverse in NC_001136 between 987525 and 991034 with 100% identity.
3379_f_at 6404.8 P
Ty1 LTR
3380_i_at 111.3 P
Ty3 LTR
3381_f_at 17.3 A
Ty3 LTR
3382_f_at -160.1 P
tRNA-Gly
3383_f_at 1705.6 P
tRNA-Glu
3384_f_at 5854.5 P
Ty3 LTR
3385_s_at 3944.3 P
tRNA-Val
3386_f_at 10120.9 P
Ty1 LTR
3387_f_at 6633.6 P
Full length Ty1
3388_f_at 10789.3 P
Ty1 LTR
3389_f_at 4182.7 P
Ty1 LTR
3390_at 157.5 A
Ty3 LTR
3391_f_at 4260.0 P
Ty1 LTR
3392_f_at 10365.5 P
Ty1 LTR
3393_f_at 13480.2 P
Saccharomyces cerevisiae chromosome IV, complete chromosome sequence. Found forward in NC_001136 between 1208292 and 1212254 with 100% identity.
3394_f_at 7660.6 P
Full length Ty1
3395_f_at 10741.0 P
Full length Ty1
3396_f_at 8397.2 P
Ty1 LTR

3397_f_at 389.9 A
tRNA-Gly
3398_f_at 1765.4 P
tRNA-Ser
3399_f_at 5585.2 P
Ty1 LTR
3400_i_at 52.4 P
Ty1 LTR
3401_f_at -20.0 A
Ty1 LTR
3402_at 3.1 A
Ty1 LTR
3403_f_at 1555.6 P
strong similarity to subtelomeric encoded proteins
3356_f_at 672.7 P
strong similarity to subtelomeric encoded proteins
3357_at 241.8 P
strong similarity to subtelomeric encoded proteins
3358_f_at -582.1 P
tRNA-Gly
3359_f_at 7405.4 P
Ty1 LTR
3360_at -42.9 A
Ty1 LTR
3361_f_at 3164.0 P
tRNA-Ser
3362_at -79.9 A
Ty1 LTR
3363_at -157.4 A
Ty4 LTR
3364_f_at 6291.9 P
tRNA-Gln
3365_f_at 7321.1 P
Ty1 LTR
3366_at 16.0 A
Ty1 LTR
3367_f_at 1377.3 P
Ty1 LTR
3368_f_at 1426.3 P
tRNA-Arg
3369_i_at 2.1 A
Ty1 LTR
3370_f_at 475.0 P
Ty1 LTR
3371_f_at 2983.8 P
tRNA-Glu
3372_f_at 1968.9 P
tRNA-His
3373_at 463.4 P
Ty1 LTR
3374_at 291.0 P
Ty1 LTR
3375_f_at 7325.5 P
Ty3 LTR
3376_f_at 7034.3 P
tRNA-Gln

3377_at	86.8	A	Ty1 LTR
3378_f_at	3737.5	P	tRNA-Ser
3332_i_at	-43.8	A	Ty1 LTR
3333_f_at	4749.8	P	Ty1 LTR
3334_at	75.0	P	Ty1 LTR
3335_at	90.6	A	Ty1 LTR
3336_f_at	1325.5	P	Ty4 LTR
3337_i_at	539.8	P	Ty3 LTR
3338_f_at	-50.2	A	Ty3 LTR
3340_f_at	7677.3	P	Ty1 LTR
3342_f_at	7330.1	P	Ty3 LTR
3343_i_at	1368.0	P	Ty1 LTR
3344_f_at	2066.2	P	Ty1 LTR
3345_f_at	2360.2	P	Ty1 LTR
3346_at	300.4	M	Ty4 LTR
3347_s_at	2173.0	P	Ty1 LTR
3348_f_at	6241.2	P	Ty1 LTR
3350_f_at	9958.5	P	Full length Ty1
3352_s_at	7724.3	P	Ty1 LTR
3354_s_at	281.3	P	Ty1 LTR
3355_s_at	651.8	P	Ty1 LTR
3307_s_at	200.3	P	Ty1 LTR
3308_s_at	950.4	P	Ty1 LTR
3309_s_at	-15.8	P	Ty1 LTR
3310_s_at	827.1	P	Ty1 LTR
3311_f_at	6791.5	P	Ty1 LTR
3313_f_at	4088.6	P	Ty1 LTR
3315_f_at	12073.4	P	Ty3 LTR

3316_f_at	13770.9	P	Ty3 LTR
3317_f_at	12823.3	P	Ty1 LTR
3319_f_at	13295.4	P	Ty1 LTR
3320_i_at	-109.5	A	Ty1 LTR
3321_f_at	159.9	A	Ty1 LTR
3322_at	-16.9	A	Ty1 LTR
3323_i_at	-292.4	A	Ty5 LTR
3324_at	140.0	A	Ty5 LTR
3325_f_at	1413.6	P	strong similarity to subtelomeric encoded proteins
3326_at	276.3	A	strong similarity to subtelomeric encoded proteins
3327_f_at	10106.1	P	Protein with strong similarity to subtelomerically-encoded proteins such as Cos5p, Ybr302p, Cos3p, Cos1p, Cos4p, Cos8p, Cos6p, Cos9p
3328_at	36.5	A	Ty1 LTR
3329_f_at	3456.8	P	Ty1 LTR
3330_f_at	7260.5	P	Ty2 LTR
3283_f_at	11290.1	P	Saccharomyces cerevisiae chromosome VI, complete chromosome sequence. Found forward in NC_001138 between 139492 and 143511 with 100% identity.
3284_f_at	9401.4	P	Full length Ty2
3285_f_at	5323.3	P	Ty2 LTR
3286_f_at	2195.3	P	Ty1 LTR
3287_s_at	192.6	P	Ty4 LTR
3288_at	9.9	A	Ty1 LTR
3289_i_at	123.5	P	Ty1 LTR
3290_f_at	213.9	P	Ty1 LTR
3291_f_at	2866.8	P	Ty1 LTR
3294_at	-26.6	A	Ty1 LTR
3296_at	-18.7	A	Ty1 LTR
3297_i_at	-113.6	A	Ty5 LTR
3298_f_at	-89.2	A	

Ty5 LTR		
3299_f_at	32.3	A
strong similarity to subtelomeric encoded proteins		
3301_f_at	1133.7	P
Ty4 LTR		
3302_f_at	5746.7	P
Ty1 LTR		
3303_f_at	745.3	P
Ty1 LTR		
3304_f_at	554.6	P
Ty1 LTR		
3305_at	-93.5	A
Ty4 LTR		
3306_i_at	1011.3	P
Ty1 LTR		
3258_f_at	929.5	P
Ty1 LTR		
3259_at	3514.2	P
Ty1 LTR		
3260_f_at	7744.2	P
Ty3 LTR		
3262_at	-18.2	A
Ty4 LTR		
3263_i_at	61.9	P
Ty1 LTR		
3264_f_at	184.2	P
Ty1 LTR		
3267_f_at	3030.6	P
Ty3 LTR		
3268_f_at	10070.6	P
Ty1 LTR		
3269_f_at	1301.1	P
Ty1 LTR		
3270_f_at	6408.6	P
Ty1 LTR		
3271_i_at	131.1	P
Ty3 LTR		
3272_f_at	3985.8	P
Ty3 LTR		
3274_at	107.4	A
Ty1 LTR		
3276_i_at	8.9	A
Ty1 LTR		
3277_f_at	80.6	A
Ty1 LTR		
3279_f_at	6805.0	P
Full length Ty1		
3235_f_at	6680.2	P
Ty1 LTR		
3236_f_at	7932.8	P
Full length Ty1		
3237_f_at	10797.1	P
Full length Ty1		
3239_f_at	9301.8	P
Ty1 LTR		
3240_f_at	7602.4	P

Ty2 LTR
3241_f_at 7634.1 P
Full length Ty2
3243_at 1123.6 P
tRNA-Leu
3244_i_at 52.7 P
Ty1 LTR
3245_f_at 367.0 P
Ty1 LTR
3247_s_at 627.8 P
TY3B protein Found forward in NC_001139 between 707604 and 708461 with 100% identity.
3248_s_at 1761.0 P
Saccharomyces cerevisiae chromosome VII, complete chromosome sequence. Found forward in NC_001139 between 708460 and 712248 with 100% identity.
3249_s_at 3407.2 P
Saccharomyces cerevisiae chromosome VII, complete chromosome sequence. Found forward in NC_001139 between 708460 and 712248 with 100% identity.
3250_s_at 1238.4 P
Saccharomyces cerevisiae chromosome VII, complete chromosome sequence. Found forward in NC_001139 between 708460 and 712248 with 100% identity.
3251_s_at 266.1 P
Full length Ty3
3252_s_at 2299.8 P
Full length Ty3
3253_f_at 9162.0 P
Full length Ty3
3255_at 838.0 P
Ty1 LTR
3256_at 7.9 A
Ty1 LTR
3257_f_at 7014.4 P
Ty3 LTR
3212_f_at 1126.4 P
Ty1 LTR
3214_at 207.0 P
Ty1 LTR
3215_f_at 139.0 P
Ty1 LTR
3216_at -100.8 A
Ty1 LTR
3218_at -21.0 A
Ty1 LTR
3222_f_at 9280.1 P
Full length Ty2
3223_f_at 7518.0 P
Ty2 LTR
3225_f_at 7932.9 P
Full length Ty1
3226_f_at 9420.2 P
Ty1 LTR
3228_at 246.6 P
Ty3 LTR
3230_f_at 5149.1 P
Ty1 LTR
3232_f_at 1919.3 P
Ty4 LTR

3233_f_at	11269.2	P	Ty1 LTR
3234_at	7182.8	P	Protein with strong similarity to other subtelomerically-encoded proteins such as Cos5p, Ybr302p, Cos3p, Cos1p, Cos4p, Cos8p, Cos6p, Cos9p
3187_s_at	4106.0	P	strong similarity to subtelomeric encoded proteins
3188_at	1071.9	P	Protein with similarity to subtelomerically-encoded proteins such as Cos5p, Ybr302p, Cos3p, Cos1p, Cos4p, Cos8p, Cos6p, Cos9p
3189_i_at	-399.1	A	Protein with similarity to subtelomerically-encoded proteins such as Cos5p, Ybr302p, Cos3p, Cos1p, Cos4p, Cos8p, Cos6p, Cos9p
3190_f_at	250.2	P	Protein with similarity to subtelomerically-encoded proteins such as Cos5p, Ybr302p, Cos3p, Cos1p, Cos4p, Cos8p, Cos6p, Cos9p
3191_i_at	39.6	P	Ty5 LTR
3192_f_at	-66.1	A	Ty5 LTR
3193_at	1357.4	A	strong similarity to subtelomeric encoded proteins
3195_f_at	8644.7	P	Ty3 LTR
3196_f_at	1108.4	P	Ty4 LTR
3199_f_at	6181.9	P	Ty1 LTR
3200_i_at	52.0	M	Ty1 LTR
3201_r_at	3.2	A	Ty1 LTR
3202_f_at	-24.1	A	Ty1 LTR
3203_f_at	10111.7	P	Ty1 LTR
3204_at	375.7	M	Ty1 LTR
3206_at	-0.2	A	Ty1 LTR
3207_i_at	109.3	A	Ty1 LTR
3208_f_at	55.1	A	Ty1 LTR
3209_f_at	7479.6	P	Ty1 LTR
3161_f_at	5357.9	P	Ty3 LTR
3162_at	1022.1	P	Ty4 LTR
3163_i_at	50.5	A	Ty1 LTR
3164_f_at	71.4	A	Ty1 LTR
3165_at	-18.8	A	Ty4 LTR

3166_i_at 33.3 A
Ty1 LTR
3167_r_at 65.1 P
Ty1 LTR
3168_f_at 14.9 A
Ty1 LTR
3169_f_at 9855.3 P
Ty2 LTR
3170_i_at 42.2 A
Ty1 LTR
3171_r_at 23.1 A
Ty1 LTR
3172_f_at 214.2 A
Ty1 LTR
3173_i_at 21.6 M
Ty1 LTR
3174_f_at 36.6 A
Ty1 LTR
3175_i_at 343.8 P
Ty1 LTR
3176_f_at 1342.6 P
Ty1 LTR
3177_f_at 364.1 P
Ty3 LTR
3178_f_at 63.7 P
Ty1 LTR
3180_f_at 9190.2 P
Full length Ty1
3181_f_at 11436.8 P
Ty1 LTR
3182_i_at 63.7 A
strong similarity to subtelomeric encoded YDR544c
3183_f_at 10113.7 P
strong similarity to subtelomeric encoded proteins
3184_s_at 248.8 P
strong similarity to subtelomeric encoded proteins
3185_s_at 99.8 P
strong similarity to subtelomeric encoded proteins
3133_f_at 3995.5 P
Ty1 LTR
3136_s_at 4036.3 P
Saccharomyces cerevisiae chromosome IX, complete chromosome sequence. Found forward in NC_001141 between 206488 and 210129 with 100% identity.
3137_s_at 1616.0 P
Full length Ty3
3139_f_at 159.0 P
Ty2 LTR
3141_i_at 30.6 A
Ty1 LTR
3142_f_at 5081.4 P
Ty1 LTR
3143_f_at 1085.2 P
Ty3 LTR
3144_f_at 1667.5 P
Ty1 LTR
3145_at 376.1 P

Ty1 LTR
3147_at -19.6 A
Ty1 LTR
3148_s_at 4903.5 P
mating hormone a2
3149_at 923.8 P
Saccharomyces cerevisiae chromosome I, complete chromosome sequence. Found forward in NC_001133 between 13744 and 14743 with 100% identity.
3150_at 1468.0 P
Saccharomyces cerevisiae chromosome I, complete chromosome sequence. Found forward in NC_001133 between 14744 and 15743 with 100% identity.
3151_g_at 577.5 P
Saccharomyces cerevisiae chromosome I, complete chromosome sequence. Found forward in NC_001133 between 14744 and 15743 with 100% identity.
3152_at 2712.3 P
Saccharomyces cerevisiae chromosome I, complete chromosome sequence. Found forward in NC_001133 between 15744 and 16743 with 100% identity.
3153_at 62.9 P
Saccharomyces cerevisiae chromosome I, complete chromosome sequence. Found forward in NC_001133 between 16744 and 17743 with 100% identity.
3154_at 442.7 P
Saccharomyces cerevisiae chromosome I, complete chromosome sequence. Found forward in NC_001133 between 17744 and 18743 with 100% identity.
3155_at -620.5 A
Saccharomyces cerevisiae chromosome I, complete chromosome sequence. Found forward in NC_001133 between 18744 and 19729 with 100% identity.
3156_at 43.8 A
Saccharomyces cerevisiae chromosome I, complete chromosome sequence. Found forward in NC_001133 between 88357 and 89356 with 100% identity.
3157_at 206.4 P
Saccharomyces cerevisiae chromosome I, complete chromosome sequence. Found forward in NC_001133 between 89357 and 90356 with 100% identity.
3158_at 267.4 P
Saccharomyces cerevisiae chromosome I, complete chromosome sequence. Found forward in NC_001133 between 90357 and 91356 with 100% identity.
3159_at 438.3 A
Saccharomyces cerevisiae chromosome I, complete chromosome sequence. Found forward in NC_001133 between 91357 and 92356 with 100% identity.
3088_at 52.9 A
Saccharomyces cerevisiae chromosome I, complete chromosome sequence. Found forward in NC_001133 between 92357 and 93356 with 100% identity.
3089_g_at 498.9 A
Saccharomyces cerevisiae chromosome I, complete chromosome sequence. Found forward in NC_001133 between 92357 and 93356 with 100% identity.
3090_s_at -119.9 A
Saccharomyces cerevisiae chromosome I, complete chromosome sequence. Found forward in NC_001133 between 93357 and 93988 with 100% identity.
3091_at -231.6 A
Saccharomyces cerevisiae chromosome I, complete chromosome sequence. Found forward in NC_001133 between 159789 and 160788 with 100% identity.
3092_f_at -33.6 A
Saccharomyces cerevisiae chromosome I, complete chromosome sequence. Found forward in NC_001133 between 160789 and 161788 with 100% identity.
3093_f_at -98.9 P
Saccharomyces cerevisiae chromosome I, complete chromosome sequence. Found forward in NC_001133 between 161789 and 162788 with 100% identity.

3096_f_at 133.5 P
Saccharomyces cerevisiae chromosome I, complete chromosome sequence. Found forward in NC_001133 between 164789 and 165788 with 100% identity.
3097_at 88.9 A
Saccharomyces cerevisiae chromosome I, complete chromosome sequence. Found forward in NC_001133 between 165789 and 166468 with 100% identity.
3098_at 434.5 A
Saccharomyces cerevisiae chromosome I, complete chromosome sequence. Found forward in NC_001133 between 208649 and 209648 with 100% identity.
3099_at 130.3 P
Saccharomyces cerevisiae chromosome I, complete chromosome sequence. Found forward in NC_001133 between 209649 and 210648 with 100% identity.
3100_s_at 702.0 P
Saccharomyces cerevisiae chromosome I, complete chromosome sequence. Found forward in NC_001133 between 210649 and 211648 with 100% identity.
3101_at 199.8 A
Saccharomyces cerevisiae chromosome I, complete chromosome sequence. Found forward in NC_001133 between 211649 and 212648 with 100% identity.
3102_s_at 228.4 P
Saccharomyces cerevisiae chromosome I, complete chromosome sequence. Found forward in NC_001133 between 212649 and 213648 with 100% identity.
3103_at 85.3 P
Saccharomyces cerevisiae chromosome I, complete chromosome sequence. Found forward in NC_001133 between 213649 and 214648 with 100% identity.
3104_at 69.8 P
Saccharomyces cerevisiae chromosome I, complete chromosome sequence. Found forward in NC_001133 between 214649 and 215648 with 100% identity.
3105_g_at 205.4 A
Saccharomyces cerevisiae chromosome I, complete chromosome sequence. Found forward in NC_001133 between 214649 and 215648 with 100% identity.
3106_s_at 287.2 A
Saccharomyces cerevisiae chromosome I, complete chromosome sequence. Found forward in NC_001133 between 215649 and 216648 with 100% identity.
3107_s_at 3417.3 A
Saccharomyces cerevisiae chromosome I, complete chromosome sequence. Found forward in NC_001133 between 216649 and 217143 with 100% identity.
3108_at 62.9 A
Saccharomyces cerevisiae chromosome X, complete chromosome sequence. Found forward in NC_001142 between 9138 and 10137 with 100% identity.
3109_at -442.1 A
Saccharomyces cerevisiae chromosome X, complete chromosome sequence. Found forward in NC_001142 between 10138 and 11137 with 100% identity.
3110_s_at -376.2 A
Saccharomyces cerevisiae chromosome X, complete chromosome sequence. Found forward in NC_001142 between 11138 and 12137 with 100% identity.
3111_s_at 149.2 P
Saccharomyces cerevisiae chromosome X, complete chromosome sequence. Found forward in NC_001142 between 12138 and 13137 with 100% identity.
3112_s_at 14.5 A
Saccharomyces cerevisiae chromosome X, complete chromosome sequence. Found forward in NC_001142 between 13138 and 14137 with 100% identity.
3113_s_at 1345.9 P
Saccharomyces cerevisiae chromosome X, complete chromosome sequence. Found forward in NC_001142 between 14138 and 15137 with 100% identity.
3114_s_at 2356.2 P
Saccharomyces cerevisiae chromosome X, complete chromosome sequence. Found forward in

NC_001142 between 15138 and 15624 with 100% identity.
3115_at -12.4 A
Saccharomyces cerevisiae chromosome X, complete chromosome sequence. Found forward in NC_001142 between 41889 and 42888 with 100% identity.
3116_at 1618.8 A
Saccharomyces cerevisiae chromosome X, complete chromosome sequence. Found forward in NC_001142 between 42889 and 43888 with 100% identity.
3117_at -207.1 P
Saccharomyces cerevisiae chromosome X, complete chromosome sequence. Found forward in NC_001142 between 43889 and 44888 with 100% identity.
3118_at -2193.1 A
Saccharomyces cerevisiae chromosome X, complete chromosome sequence. Found forward in NC_001142 between 44889 and 45888 with 100% identity.
3119_at -423.2 A
Saccharomyces cerevisiae chromosome X, complete chromosome sequence. Found forward in NC_001142 between 45889 and 46888 with 100% identity.
3120_at 255.8 P
Saccharomyces cerevisiae chromosome X, complete chromosome sequence. Found forward in NC_001142 between 46889 and 47659 with 100% identity.
3121_at 1276.5 A
Saccharomyces cerevisiae chromosome X, complete chromosome sequence. Found forward in NC_001142 between 165921 and 166920 with 100% identity.
3122_at 798.8 P
Saccharomyces cerevisiae chromosome X, complete chromosome sequence. Found forward in NC_001142 between 166921 and 167920 with 100% identity.
3123_at -855.5 A
Saccharomyces cerevisiae chromosome X, complete chromosome sequence. Found forward in NC_001142 between 167921 and 168920 with 100% identity.
3124_at 254.2 P
Saccharomyces cerevisiae chromosome X, complete chromosome sequence. Found forward in NC_001142 between 168921 and 169920 with 100% identity.
3125_at 1168.3 P
Saccharomyces cerevisiae chromosome X, complete chromosome sequence. Found forward in NC_001142 between 169921 and 170920 with 100% identity.
3126_at 37.5 A
Saccharomyces cerevisiae chromosome X, complete chromosome sequence. Found forward in NC_001142 between 170921 and 171920 with 100% identity.
3127_at -336.7 A
Saccharomyces cerevisiae chromosome X, complete chromosome sequence. Found forward in NC_001142 between 171921 and 172694 with 100% identity.
3128_at 446.3 P
Saccharomyces cerevisiae chromosome X, complete chromosome sequence. Found forward in NC_001142 between 196825 and 197824 with 100% identity.
3129_at -428.0 A
Saccharomyces cerevisiae chromosome X, complete chromosome sequence. Found forward in NC_001142 between 203825 and 204824 with 100% identity.
3130_at -24.9 P
Saccharomyces cerevisiae chromosome X, complete chromosome sequence. Found forward in NC_001142 between 204825 and 205824 with 100% identity.
3131_g_at 854.9 P
Saccharomyces cerevisiae chromosome X, complete chromosome sequence. Found forward in NC_001142 between 204825 and 205824 with 100% identity.
3045_s_at 1040.9 P
Saccharomyces cerevisiae chromosome X, complete chromosome sequence. Found forward in NC_001142 between 205825 and 206646 with 100% identity.
3046_at -422.7 A

Saccharomyces cerevisiae chromosome X, complete chromosome sequence. Found forward in NC_001142 between 212197 and 213196 with 100% identity.
3047_at	581.0	P
Saccharomyces cerevisiae chromosome X, complete chromosome sequence. Found forward in NC_001142 between 213197 and 214196 with 100% identity.
3048_at	-87.7	A
Saccharomyces cerevisiae chromosome X, complete chromosome sequence. Found forward in NC_001142 between 214197 and 215196 with 100% identity.
3049_at	-74.2	A
Saccharomyces cerevisiae chromosome X, complete chromosome sequence. Found forward in NC_001142 between 215197 and 216196 with 100% identity.
3050_at	439.3	A
Saccharomyces cerevisiae chromosome X, complete chromosome sequence. Found forward in NC_001142 between 216197 and 217196 with 100% identity.
3051_at	212.6	A
Saccharomyces cerevisiae chromosome X, complete chromosome sequence. Found forward in NC_001142 between 217197 and 217402 with 100% identity.
3052_at	-144.0	A
Saccharomyces cerevisiae chromosome X, complete chromosome sequence. Found forward in NC_001142 between 254933 and 255932 with 100% identity.
3053_at	-1147.0	A
Saccharomyces cerevisiae chromosome X, complete chromosome sequence. Found forward in NC_001142 between 255933 and 256932 with 100% identity.
3054_at	-559.7	A
Saccharomyces cerevisiae chromosome X, complete chromosome sequence. Found forward in NC_001142 between 256933 and 257932 with 100% identity.
3055_g_at	312.6	P
Saccharomyces cerevisiae chromosome X, complete chromosome sequence. Found forward in NC_001142 between 256933 and 257932 with 100% identity.
3056_s_at	276.7	A
Saccharomyces cerevisiae chromosome X, complete chromosome sequence. Found forward in NC_001142 between 257933 and 258932 with 100% identity.
3057_s_at	2433.8	P
Saccharomyces cerevisiae chromosome X, complete chromosome sequence. Found forward in NC_001142 between 258933 and 259932 with 100% identity.
3058_s_at	1027.8	P
Saccharomyces cerevisiae chromosome X, complete chromosome sequence. Found forward in NC_001142 between 259933 and 260143 with 100% identity.
3059_at	-66.0	A
Saccharomyces cerevisiae chromosome X, complete chromosome sequence. Found forward in NC_001142 between 368944 and 369943 with 100% identity.
3060_at	923.2	P
Saccharomyces cerevisiae chromosome X, complete chromosome sequence. Found forward in NC_001142 between 369944 and 370943 with 100% identity.
3061_at	-328.9	A
Saccharomyces cerevisiae chromosome X, complete chromosome sequence. Found forward in NC_001142 between 370944 and 371943 with 100% identity.
3062_at	1167.4	A
Saccharomyces cerevisiae chromosome X, complete chromosome sequence. Found forward in NC_001142 between 371944 and 372943 with 100% identity.
3063_at	-188.9	A
Saccharomyces cerevisiae chromosome X, complete chromosome sequence. Found forward in NC_001142 between 372944 and 373943 with 100% identity.
3064_at	1465.3	A
Saccharomyces cerevisiae chromosome X, complete chromosome sequence. Found forward in NC_001142 between 373944 and 374811 with 100% identity.

3065_g_at 669.6 A
Saccharomyces cerevisiae chromosome X, complete chromosome sequence. Found forward in NC_001142 between 373944 and 374811 with 100% identity.
3066_at -13.1 A
Saccharomyces cerevisiae chromosome X, complete chromosome sequence. Found forward in NC_001142 between 424301 and 425300 with 100% identity.
3067_g_at -58.5 A
Saccharomyces cerevisiae chromosome X, complete chromosome sequence. Found forward in NC_001142 between 424301 and 425300 with 100% identity.
3068_s_at 784.8 P
Saccharomyces cerevisiae chromosome X, complete chromosome sequence. Found forward in NC_001142 between 425301 and 426300 with 100% identity.
3069_s_at -751.5 A
Saccharomyces cerevisiae chromosome X, complete chromosome sequence. Found forward in NC_001142 between 426301 and 427300 with 100% identity.
3070_s_at -1064.3 A
Saccharomyces cerevisiae chromosome X, complete chromosome sequence. Found forward in NC_001142 between 427301 and 428300 with 100% identity.
3071_s_at 1487.2 A
Saccharomyces cerevisiae chromosome X, complete chromosome sequence. Found forward in NC_001142 between 428301 and 429300 with 100% identity.
3072_s_at 3855.1 P
Saccharomyces cerevisiae chromosome X, complete chromosome sequence. Found forward in NC_001142 between 429301 and 430300 with 100% identity.
3073_s_at 153.1 P
Saccharomyces cerevisiae chromosome X, complete chromosome sequence. Found forward in NC_001142 between 430301 and 430425 with 100% identity.
3074_at -10.5 A
Saccharomyces cerevisiae chromosome X, complete chromosome sequence. Found forward in NC_001142 between 510427 and 511426 with 100% identity.
3075_at 248.5 P
Saccharomyces cerevisiae chromosome X, complete chromosome sequence. Found forward in NC_001142 between 511427 and 512426 with 100% identity.
3076_at -71.7 A
Saccharomyces cerevisiae chromosome X, complete chromosome sequence. Found forward in NC_001142 between 512427 and 513426 with 100% identity.
3077_at 373.8 A
Saccharomyces cerevisiae chromosome X, complete chromosome sequence. Found forward in NC_001142 between 513427 and 514426 with 100% identity.
3078_g_at 1392.8 P
Saccharomyces cerevisiae chromosome X, complete chromosome sequence. Found forward in NC_001142 between 513427 and 514426 with 100% identity.
3079_s_at 2445.9 P
Saccharomyces cerevisiae chromosome X, complete chromosome sequence. Found forward in NC_001142 between 514427 and 515426 with 100% identity.
3080_f_at 3572.4 P
Saccharomyces cerevisiae chromosome X, complete chromosome sequence. Found forward in NC_001142 between 515427 and 515477 with 100% identity.
3081_at 1174.8 P
Saccharomyces cerevisiae chromosome X, complete chromosome sequence. Found forward in NC_001142 between 557997 and 558996 with 100% identity.
3082_at -175.2 A
Saccharomyces cerevisiae chromosome X, complete chromosome sequence. Found forward in NC_001142 between 558997 and 559996 with 100% identity.
3083_g_at -151.9 A
Saccharomyces cerevisiae chromosome X, complete chromosome sequence. Found forward in

NC_001142 between 558997 and 559996 with 100% identity.
3084_s_at 306.5 A
Saccharomyces cerevisiae chromosome X, complete chromosome sequence. Found forward in NC_001142 between 559997 and 560996 with 100% identity.
3085_s_at 841.1 P
Saccharomyces cerevisiae chromosome X, complete chromosome sequence. Found forward in NC_001142 between 560997 and 561996 with 100% identity.
3086_s_at 428.3 P
Saccharomyces cerevisiae chromosome X, complete chromosome sequence. Found forward in NC_001142 between 561997 and 562996 with 100% identity.
3087_s_at -117.4 A
Saccharomyces cerevisiae chromosome X, complete chromosome sequence. Found forward in NC_001142 between 562997 and 563996 with 100% identity.
3003_s_at 1881.9 P
Saccharomyces cerevisiae chromosome X, complete chromosome sequence. Found forward in NC_001142 between 563997 and 564996 with 100% identity.
3004_s_at 2722.1 P
Saccharomyces cerevisiae chromosome X, complete chromosome sequence. Found forward in NC_001142 between 564997 and 565996 with 100% identity.
3005_at 278.9 A
Saccharomyces cerevisiae chromosome X, complete chromosome sequence. Found forward in NC_001142 between 595249 and 596248 with 100% identity.
3006_at 279.5 P
Saccharomyces cerevisiae chromosome X, complete chromosome sequence. Found forward in NC_001142 between 596249 and 597248 with 100% identity.
3007_at 441.4 M
Saccharomyces cerevisiae chromosome X, complete chromosome sequence. Found forward in NC_001142 between 597249 and 598248 with 100% identity.
3008_at 473.9 P
Saccharomyces cerevisiae chromosome X, complete chromosome sequence. Found forward in NC_001142 between 598249 and 599248 with 100% identity.
3009_g_at 1242.7 P
Saccharomyces cerevisiae chromosome X, complete chromosome sequence. Found forward in NC_001142 between 598249 and 599248 with 100% identity.
3010_s_at -116.0 A
Saccharomyces cerevisiae chromosome X, complete chromosome sequence. Found forward in NC_001142 between 599249 and 600248 with 100% identity.
3011_s_at 648.4 P
Saccharomyces cerevisiae chromosome X, complete chromosome sequence. Found forward in NC_001142 between 600249 and 601248 with 100% identity.
3012_s_at 909.4 P
Saccharomyces cerevisiae chromosome X, complete chromosome sequence. Found forward in NC_001142 between 601249 and 602248 with 100% identity.
3013_at -317.0 A
Saccharomyces cerevisiae chromosome X, complete chromosome sequence. Found forward in NC_001142 between 629774 and 630773 with 100% identity.
3014_at 35.8 A
Saccharomyces cerevisiae chromosome X, complete chromosome sequence. Found forward in NC_001142 between 630774 and 631773 with 100% identity.
3015_at 415.7 P
Saccharomyces cerevisiae chromosome X, complete chromosome sequence. Found forward in NC_001142 between 631774 and 632773 with 100% identity.
3016_at 244.1 P
Saccharomyces cerevisiae chromosome X, complete chromosome sequence. Found forward in NC_001142 between 632774 and 633773 with 100% identity.
3017_g_at 622.9 P

Saccharomyces cerevisiae chromosome X, complete chromosome sequence. Found forward in NC_001142 between 632774 and 633773 with 100% identity.

3018_s_at 370.6 P

Saccharomyces cerevisiae chromosome X, complete chromosome sequence. Found forward in NC_001142 between 633774 and 634773 with 100% identity.

3019_at -687.3 A

Saccharomyces cerevisiae chromosome X, complete chromosome sequence. Found forward in NC_001142 between 690939 and 691938 with 100% identity.

3020_at 229.4 A

Saccharomyces cerevisiae chromosome X, complete chromosome sequence. Found forward in NC_001142 between 691939 and 692938 with 100% identity.

3021_at -428.6 A

Saccharomyces cerevisiae chromosome X, complete chromosome sequence. Found forward in NC_001142 between 692939 and 693938 with 100% identity.

3022_at -532.1 A

Saccharomyces cerevisiae chromosome X, complete chromosome sequence. Found forward in NC_001142 between 693939 and 694938 with 100% identity.

3023_at -127.8 A

Saccharomyces cerevisiae chromosome X, complete chromosome sequence. Found forward in NC_001142 between 694939 and 695938 with 100% identity.

3024_g_at 1632.6 P

Saccharomyces cerevisiae chromosome X, complete chromosome sequence. Found forward in NC_001142 between 694939 and 695938 with 100% identity.

3025_s_at 755.5 P

Saccharomyces cerevisiae chromosome X, complete chromosome sequence. Found forward in NC_001142 between 695939 and 696138 with 100% identity.

3026_at -152.1 A

Saccharomyces cerevisiae chromosome X, complete chromosome sequence. Found forward in NC_001142 between 712444 and 713443 with 100% identity.

3027_at 22.4 A

Saccharomyces cerevisiae chromosome X, complete chromosome sequence. Found forward in NC_001142 between 713444 and 714443 with 100% identity.

3028_at 260.1 A

Saccharomyces cerevisiae chromosome X, complete chromosome sequence. Found forward in NC_001142 between 714444 and 715443 with 100% identity.

3029_at 32.9 A

Saccharomyces cerevisiae chromosome X, complete chromosome sequence. Found forward in NC_001142 between 715444 and 716443 with 100% identity.

3030_at -1544.0 A

Saccharomyces cerevisiae chromosome X, complete chromosome sequence. Found forward in NC_001142 between 716444 and 717443 with 100% identity.

3031_at -301.5 A

Saccharomyces cerevisiae chromosome X, complete chromosome sequence. Found forward in NC_001142 between 717444 and 718443 with 100% identity.

3032_at 191.0 P

Saccharomyces cerevisiae chromosome X, complete chromosome sequence. Found forward in NC_001142 between 718444 and 719443 with 100% identity.

3033_s_at 1295.5 P

Saccharomyces cerevisiae chromosome X, complete chromosome sequence. Found forward in NC_001142 between 719444 and 720443 with 100% identity.

3034_at 104.0 A

Saccharomyces cerevisiae chromosome XI, complete chromosome sequence. Found forward in NC_001143 between 9592 and 10591 with 100% identity.

3035_at 521.0 P

Saccharomyces cerevisiae chromosome XI, complete chromosome sequence. Found forward in NC_001143 between 10592 and 11591 with 100% identity.

3036_at 1014.8 P
Saccharomyces cerevisiae chromosome XI, complete chromosome sequence. Found forward in NC_001143 between 11592 and 12591 with 100% identity.
3037_at -38.1 A
Saccharomyces cerevisiae chromosome XI, complete chromosome sequence. Found forward in NC_001143 between 12592 and 13591 with 100% identity.
3038_at 222.9 A
Saccharomyces cerevisiae chromosome XI, complete chromosome sequence. Found forward in NC_001143 between 13592 and 14591 with 100% identity.
3039_s_at 3550.2 P
Saccharomyces cerevisiae chromosome XI, complete chromosome sequence. Found forward in NC_001143 between 14592 and 15208 with 100% identity.
3040_at 519.4 P
Saccharomyces cerevisiae chromosome XI, complete chromosome sequence. Found forward in NC_001143 between 56435 and 57434 with 100% identity.
3041_at 122.8 A
Saccharomyces cerevisiae chromosome XI, complete chromosome sequence. Found forward in NC_001143 between 57435 and 58434 with 100% identity.
3042_at 246.7 P
Saccharomyces cerevisiae chromosome XI, complete chromosome sequence. Found forward in NC_001143 between 58435 and 59434 with 100% identity.
3043_at -80.5 A
Saccharomyces cerevisiae chromosome XI, complete chromosome sequence. Found forward in NC_001143 between 59435 and 60434 with 100% identity.
3044_at 78.8 A
Saccharomyces cerevisiae chromosome XI, complete chromosome sequence. Found forward in NC_001143 between 60435 and 61434 with 100% identity.
2960_at -52.8 M
Saccharomyces cerevisiae chromosome XI, complete chromosome sequence. Found forward in NC_001143 between 61435 and 62434 with 100% identity.
2961_at 838.7 P
Saccharomyces cerevisiae chromosome XI, complete chromosome sequence. Found forward in NC_001143 between 62435 and 63434 with 100% identity.
2962_at 1276.8 P
Saccharomyces cerevisiae chromosome XI, complete chromosome sequence. Found forward in NC_001143 between 63435 and 63899 with 100% identity.
2963_at 303.9 A
Saccharomyces cerevisiae chromosome XI, complete chromosome sequence. Found forward in NC_001143 between 99643 and 100642 with 100% identity.
2964_at 14403.7 P
Saccharomyces cerevisiae chromosome XI, complete chromosome sequence. Found forward in NC_001143 between 100643 and 101642 with 100% identity.
2965_g_at 8293.7 P
Saccharomyces cerevisiae chromosome XI, complete chromosome sequence. Found forward in NC_001143 between 100643 and 101642 with 100% identity.
2966_s_at 12208.2 P
Saccharomyces cerevisiae chromosome XI, complete chromosome sequence. Found forward in NC_001143 between 101643 and 102642 with 100% identity.
2967_s_at 8236.3 P
Saccharomyces cerevisiae chromosome XI, complete chromosome sequence. Found forward in NC_001143 between 102643 and 103642 with 100% identity.
2968_s_at 9688.7 P
Saccharomyces cerevisiae chromosome XI, complete chromosome sequence. Found forward in NC_001143 between 103643 and 104642 with 100% identity.
2969_s_at 9218.9 P
Saccharomyces cerevisiae chromosome XI, complete chromosome sequence. Found forward in

NC_001143 between 104643 and 105642 with 100% identity.

2970_s_at 15672.6 P

Saccharomyces cerevisiae chromosome XI, complete chromosome sequence. Found forward in NC_001143 between 105643 and 106328 with 100% identity.

2971_at -1292.2 A

Saccharomyces cerevisiae chromosome XI, complete chromosome sequence. Found forward in NC_001143 between 411757 and 412756 with 100% identity.

2972_at 149.1 P

Saccharomyces cerevisiae chromosome XI, complete chromosome sequence. Found forward in NC_001143 between 412757 and 413756 with 100% identity.

2973_at 142.0 P

Saccharomyces cerevisiae chromosome XI, complete chromosome sequence. Found forward in NC_001143 between 413757 and 414756 with 100% identity.

2974_at -1074.9 A

Saccharomyces cerevisiae chromosome XI, complete chromosome sequence. Found forward in NC_001143 between 414757 and 415756 with 100% identity.

2975_at 460.7 P

Saccharomyces cerevisiae chromosome XI, complete chromosome sequence. Found forward in NC_001143 between 415757 and 416756 with 100% identity.

2976_at 86.2 P

Saccharomyces cerevisiae chromosome XI, complete chromosome sequence. Found forward in NC_001143 between 416757 and 417146 with 100% identity.

2977_at -36.9 P

Saccharomyces cerevisiae chromosome XI, complete chromosome sequence. Found forward in NC_001143 between 535784 and 536783 with 100% identity.

2978_at 233.7 P

Saccharomyces cerevisiae chromosome XI, complete chromosome sequence. Found forward in NC_001143 between 536784 and 537783 with 100% identity.

2979_at 1739.5 A

Saccharomyces cerevisiae chromosome XI, complete chromosome sequence. Found forward in NC_001143 between 537784 and 538783 with 100% identity.

2980_at 170.4 A

Saccharomyces cerevisiae chromosome XI, complete chromosome sequence. Found forward in NC_001143 between 538784 and 539783 with 100% identity.

2981_at 94.5 A

Saccharomyces cerevisiae chromosome XI, complete chromosome sequence. Found forward in NC_001143 between 539784 and 540783 with 100% identity.

2982_at 75.9 A

Saccharomyces cerevisiae chromosome XI, complete chromosome sequence. Found forward in NC_001143 between 540784 and 541783 with 100% identity.

2983_at -270.8 A

Saccharomyces cerevisiae chromosome XI, complete chromosome sequence. Found forward in NC_001143 between 541784 and 542783 with 100% identity.

2984_at 16.7 A

Saccharomyces cerevisiae chromosome XI, complete chromosome sequence. Found forward in NC_001143 between 542784 and 543783 with 100% identity.

2985_at -153.3 A

Saccharomyces cerevisiae chromosome XI, complete chromosome sequence. Found forward in NC_001143 between 543784 and 544783 with 100% identity.

2986_at 108.6 A

Saccharomyces cerevisiae chromosome XI, complete chromosome sequence. Found forward in NC_001143 between 544784 and 545783 with 100% identity.

2987_at 536.1 P

Saccharomyces cerevisiae chromosome XI, complete chromosome sequence. Found forward in NC_001143 between 545784 and 546783 with 100% identity.

2988_at -1896.5 A

Saccharomyces cerevisiae chromosome XI, complete chromosome sequence. Found forward in NC_001143 between 546784 and 547783 with 100% identity.

2989_at 98.3 P

Saccharomyces cerevisiae chromosome XI, complete chromosome sequence. Found forward in NC_001143 between 547784 and 548228 with 100% identity.

2990_g_at 1222.4 P

Saccharomyces cerevisiae chromosome XI, complete chromosome sequence. Found forward in NC_001143 between 547784 and 548228 with 100% identity.

2991_at 431.6 P

Saccharomyces cerevisiae chromosome XI, complete chromosome sequence. Found forward in NC_001143 between 619375 and 620374 with 100% identity.

2992_g_at 350.9 P

Saccharomyces cerevisiae chromosome XI, complete chromosome sequence. Found forward in NC_001143 between 619375 and 620374 with 100% identity.

2993_s_at 281.9 P

Saccharomyces cerevisiae chromosome XI, complete chromosome sequence. Found forward in NC_001143 between 620375 and 621374 with 100% identity.

2994_s_at 402.0 P

Saccharomyces cerevisiae chromosome XI, complete chromosome sequence. Found forward in NC_001143 between 621375 and 622374 with 100% identity.

2995_s_at 674.3 P

Saccharomyces cerevisiae chromosome XI, complete chromosome sequence. Found forward in NC_001143 between 622375 and 623374 with 100% identity.

2996_s_at 539.0 P

Saccharomyces cerevisiae chromosome XI, complete chromosome sequence. Found forward in NC_001143 between 623375 and 624374 with 100% identity.

2997_s_at 1965.1 P

Saccharomyces cerevisiae chromosome XI, complete chromosome sequence. Found forward in NC_001143 between 624375 and 624566 with 100% identity.

2998_at 314.6 P

Saccharomyces cerevisiae chromosome XI, complete chromosome sequence. Found forward in NC_001143 between 642133 and 643132 with 100% identity.

2999_at 182.7 A

Saccharomyces cerevisiae chromosome XI, complete chromosome sequence. Found forward in NC_001143 between 643133 and 644132 with 100% identity.

3000_at -75.8 A

Saccharomyces cerevisiae chromosome XI, complete chromosome sequence. Found forward in NC_001143 between 644133 and 645132 with 100% identity.

3001_at 521.3 P

Saccharomyces cerevisiae chromosome XI, complete chromosome sequence. Found forward in NC_001143 between 645133 and 646132 with 100% identity.

3002_g_at 176.5 A

Saccharomyces cerevisiae chromosome XI, complete chromosome sequence. Found forward in NC_001143 between 645133 and 646132 with 100% identity.

2917_s_at 541.5 A

Saccharomyces cerevisiae chromosome XI, complete chromosome sequence. Found forward in NC_001143 between 646133 and 647132 with 100% identity.

2918_s_at 499.4 P

Saccharomyces cerevisiae chromosome XI, complete chromosome sequence. Found forward in NC_001143 between 647133 and 648132 with 100% identity.

2919_s_at 2065.5 P

Saccharomyces cerevisiae chromosome XI, complete chromosome sequence. Found forward in NC_001143 between 648133 and 648994 with 100% identity.

2920_at 1582.4 P

Saccharomyces cerevisiae chromosome XI, complete chromosome sequence. Found forward in NC_001143 between 649494 and 650493 with 100% identity.

2921_at 684.4 P
Saccharomyces cerevisiae chromosome XI, complete chromosome sequence. Found forward in NC_001143 between 650494 and 651493 with 100% identity.
2922_at 588.7 P
Saccharomyces cerevisiae chromosome XI, complete chromosome sequence. Found forward in NC_001143 between 651494 and 652493 with 100% identity.
2923_at 858.9 P
Saccharomyces cerevisiae chromosome XI, complete chromosome sequence. Found forward in NC_001143 between 652494 and 653493 with 100% identity.
2924_g_at -482.8 P
Saccharomyces cerevisiae chromosome XI, complete chromosome sequence. Found forward in NC_001143 between 652494 and 653493 with 100% identity.
2925_s_at 1043.8 P
Saccharomyces cerevisiae chromosome XI, complete chromosome sequence. Found forward in NC_001143 between 653494 and 654493 with 100% identity.
2926_s_at 330.3 P
Saccharomyces cerevisiae chromosome XI, complete chromosome sequence. Found forward in NC_001143 between 654494 and 655493 with 100% identity.
2927_s_at 417.6 P
Saccharomyces cerevisiae chromosome XI, complete chromosome sequence. Found forward in NC_001143 between 655494 and 655865 with 100% identity.
2928_at 1110.4 A
Saccharomyces cerevisiae chromosome XI, complete chromosome sequence. Found forward in NC_001143 between 662918 and 663917 with 100% identity.
2929_at 417.2 A
Saccharomyces cerevisiae chromosome XI, complete chromosome sequence. Found forward in NC_001143 between 663918 and 664917 with 100% identity.
2930_at 342.5 M
Saccharomyces cerevisiae chromosome XI, complete chromosome sequence. Found forward in NC_001143 between 664918 and 665917 with 100% identity.
2931_at 29.4 A
Saccharomyces cerevisiae chromosome XI, complete chromosome sequence. Found forward in NC_001143 between 665918 and 666445 with 100% identity.
2932_at -38.4 A
Saccharomyces cerevisiae chromosome XII, complete chromosome sequence. Found forward in NC_001144 between 54710 and 55709 with 100% identity.
2933_at 694.0 P
Saccharomyces cerevisiae chromosome XII, complete chromosome sequence. Found forward in NC_001144 between 55710 and 56709 with 100% identity.
2934_at 70.2 A
Saccharomyces cerevisiae chromosome XII, complete chromosome sequence. Found forward in NC_001144 between 56710 and 57709 with 100% identity.
2935_at 2477.1 P
Saccharomyces cerevisiae chromosome XII, complete chromosome sequence. Found forward in NC_001144 between 57710 and 58709 with 100% identity.
2936_at 175.0 P
Saccharomyces cerevisiae chromosome XII, complete chromosome sequence. Found forward in NC_001144 between 58710 and 59709 with 100% identity.
2937_at -88.8 A
Saccharomyces cerevisiae chromosome XII, complete chromosome sequence. Found forward in NC_001144 between 59710 and 60709 with 100% identity.
2938_at -65.1 A
Saccharomyces cerevisiae chromosome XII, complete chromosome sequence. Found forward in NC_001144 between 60710 and 61709 with 100% identity.
2939_at -206.9 A
Saccharomyces cerevisiae chromosome XII, complete chromosome sequence. Found forward in

NC_001144 between 61710 and 62709 with 100% identity.
2940_at 256.1 A
Saccharomyces cerevisiae chromosome XII, complete chromosome sequence. Found forward in NC_001144 between 62710 and 63709 with 100% identity.
2941_at -387.8 A
Saccharomyces cerevisiae chromosome XII, complete chromosome sequence. Found forward in NC_001144 between 63710 and 64061 with 100% identity.
2942_at -896.5 A
Saccharomyces cerevisiae chromosome XII, complete chromosome sequence. Found forward in NC_001144 between 99543 and 100542 with 100% identity.
2943_at 1066.8 P
Saccharomyces cerevisiae chromosome XII, complete chromosome sequence. Found forward in NC_001144 between 100543 and 101542 with 100% identity.
2944_g_at 2403.8 P
Saccharomyces cerevisiae chromosome XII, complete chromosome sequence. Found forward in NC_001144 between 100543 and 101542 with 100% identity.
2945_s_at 864.3 P
Saccharomyces cerevisiae chromosome XII, complete chromosome sequence. Found forward in NC_001144 between 101543 and 102542 with 100% identity.
2946_s_at 1494.6 P
Saccharomyces cerevisiae chromosome XII, complete chromosome sequence. Found forward in NC_001144 between 102543 and 103542 with 100% identity.
2947_s_at 4547.2 P
Saccharomyces cerevisiae chromosome XII, complete chromosome sequence. Found forward in NC_001144 between 103543 and 104542 with 100% identity.
2948_s_at 1362.3 P
Saccharomyces cerevisiae chromosome XII, complete chromosome sequence. Found forward in NC_001144 between 104543 and 104846 with 100% identity.
2949_at 110.0 A
Saccharomyces cerevisiae chromosome XII, complete chromosome sequence. Found forward in NC_001144 between 188164 and 189163 with 100% identity.
2950_at 532.8 P
Saccharomyces cerevisiae chromosome XII, complete chromosome sequence. Found forward in NC_001144 between 189164 and 190163 with 100% identity.
2951_at 521.4 A
Saccharomyces cerevisiae chromosome XII, complete chromosome sequence. Found forward in NC_001144 between 190164 and 191163 with 100% identity.
2952_at 216.0 A
Saccharomyces cerevisiae chromosome XII, complete chromosome sequence. Found forward in NC_001144 between 191164 and 192163 with 100% identity.
2953_at 504.6 A
Saccharomyces cerevisiae chromosome XII, complete chromosome sequence. Found forward in NC_001144 between 192164 and 193163 with 100% identity.
2954_at -8.4 A
Saccharomyces cerevisiae chromosome XII, complete chromosome sequence. Found forward in NC_001144 between 193164 and 194163 with 100% identity.
2955_at -697.5 A
Saccharomyces cerevisiae chromosome XII, complete chromosome sequence. Found forward in NC_001144 between 194164 and 194675 with 100% identity.
2956_g_at 1754.3 P
Saccharomyces cerevisiae chromosome XII, complete chromosome sequence. Found forward in NC_001144 between 194164 and 194675 with 100% identity.
2957_at 331.2 A
Saccharomyces cerevisiae chromosome XII, complete chromosome sequence. Found forward in NC_001144 between 307356 and 308355 with 100% identity.
2958_at -114.2 A

Saccharomyces cerevisiae chromosome XII, complete chromosome sequence. Found forward in NC_001144 between 308356 and 309355 with 100% identity.
2959_at 197.9 A
Saccharomyces cerevisiae chromosome XII, complete chromosome sequence. Found forward in NC_001144 between 309356 and 310355 with 100% identity.
2875_at -1125.1 A
Saccharomyces cerevisiae chromosome XII, complete chromosome sequence. Found forward in NC_001144 between 310356 and 311355 with 100% identity.
2876_at -845.6 A
Saccharomyces cerevisiae chromosome XII, complete chromosome sequence. Found forward in NC_001144 between 311356 and 312355 with 100% identity.
2877_at -571.0 A
Saccharomyces cerevisiae chromosome XII, complete chromosome sequence. Found forward in NC_001144 between 312356 and 313355 with 100% identity.
2878_at 414.3 A
Saccharomyces cerevisiae chromosome XII, complete chromosome sequence. Found forward in NC_001144 between 313356 and 314355 with 100% identity.
2879_at 400.4 P
Saccharomyces cerevisiae chromosome XII, complete chromosome sequence. Found forward in NC_001144 between 314356 and 315355 with 100% identity.
2880_at 296.5 A
Saccharomyces cerevisiae chromosome XII, complete chromosome sequence. Found forward in NC_001144 between 315356 and 315877 with 100% identity.
2881_at 1157.6 P
Saccharomyces cerevisiae chromosome XII, complete chromosome sequence. Found forward in NC_001144 between 330178 and 331177 with 100% identity.
2882_at 1384.2 A
Saccharomyces cerevisiae chromosome XII, complete chromosome sequence. Found forward in NC_001144 between 331178 and 332177 with 100% identity.
2883_at -842.8 A
Saccharomyces cerevisiae chromosome XII, complete chromosome sequence. Found forward in NC_001144 between 332178 and 333177 with 100% identity.
2884_g_at 1390.5 P
Saccharomyces cerevisiae chromosome XII, complete chromosome sequence. Found forward in NC_001144 between 332178 and 333177 with 100% identity.
2885_s_at 1270.5 P
Saccharomyces cerevisiae chromosome XII, complete chromosome sequence. Found forward in NC_001144 between 333178 and 334177 with 100% identity.
2886_s_at 2112.3 P
Saccharomyces cerevisiae chromosome XII, complete chromosome sequence. Found forward in NC_001144 between 334178 and 335177 with 100% identity.
2887_s_at 2552.8 P
Saccharomyces cerevisiae chromosome XII, complete chromosome sequence. Found forward in NC_001144 between 335178 and 335534 with 100% identity.
2888_at 1100.6 P
Saccharomyces cerevisiae chromosome XII, complete chromosome sequence. Found forward in NC_001144 between 349507 and 350506 with 100% identity.
2889_at 427.1 P
Saccharomyces cerevisiae chromosome XII, complete chromosome sequence. Found forward in NC_001144 between 350507 and 351506 with 100% identity.
2890_at -103.6 A
Saccharomyces cerevisiae chromosome XII, complete chromosome sequence. Found forward in NC_001144 between 351507 and 352506 with 100% identity.
2891_at 336.3 A
Saccharomyces cerevisiae chromosome XII, complete chromosome sequence. Found forward in NC_001144 between 352507 and 353506 with 100% identity.

2892_at -1179.7 A

Saccharomyces cerevisiae chromosome XII, complete chromosome sequence. Found forward in NC_001144 between 353507 and 354506 with 100% identity.

2893_at -130.1 A

Saccharomyces cerevisiae chromosome XII, complete chromosome sequence. Found forward in NC_001144 between 354507 and 355506 with 100% identity.

2894_at -563.8 A

Saccharomyces cerevisiae chromosome XII, complete chromosome sequence. Found forward in NC_001144 between 355507 and 356506 with 100% identity.

2895_at 6.8 A

Saccharomyces cerevisiae chromosome XII, complete chromosome sequence. Found forward in NC_001144 between 356507 and 357506 with 100% identity.

2896_at -97.6 A

Saccharomyces cerevisiae chromosome XII, complete chromosome sequence. Found forward in NC_001144 between 357507 and 358506 with 100% identity.

2897_at -159.9 A

Saccharomyces cerevisiae chromosome XII, complete chromosome sequence. Found forward in NC_001144 between 358507 and 359506 with 100% identity.

2898_at -115.6 A

Saccharomyces cerevisiae chromosome XII, complete chromosome sequence. Found forward in NC_001144 between 359507 and 360506 with 100% identity.

2899_at 640.6 A

Saccharomyces cerevisiae chromosome XII, complete chromosome sequence. Found forward in NC_001144 between 360507 and 361506 with 100% identity.

2900_at -118.3 A

Saccharomyces cerevisiae chromosome XII, complete chromosome sequence. Found forward in NC_001144 between 361507 and 362506 with 100% identity.

2901_at 290.1 A

Saccharomyces cerevisiae chromosome XII, complete chromosome sequence. Found forward in NC_001144 between 362507 and 363506 with 100% identity.

2902_at -60.8 A

Saccharomyces cerevisiae chromosome XII, complete chromosome sequence. Found forward in NC_001144 between 363507 and 364506 with 100% identity.

2903_g_at 1937.6 A

Saccharomyces cerevisiae chromosome XII, complete chromosome sequence. Found forward in NC_001144 between 363507 and 364506 with 100% identity.

2904_s_at 2136.0 P

Saccharomyces cerevisiae chromosome XII, complete chromosome sequence. Found forward in NC_001144 between 364507 and 364831 with 100% identity.

2905_at -317.8 A

Saccharomyces cerevisiae chromosome XII, complete chromosome sequence. Found forward in NC_001144 between 629184 and 630183 with 100% identity.

2906_at 130.9 P

Saccharomyces cerevisiae chromosome XII, complete chromosome sequence. Found forward in NC_001144 between 630184 and 631183 with 100% identity.

2907_at -212.9 A

Saccharomyces cerevisiae chromosome XII, complete chromosome sequence. Found forward in NC_001144 between 631184 and 632183 with 100% identity.

2908_at 48.9 M

Saccharomyces cerevisiae chromosome XII, complete chromosome sequence. Found forward in NC_001144 between 632184 and 633183 with 100% identity.

2909_at 45.0 A

Saccharomyces cerevisiae chromosome XII, complete chromosome sequence. Found forward in NC_001144 between 633184 and 634183 with 100% identity.

2910_at 31.4 P

Saccharomyces cerevisiae chromosome XII, complete chromosome sequence. Found forward in

NC_001144 between 634184 and 635183 with 100% identity.
2911_s_at 4925.3 P
Saccharomyces cerevisiae chromosome XII, complete chromosome sequence. Found forward in NC_001144 between 635184 and 635584 with 100% identity.
2912_at 350.2 A
Saccharomyces cerevisiae chromosome XII, complete chromosome sequence. Found forward in NC_001144 between 769817 and 770816 with 100% identity.
2913_at 2328.7 P
Saccharomyces cerevisiae chromosome XII, complete chromosome sequence. Found forward in NC_001144 between 770817 and 771816 with 100% identity.
2914_at -80.4 A
Saccharomyces cerevisiae chromosome XII, complete chromosome sequence. Found forward in NC_001144 between 771817 and 772816 with 100% identity.
2915_g_at 200.9 P
Saccharomyces cerevisiae chromosome XII, complete chromosome sequence. Found forward in NC_001144 between 771817 and 772816 with 100% identity.
2916_s_at 125.6 A
Saccharomyces cerevisiae chromosome XII, complete chromosome sequence. Found forward in NC_001144 between 772817 and 773816 with 100% identity.
2832_s_at 595.3 P
Saccharomyces cerevisiae chromosome XII, complete chromosome sequence. Found forward in NC_001144 between 773817 and 774816 with 100% identity.
2833_s_at 633.2 P
Saccharomyces cerevisiae chromosome XII, complete chromosome sequence. Found forward in NC_001144 between 774817 and 775803 with 100% identity.
2834_at -79.1 A
Saccharomyces cerevisiae chromosome XII, complete chromosome sequence. Found forward in NC_001144 between 808817 and 809816 with 100% identity.
2835_at 2865.9 P
Saccharomyces cerevisiae chromosome XII, complete chromosome sequence. Found forward in NC_001144 between 809817 and 810816 with 100% identity.
2836_g_at 6667.8 P
Saccharomyces cerevisiae chromosome XII, complete chromosome sequence. Found forward in NC_001144 between 809817 and 810816 with 100% identity.
2837_s_at 3235.4 A
Saccharomyces cerevisiae chromosome XII, complete chromosome sequence. Found forward in NC_001144 between 810817 and 811816 with 100% identity.
2838_s_at 7334.0 P
Saccharomyces cerevisiae chromosome XII, complete chromosome sequence. Found forward in NC_001144 between 811817 and 812816 with 100% identity.
2839_s_at 10256.0 P
Saccharomyces cerevisiae chromosome XII, complete chromosome sequence. Found forward in NC_001144 between 812817 and 813816 with 100% identity.
2840_s_at 11300.3 P
Saccharomyces cerevisiae chromosome XII, complete chromosome sequence. Found forward in NC_001144 between 813817 and 814816 with 100% identity.
2841_s_at 13332.4 P
Saccharomyces cerevisiae chromosome XII, complete chromosome sequence. Found forward in NC_001144 between 814817 and 815126 with 100% identity.
2842_at 720.1 A
Saccharomyces cerevisiae chromosome XII, complete chromosome sequence. Found forward in NC_001144 between 934909 and 935908 with 100% identity.
2843_at 896.5 A
Saccharomyces cerevisiae chromosome XII, complete chromosome sequence. Found forward in NC_001144 between 935909 and 936908 with 100% identity.
2844_at -124.6 A

Saccharomyces cerevisiae chromosome XII, complete chromosome sequence. Found forward in NC_001144 between 936909 and 937908 with 100% identity.
2845_g_at 1227.9 P
Saccharomyces cerevisiae chromosome XII, complete chromosome sequence. Found forward in NC_001144 between 936909 and 937908 with 100% identity.
2846_s_at 2561.1 P
Saccharomyces cerevisiae chromosome XII, complete chromosome sequence. Found forward in NC_001144 between 937909 and 938908 with 100% identity.
2847_s_at 3875.5 P
Saccharomyces cerevisiae chromosome XII, complete chromosome sequence. Found forward in NC_001144 between 938909 and 939908 with 100% identity.
2848_s_at 5546.3 P
Saccharomyces cerevisiae chromosome XII, complete chromosome sequence. Found forward in NC_001144 between 939909 and 940476 with 100% identity.
2849_at 920.7 P
Saccharomyces cerevisiae chromosome XII, complete chromosome sequence. Found forward in NC_001144 between 965554 and 966553 with 100% identity.
2850_g_at 815.6 P
Saccharomyces cerevisiae chromosome XII, complete chromosome sequence. Found forward in NC_001144 between 965554 and 966553 with 100% identity.
2851_s_at 1390.7 P
Saccharomyces cerevisiae chromosome XII, complete chromosome sequence. Found forward in NC_001144 between 966554 and 967553 with 100% identity.
2852_s_at 1244.3 P
Saccharomyces cerevisiae chromosome XII, complete chromosome sequence. Found forward in NC_001144 between 967554 and 968553 with 100% identity.
2853_s_at 350.5 P
Saccharomyces cerevisiae chromosome XII, complete chromosome sequence. Found forward in NC_001144 between 968554 and 969553 with 100% identity.
2854_s_at 736.7 P
Saccharomyces cerevisiae chromosome XII, complete chromosome sequence. Found forward in NC_001144 between 969554 and 970553 with 100% identity.
2855_s_at 2575.3 P
Saccharomyces cerevisiae chromosome XII, complete chromosome sequence. Found forward in NC_001144 between 970554 and 971189 with 100% identity.
2856_at 806.2 P
Saccharomyces cerevisiae chromosome XII, complete chromosome sequence. Found forward in NC_001144 between 979430 and 980429 with 100% identity.
2857_at 694.3 P
Saccharomyces cerevisiae chromosome XII, complete chromosome sequence. Found forward in NC_001144 between 980430 and 981429 with 100% identity.
2858_at 119.4 A
Saccharomyces cerevisiae chromosome XII, complete chromosome sequence. Found forward in NC_001144 between 981430 and 982429 with 100% identity.
2859_at 1761.8 P
Saccharomyces cerevisiae chromosome XII, complete chromosome sequence. Found forward in NC_001144 between 982430 and 983429 with 100% identity.
2860_g_at -27.3 P
Saccharomyces cerevisiae chromosome XII, complete chromosome sequence. Found forward in NC_001144 between 982430 and 983429 with 100% identity.
2861_s_at 165.6 A
Saccharomyces cerevisiae chromosome XII, complete chromosome sequence. Found forward in NC_001144 between 983430 and 984429 with 100% identity.
2862_s_at 589.8 P
Saccharomyces cerevisiae chromosome XII, complete chromosome sequence. Found forward in NC_001144 between 984430 and 985429 with 100% identity.

2863_s_at 88.6 P
Saccharomyces cerevisiae chromosome XII, complete chromosome sequence. Found forward in NC_001144 between 985430 and 986311 with 100% identity.

2864_at 511.0 P
Saccharomyces cerevisiae chromosome XII, complete chromosome sequence. Found forward in NC_001144 between 992726 and 993725 with 100% identity.

2865_g_at 615.8 P
Saccharomyces cerevisiae chromosome XII, complete chromosome sequence. Found forward in NC_001144 between 992726 and 993725 with 100% identity.

2866_s_at 466.6 P
Saccharomyces cerevisiae chromosome XII, complete chromosome sequence. Found forward in NC_001144 between 993726 and 994725 with 100% identity.

2867_s_at 1162.5 P
Saccharomyces cerevisiae chromosome XII, complete chromosome sequence. Found forward in NC_001144 between 994726 and 995725 with 100% identity.

2868_s_at -878.5 A
Saccharomyces cerevisiae chromosome XII, complete chromosome sequence. Found forward in NC_001144 between 995726 and 996725 with 100% identity.

2869_s_at 767.0 P
Saccharomyces cerevisiae chromosome XII, complete chromosome sequence. Found forward in NC_001144 between 996726 and 997725 with 100% identity.

2870_s_at -108.7 P
Saccharomyces cerevisiae chromosome XII, complete chromosome sequence. Found forward in NC_001144 between 997726 and 998725 with 100% identity.

2871_s_at 3628.9 P
Saccharomyces cerevisiae chromosome XII, complete chromosome sequence. Found forward in NC_001144 between 998726 and 999623 with 100% identity.

2872_at 185.1 A
Saccharomyces cerevisiae chromosome XII, complete chromosome sequence. Found forward in NC_001144 between 1042294 and 1043293 with 100% identity.

2873_at 643.2 P
Saccharomyces cerevisiae chromosome XII, complete chromosome sequence. Found forward in NC_001144 between 1043294 and 1044293 with 100% identity.

2874_g_at 140.1 P
Saccharomyces cerevisiae chromosome XII, complete chromosome sequence. Found forward in NC_001144 between 1043294 and 1044293 with 100% identity.

2789_s_at 234.0 A
Saccharomyces cerevisiae chromosome XII, complete chromosome sequence. Found forward in NC_001144 between 1044294 and 1045293 with 100% identity.

2790_s_at 304.7 P
Saccharomyces cerevisiae chromosome XII, complete chromosome sequence. Found forward in NC_001144 between 1045294 and 1046293 with 100% identity.

2791_s_at 218.2 A
Saccharomyces cerevisiae chromosome XII, complete chromosome sequence. Found forward in NC_001144 between 1046294 and 1047293 with 100% identity.

2792_s_at 74.8 A
Saccharomyces cerevisiae chromosome XII, complete chromosome sequence. Found forward in NC_001144 between 1047294 and 1048293 with 100% identity.

2793_s_at 428.2 P
Saccharomyces cerevisiae chromosome XII, complete chromosome sequence. Found forward in NC_001144 between 1048294 and 1049293 with 100% identity.

2794_s_at 1780.5 P
Saccharomyces cerevisiae chromosome XII, complete chromosome sequence. Found forward in NC_001144 between 1049294 and 1050293 with 100% identity.

2795_s_at 1859.0 P
Saccharomyces cerevisiae chromosome XII, complete chromosome sequence. Found forward in

NC_001144 between 1050294 and 1051293 with 100% identity.
2796_f_at 3472.4 P
Saccharomyces cerevisiae chromosome XII, complete chromosome sequence. Found forward in NC_001144 between 1051294 and 1051379 with 100% identity.
2797_at 160.6 P
Saccharomyces cerevisiae chromosome XII, complete chromosome sequence. Found forward in NC_001144 between 1071425 and 1072424 with 100% identity.
2798_g_at 215.4 P
Saccharomyces cerevisiae chromosome XII, complete chromosome sequence. Found forward in NC_001144 between 1071425 and 1072424 with 100% identity.
2799_at -60.6 A
Saccharomyces cerevisiae chromosome XIII, complete chromosome sequence. Found forward in NC_001145 between 63082 and 64081 with 100% identity.
2800_at 392.6 P
Saccharomyces cerevisiae chromosome XIII, complete chromosome sequence. Found forward in NC_001145 between 64082 and 65081 with 100% identity.
2801_at 222.5 A
Saccharomyces cerevisiae chromosome XIII, complete chromosome sequence. Found forward in NC_001145 between 65082 and 66081 with 100% identity.
2802_at 589.9 A
Saccharomyces cerevisiae chromosome XIII, complete chromosome sequence. Found forward in NC_001145 between 66082 and 67081 with 100% identity.
2803_at -302.4 A
Saccharomyces cerevisiae chromosome XIII, complete chromosome sequence. Found forward in NC_001145 between 67082 and 68081 with 100% identity.
2804_at 493.8 P
Saccharomyces cerevisiae chromosome XIII, complete chromosome sequence. Found forward in NC_001145 between 68082 and 69081 with 100% identity.
2805_g_at 2272.5 P
Saccharomyces cerevisiae chromosome XIII, complete chromosome sequence. Found forward in NC_001145 between 68082 and 69081 with 100% identity.
2806_s_at 2402.8 P
Saccharomyces cerevisiae chromosome XIII, complete chromosome sequence. Found forward in NC_001145 between 69082 and 69200 with 100% identity.
2807_at 1282.9 P
Saccharomyces cerevisiae chromosome XIII, complete chromosome sequence. Found forward in NC_001145 between 153719 and 154718 with 100% identity.
2808_at -1536.4 A
Saccharomyces cerevisiae chromosome XIII, complete chromosome sequence. Found forward in NC_001145 between 154719 and 155718 with 100% identity.
2809_at -58.5 A
Saccharomyces cerevisiae chromosome XIII, complete chromosome sequence. Found forward in NC_001145 between 155719 and 156718 with 100% identity.
2810_at 323.3 P
Saccharomyces cerevisiae chromosome XIII, complete chromosome sequence. Found forward in NC_001145 between 156719 and 157718 with 100% identity.
2811_at 436.2 A
Saccharomyces cerevisiae chromosome XIII, complete chromosome sequence. Found forward in NC_001145 between 157719 and 158718 with 100% identity.
2812_at 30.4 A
Saccharomyces cerevisiae chromosome XIII, complete chromosome sequence. Found forward in NC_001145 between 183363 and 184362 with 100% identity.
2813_at 823.0 P
Saccharomyces cerevisiae chromosome XIII, complete chromosome sequence. Found forward in NC_001145 between 189363 and 190244 with 100% identity.
2814_at -44.3 A

Saccharomyces cerevisiae chromosome XIII, complete chromosome sequence. Found forward in NC_001145 between 195413 and 196412 with 100% identity.
2815_at 2760.5 P
Saccharomyces cerevisiae chromosome XIII, complete chromosome sequence. Found forward in NC_001145 between 201413 and 202412 with 100% identity.
2816_at 5954.9 P
Saccharomyces cerevisiae chromosome XIII, complete chromosome sequence. Found forward in NC_001145 between 202413 and 202775 with 100% identity.
2817_at 3355.5 P
Saccharomyces cerevisiae chromosome XIII, complete chromosome sequence. Found forward in NC_001145 between 356810 and 357809 with 100% identity.
2818_at 443.5 P
Saccharomyces cerevisiae chromosome XIII, complete chromosome sequence. Found forward in NC_001145 between 357810 and 358809 with 100% identity.
2819_s_at 1821.0 P
Saccharomyces cerevisiae chromosome XIII, complete chromosome sequence. Found forward in NC_001145 between 358810 and 359809 with 100% identity.
2821_at -177.7 A
Saccharomyces cerevisiae chromosome XIII, complete chromosome sequence. Found forward in NC_001145 between 360810 and 361809 with 100% identity.
2822_at 1401.4 P
Saccharomyces cerevisiae chromosome XIII, complete chromosome sequence. Found forward in NC_001145 between 361810 and 362701 with 100% identity.
2823_at -43.5 P
Saccharomyces cerevisiae chromosome XIII, complete chromosome sequence. Found forward in NC_001145 between 368593 and 369592 with 100% identity.
2824_at 1900.8 P
Saccharomyces cerevisiae chromosome XIII, complete chromosome sequence. Found forward in NC_001145 between 369593 and 370592 with 100% identity.
2825_at 222.3 P
Saccharomyces cerevisiae chromosome XIII, complete chromosome sequence. Found forward in NC_001145 between 370593 and 371592 with 100% identity.
2826_at 302.9 A
Saccharomyces cerevisiae chromosome XIII, complete chromosome sequence. Found forward in NC_001145 between 371593 and 372592 with 100% identity.
2827_g_at 187.5 A
Saccharomyces cerevisiae chromosome XIII, complete chromosome sequence. Found forward in NC_001145 between 371593 and 372592 with 100% identity.
2828_at -11.1 A
Saccharomyces cerevisiae chromosome XIII, complete chromosome sequence. Found forward in NC_001145 between 372593 and 373592 with 100% identity.
2829_f_at 2681.4 P
Saccharomyces cerevisiae chromosome XIII, complete chromosome sequence. Found forward in NC_001145 between 373593 and 374592 with 100% identity.
2748_at -255.3 A
Saccharomyces cerevisiae chromosome XIII, complete chromosome sequence. Found forward in NC_001145 between 378593 and 379592 with 100% identity.
2749_s_at 565.3 P
Saccharomyces cerevisiae chromosome XIII, complete chromosome sequence. Found forward in NC_001145 between 379593 and 379699 with 100% identity.
2750_at 204.2 A
Saccharomyces cerevisiae chromosome XIII, complete chromosome sequence. Found forward in NC_001145 between 677692 and 678691 with 100% identity.
2751_at 893.7 A
Saccharomyces cerevisiae chromosome XIII, complete chromosome sequence. Found forward in NC_001145 between 678692 and 679691 with 100% identity.

2752_at -30.5 A
Saccharomyces cerevisiae chromosome XIII, complete chromosome sequence. Found forward in NC_001145 between 679692 and 680691 with 100% identity.
2753_at 157.2 A
Saccharomyces cerevisiae chromosome XIII, complete chromosome sequence. Found forward in NC_001145 between 680692 and 681691 with 100% identity.
2754_at -135.1 A
Saccharomyces cerevisiae chromosome XIII, complete chromosome sequence. Found forward in NC_001145 between 681692 and 682691 with 100% identity.
2755_at -5.8 A
Saccharomyces cerevisiae chromosome XIII, complete chromosome sequence. Found forward in NC_001145 between 682692 and 683691 with 100% identity.
2756_at 309.0 P
Saccharomyces cerevisiae chromosome XIII, complete chromosome sequence. Found forward in NC_001145 between 683692 and 684691 with 100% identity.
2757_g_at 6419.6 P
Saccharomyces cerevisiae chromosome XIII, complete chromosome sequence. Found forward in NC_001145 between 683692 and 684691 with 100% identity.
2758_s_at 8208.0 P
Saccharomyces cerevisiae chromosome XIII, complete chromosome sequence. Found forward in NC_001145 between 684692 and 685297 with 100% identity.
2759_at -256.4 A
Saccharomyces cerevisiae chromosome XIII, complete chromosome sequence. Found forward in NC_001145 between 704078 and 705077 with 100% identity.
2760_at 877.5 P
Saccharomyces cerevisiae chromosome XIII, complete chromosome sequence. Found forward in NC_001145 between 705078 and 706077 with 100% identity.
2761_at 888.8 A
Saccharomyces cerevisiae chromosome XIII, complete chromosome sequence. Found forward in NC_001145 between 706078 and 707077 with 100% identity.
2762_at 20.9 A
Saccharomyces cerevisiae chromosome XIII, complete chromosome sequence. Found forward in NC_001145 between 707078 and 708077 with 100% identity.
2763_s_at 51.4 A
Saccharomyces cerevisiae chromosome XIII, complete chromosome sequence. Found forward in NC_001145 between 708078 and 709077 with 100% identity.
2764_s_at 589.5 P
Saccharomyces cerevisiae chromosome XIII, complete chromosome sequence. Found forward in NC_001145 between 709078 and 710077 with 100% identity.
2765_s_at -444.2 A
Saccharomyces cerevisiae chromosome XIII, complete chromosome sequence. Found forward in NC_001145 between 710078 and 711077 with 100% identity.
2766_s_at 2642.6 P
Saccharomyces cerevisiae chromosome XIII, complete chromosome sequence. Found forward in NC_001145 between 711078 and 711608 with 100% identity.
2767_at 543.4 A
Saccharomyces cerevisiae chromosome XIII, complete chromosome sequence. Found forward in NC_001145 between 726433 and 727432 with 100% identity.
2768_at 356.1 A
Saccharomyces cerevisiae chromosome XIII, complete chromosome sequence. Found forward in NC_001145 between 727433 and 728432 with 100% identity.
2769_at -714.8 A
Saccharomyces cerevisiae chromosome XIII, complete chromosome sequence. Found forward in NC_001145 between 728433 and 729432 with 100% identity.
2770_at 41.9 A
Saccharomyces cerevisiae chromosome XIII, complete chromosome sequence. Found forward in

NC_001145 between 729433 and 730432 with 100% identity.

2771_at 378.3 A

Saccharomyces cerevisiae chromosome XIII, complete chromosome sequence. Found forward in NC_001145 between 730433 and 731432 with 100% identity.

2772_at 686.3 P

Saccharomyces cerevisiae chromosome XIII, complete chromosome sequence. Found forward in NC_001145 between 731433 and 731964 with 100% identity.

2773_at -241.4 A

Saccharomyces cerevisiae chromosome XIII, complete chromosome sequence. Found forward in NC_001145 between 827528 and 828527 with 100% identity.

2774_at 265.2 A

Saccharomyces cerevisiae chromosome XIII, complete chromosome sequence. Found forward in NC_001145 between 828528 and 829527 with 100% identity.

2775_at 462.4 A

Saccharomyces cerevisiae chromosome XIII, complete chromosome sequence. Found forward in NC_001145 between 829528 and 830527 with 100% identity.

2776_at -748.6 A

Saccharomyces cerevisiae chromosome XIII, complete chromosome sequence. Found forward in NC_001145 between 830528 and 831527 with 100% identity.

2777_at 172.3 A

Saccharomyces cerevisiae chromosome XIII, complete chromosome sequence. Found forward in NC_001145 between 831528 and 832527 with 100% identity.

2778_g_at 766.0 P

Saccharomyces cerevisiae chromosome XIII, complete chromosome sequence. Found forward in NC_001145 between 831528 and 832527 with 100% identity.

2779_s_at 1449.3 P

Saccharomyces cerevisiae chromosome XIII, complete chromosome sequence. Found forward in NC_001145 between 832528 and 832753 with 100% identity.

2780_at 687.2 P

Saccharomyces cerevisiae chromosome XIII, complete chromosome sequence. Found forward in NC_001145 between 842936 and 843935 with 100% identity.

2781_at 326.0 M

Saccharomyces cerevisiae chromosome XIII, complete chromosome sequence. Found forward in NC_001145 between 843936 and 844935 with 100% identity.

2782_at 121.2 A

Saccharomyces cerevisiae chromosome XIII, complete chromosome sequence. Found forward in NC_001145 between 844936 and 845935 with 100% identity.

2783_g_at 849.6 P

Saccharomyces cerevisiae chromosome XIII, complete chromosome sequence. Found forward in NC_001145 between 844936 and 845935 with 100% identity.

2784_s_at 358.8 A

Saccharomyces cerevisiae chromosome XIII, complete chromosome sequence. Found forward in NC_001145 between 845936 and 846935 with 100% identity.

2785_s_at 1166.1 P

Saccharomyces cerevisiae chromosome XIII, complete chromosome sequence. Found forward in NC_001145 between 846936 and 847935 with 100% identity.

2786_s_at 3635.8 P

Saccharomyces cerevisiae chromosome XIII, complete chromosome sequence. Found forward in NC_001145 between 847936 and 847986 with 100% identity.

2787_at 315.7 A

Saccharomyces cerevisiae chromosome XIII, complete chromosome sequence. Found forward in NC_001145 between 879563 and 880562 with 100% identity.

2788_at 288.5 A

Saccharomyces cerevisiae chromosome XIII, complete chromosome sequence. Found forward in NC_001145 between 880563 and 881562 with 100% identity.

2703_g_at -221.3 A

Saccharomyces cerevisiae chromosome XIII, complete chromosome sequence. Found forward in NC_001145 between 880563 and 881562 with 100% identity.
2704_s_at 449.8 P
Saccharomyces cerevisiae chromosome XIII, complete chromosome sequence. Found forward in NC_001145 between 881563 and 882562 with 100% identity.
2705_s_at -134.3 A
Saccharomyces cerevisiae chromosome XIII, complete chromosome sequence. Found forward in NC_001145 between 882563 and 883562 with 100% identity.
2706_s_at 523.3 A
Saccharomyces cerevisiae chromosome XIII, complete chromosome sequence. Found forward in NC_001145 between 883563 and 884562 with 100% identity.
2707_s_at 258.6 A
Saccharomyces cerevisiae chromosome XIII, complete chromosome sequence. Found forward in NC_001145 between 884563 and 885562 with 100% identity.
2708_s_at 633.0 P
Saccharomyces cerevisiae chromosome XIII, complete chromosome sequence. Found forward in NC_001145 between 885563 and 886016 with 100% identity.
2709_s_at 1173.2 P
Saccharomyces cerevisiae chromosome XIV, complete chromosome sequence. Found forward in NC_001146 between 871 and 1870 with 100% identity.
2710_s_at 423.8 P
Saccharomyces cerevisiae chromosome XIV, complete chromosome sequence. Found forward in NC_001146 between 1871 and 2870 with 100% identity.
2711_s_at 1914.6 P
Saccharomyces cerevisiae chromosome XIV, complete chromosome sequence. Found forward in NC_001146 between 2871 and 3870 with 100% identity.
2712_s_at 556.3 P
Saccharomyces cerevisiae chromosome XIV, complete chromosome sequence. Found forward in NC_001146 between 3871 and 4870 with 100% identity.
2713_s_at 641.5 P
Saccharomyces cerevisiae chromosome XIV, complete chromosome sequence. Found forward in NC_001146 between 4871 and 5870 with 100% identity.
2714_s_at 6044.8 P
Saccharomyces cerevisiae chromosome XIV, complete chromosome sequence. Found forward in NC_001146 between 5871 and 6080 with 100% identity.
2715_at 47.5 A
Saccharomyces cerevisiae chromosome XIV, complete chromosome sequence. Found forward in NC_001146 between 130021 and 131020 with 100% identity.
2716_at 484.9 A
Saccharomyces cerevisiae chromosome XIV, complete chromosome sequence. Found forward in NC_001146 between 131021 and 132020 with 100% identity.
2717_at 1133.6 A
Saccharomyces cerevisiae chromosome XIV, complete chromosome sequence. Found forward in NC_001146 between 132021 and 133020 with 100% identity.
2718_at 1714.5 A
Saccharomyces cerevisiae chromosome XIV, complete chromosome sequence. Found forward in NC_001146 between 133021 and 134020 with 100% identity.
2719_at -694.7 A
Saccharomyces cerevisiae chromosome XIV, complete chromosome sequence. Found forward in NC_001146 between 134021 and 135020 with 100% identity.
2720_at 96.2 A
Saccharomyces cerevisiae chromosome XIV, complete chromosome sequence. Found forward in NC_001146 between 135021 and 135939 with 100% identity.
2721_at 103.3 A
Saccharomyces cerevisiae chromosome XIV, complete chromosome sequence. Found forward in NC_001146 between 147395 and 148394 with 100% identity.

2722_g_at 252.4 A
Saccharomyces cerevisiae chromosome XIV, complete chromosome sequence. Found forward in NC_001146 between 147395 and 148394 with 100% identity.
2723_s_at -1690.7 A
Saccharomyces cerevisiae chromosome XIV, complete chromosome sequence. Found forward in NC_001146 between 148395 and 149394 with 100% identity.
2724_s_at 752.4 P
Saccharomyces cerevisiae chromosome XIV, complete chromosome sequence. Found forward in NC_001146 between 149395 and 150394 with 100% identity.
2725_s_at 52.2 A
Saccharomyces cerevisiae chromosome XIV, complete chromosome sequence. Found forward in NC_001146 between 150395 and 151394 with 100% identity.
2726_s_at 469.0 P
Saccharomyces cerevisiae chromosome XIV, complete chromosome sequence. Found forward in NC_001146 between 151395 and 152394 with 100% identity.
2727_s_at 1833.7 P
Saccharomyces cerevisiae chromosome XIV, complete chromosome sequence. Found forward in NC_001146 between 152395 and 153394 with 100% identity.
2728_s_at 1380.3 P
Saccharomyces cerevisiae chromosome XIV, complete chromosome sequence. Found forward in NC_001146 between 153395 and 154379 with 100% identity.
2729_at 145.4 A
Saccharomyces cerevisiae chromosome XIV, complete chromosome sequence. Found forward in NC_001146 between 161130 and 162129 with 100% identity.
2730_at -90.2 A
Saccharomyces cerevisiae chromosome XIV, complete chromosome sequence. Found forward in NC_001146 between 162130 and 163129 with 100% identity.
2731_at 1421.2 A
Saccharomyces cerevisiae chromosome XIV, complete chromosome sequence. Found forward in NC_001146 between 163130 and 164129 with 100% identity.
2732_at 168.0 A
Saccharomyces cerevisiae chromosome XIV, complete chromosome sequence. Found forward in NC_001146 between 164130 and 165129 with 100% identity.
2733_g_at 1642.7 P
Saccharomyces cerevisiae chromosome XIV, complete chromosome sequence. Found forward in NC_001146 between 164130 and 165129 with 100% identity.
2734_s_at 1489.3 P
Saccharomyces cerevisiae chromosome XIV, complete chromosome sequence. Found forward in NC_001146 between 165130 and 166129 with 100% identity.
2735_s_at 3907.0 P
Saccharomyces cerevisiae chromosome XIV, complete chromosome sequence. Found forward in NC_001146 between 166130 and 166596 with 100% identity.
2736_at -198.0 A
Saccharomyces cerevisiae chromosome XIV, complete chromosome sequence. Found forward in NC_001146 between 173087 and 174086 with 100% identity.
2737_at 37.3 P
Saccharomyces cerevisiae chromosome XIV, complete chromosome sequence. Found forward in NC_001146 between 174087 and 175086 with 100% identity.
2738_at -1103.4 P
Saccharomyces cerevisiae chromosome XIV, complete chromosome sequence. Found forward in NC_001146 between 175087 and 176086 with 100% identity.
2739_g_at 181.9 P
Saccharomyces cerevisiae chromosome XIV, complete chromosome sequence. Found forward in NC_001146 between 175087 and 176086 with 100% identity.
2740_s_at 103.9 A
Saccharomyces cerevisiae chromosome XIV, complete chromosome sequence. Found forward in

NC_001146 between 176087 and 177086 with 100% identity.
2741_s_at 163.4 A
Saccharomyces cerevisiae chromosome XIV, complete chromosome sequence. Found forward in NC_001146 between 177087 and 178086 with 100% identity.
2742_s_at 306.1 A
Saccharomyces cerevisiae chromosome XIV, complete chromosome sequence. Found forward in NC_001146 between 178087 and 178847 with 100% identity.
2743_at -66.5 A
Saccharomyces cerevisiae chromosome XIV, complete chromosome sequence. Found forward in NC_001146 between 309454 and 310453 with 100% identity.
2744_at 512.0 P
Saccharomyces cerevisiae chromosome XIV, complete chromosome sequence. Found forward in NC_001146 between 310454 and 311453 with 100% identity.
2745_g_at 372.6 P
Saccharomyces cerevisiae chromosome XIV, complete chromosome sequence. Found forward in NC_001146 between 310454 and 311453 with 100% identity.
2660_s_at 120.6 A
Saccharomyces cerevisiae chromosome XIV, complete chromosome sequence. Found forward in NC_001146 between 311454 and 312453 with 100% identity.
2661_s_at 132.9 A
Saccharomyces cerevisiae chromosome XIV, complete chromosome sequence. Found forward in NC_001146 between 312454 and 313453 with 100% identity.
2662_s_at 1013.3 P
Saccharomyces cerevisiae chromosome XIV, complete chromosome sequence. Found forward in NC_001146 between 313454 and 314453 with 100% identity.
2663_s_at 1532.2 P
Saccharomyces cerevisiae chromosome XIV, complete chromosome sequence. Found forward in NC_001146 between 314454 and 315379 with 100% identity.
2664_at 2520.6 A
Saccharomyces cerevisiae chromosome XIV, complete chromosome sequence. Found forward in NC_001146 between 524084 and 525083 with 100% identity.
2665_at 223.8 P
Saccharomyces cerevisiae chromosome XIV, complete chromosome sequence. Found forward in NC_001146 between 525084 and 526083 with 100% identity.
2666_s_at -768.0 M
Saccharomyces cerevisiae chromosome XIV, complete chromosome sequence. Found forward in NC_001146 between 526084 and 527083 with 100% identity.
2667_s_at 655.3 P
Saccharomyces cerevisiae chromosome XIV, complete chromosome sequence. Found forward in NC_001146 between 527084 and 528083 with 100% identity.
2668_s_at 780.8 P
Saccharomyces cerevisiae chromosome XIV, complete chromosome sequence. Found forward in NC_001146 between 528084 and 529079 with 100% identity.
2669_at 2447.0 P
Saccharomyces cerevisiae chromosome XIV, complete chromosome sequence. Found forward in NC_001146 between 655170 and 656169 with 100% identity.
2670_at 190.6 P
Saccharomyces cerevisiae chromosome XIV, complete chromosome sequence. Found forward in NC_001146 between 656170 and 657169 with 100% identity.
2671_at -367.7 A
Saccharomyces cerevisiae chromosome XIV, complete chromosome sequence. Found forward in NC_001146 between 657170 and 658169 with 100% identity.
2672_at 164.8 A
Saccharomyces cerevisiae chromosome XIV, complete chromosome sequence. Found forward in NC_001146 between 658170 and 659169 with 100% identity.
2673_at 172.8 P

Saccharomyces cerevisiae chromosome XIV, complete chromosome sequence. Found forward in NC_001146 between 659170 and 660169 with 100% identity.
2674_at -203.7 A
Saccharomyces cerevisiae chromosome XIV, complete chromosome sequence. Found forward in NC_001146 between 660170 and 661169 with 100% identity.
2675_at 653.2 P
Saccharomyces cerevisiae chromosome XIV, complete chromosome sequence. Found forward in NC_001146 between 661170 and 661997 with 100% identity.
2676_at 0.3 M
Saccharomyces cerevisiae chromosome XIV, complete chromosome sequence. Found forward in NC_001146 between 681191 and 682190 with 100% identity.
2677_at 52.8 A
Saccharomyces cerevisiae chromosome XIV, complete chromosome sequence. Found forward in NC_001146 between 682191 and 683190 with 100% identity.
2678_at -2026.2 A
Saccharomyces cerevisiae chromosome XIV, complete chromosome sequence. Found forward in NC_001146 between 683191 and 684190 with 100% identity.
2679_at 715.7 A
Saccharomyces cerevisiae chromosome XIV, complete chromosome sequence. Found forward in NC_001146 between 684191 and 685190 with 100% identity.
2680_at -72.6 A
Saccharomyces cerevisiae chromosome XIV, complete chromosome sequence. Found forward in NC_001146 between 685191 and 686190 with 100% identity.
2681_g_at 2380.1 P
Saccharomyces cerevisiae chromosome XIV, complete chromosome sequence. Found forward in NC_001146 between 685191 and 686190 with 100% identity.
2682_s_at 1700.5 A
Saccharomyces cerevisiae chromosome XIV, complete chromosome sequence. Found forward in NC_001146 between 686191 and 686613 with 100% identity.
2683_at -985.3 A
Saccharomyces cerevisiae chromosome XIV, complete chromosome sequence. Found forward in NC_001146 between 761618 and 762617 with 100% identity.
2684_at -214.7 P
Saccharomyces cerevisiae chromosome XIV, complete chromosome sequence. Found forward in NC_001146 between 762618 and 763617 with 100% identity.
2685_at 1215.7 A
Saccharomyces cerevisiae chromosome XIV, complete chromosome sequence. Found forward in NC_001146 between 763618 and 764617 with 100% identity.
2686_at 959.6 M
Saccharomyces cerevisiae chromosome XIV, complete chromosome sequence. Found forward in NC_001146 between 764618 and 765617 with 100% identity.
2687_g_at 19.4 A
Saccharomyces cerevisiae chromosome XIV, complete chromosome sequence. Found forward in NC_001146 between 764618 and 765617 with 100% identity.
2688_s_at 690.6 A
Saccharomyces cerevisiae chromosome XIV, complete chromosome sequence. Found forward in NC_001146 between 765618 and 766617 with 100% identity.
2689_s_at -157.0 A
Saccharomyces cerevisiae chromosome XIV, complete chromosome sequence. Found forward in NC_001146 between 766618 and 767617 with 100% identity.
2690_s_at 842.4 A
Saccharomyces cerevisiae chromosome XIV, complete chromosome sequence. Found forward in NC_001146 between 767618 and 768617 with 100% identity.
2691_s_at -246.0 A
Saccharomyces cerevisiae chromosome XIV, complete chromosome sequence. Found forward in NC_001146 between 768618 and 768871 with 100% identity.

2692_at 117.9 A
Saccharomyces cerevisiae chromosome XV, complete chromosome sequence. Found forward in NC_001147 between 2078 and 3077 with 100% identity.
2693_at 590.0 P
Saccharomyces cerevisiae chromosome XV, complete chromosome sequence. Found forward in NC_001147 between 3078 and 4077 with 100% identity.
2694_at 1442.2 A
Saccharomyces cerevisiae chromosome XV, complete chromosome sequence. Found forward in NC_001147 between 4078 and 5077 with 100% identity.
2695_at -613.6 A
Saccharomyces cerevisiae chromosome XV, complete chromosome sequence. Found forward in NC_001147 between 5078 and 6077 with 100% identity.
2696_at 573.9 P
Saccharomyces cerevisiae chromosome XV, complete chromosome sequence. Found forward in NC_001147 between 6078 and 7077 with 100% identity.
2697_g_at 177.7 A
Saccharomyces cerevisiae chromosome XV, complete chromosome sequence. Found forward in NC_001147 between 6078 and 7077 with 100% identity.
2698_s_at 587.2 P
Saccharomyces cerevisiae chromosome XV, complete chromosome sequence. Found forward in NC_001147 between 7078 and 7615 with 100% identity.
2699_at 839.9 A
Saccharomyces cerevisiae chromosome XV, complete chromosome sequence. Found forward in NC_001147 between 169973 and 170972 with 100% identity.
2700_at 39.9 A
Saccharomyces cerevisiae chromosome XV, complete chromosome sequence. Found forward in NC_001147 between 170973 and 171972 with 100% identity.
2701_g_at 425.5 P
Saccharomyces cerevisiae chromosome XV, complete chromosome sequence. Found forward in NC_001147 between 170973 and 171972 with 100% identity.
2702_s_at 2003.5 P
Saccharomyces cerevisiae chromosome XV, complete chromosome sequence. Found forward in NC_001147 between 171973 and 172972 with 100% identity.
2618_s_at 558.9 A
Saccharomyces cerevisiae chromosome XV, complete chromosome sequence. Found forward in NC_001147 between 172973 and 173972 with 100% identity.
2619_s_at 24.6 A
Saccharomyces cerevisiae chromosome XV, complete chromosome sequence. Found forward in NC_001147 between 173973 and 174972 with 100% identity.
2620_s_at 74.6 A
Saccharomyces cerevisiae chromosome XV, complete chromosome sequence. Found forward in NC_001147 between 174973 and 175972 with 100% identity.
2621_s_at 896.0 P
Saccharomyces cerevisiae chromosome XV, complete chromosome sequence. Found forward in NC_001147 between 175973 and 176972 with 100% identity.
2622_s_at 1934.1 P
Saccharomyces cerevisiae chromosome XV, complete chromosome sequence. Found forward in NC_001147 between 176973 and 177972 with 100% identity.
2623_s_at -221.3 A
Saccharomyces cerevisiae chromosome XV, complete chromosome sequence. Found forward in NC_001147 between 177973 and 178972 with 100% identity.
2624_s_at 1444.1 P
Saccharomyces cerevisiae chromosome XV, complete chromosome sequence. Found forward in NC_001147 between 178973 and 179808 with 100% identity.
2625_at 710.0 A
Saccharomyces cerevisiae chromosome XV, complete chromosome sequence. Found forward in

NC_001147 between 346694 and 347693 with 100% identity.
2626_at 2051.7 A
Saccharomyces cerevisiae chromosome XV, complete chromosome sequence. Found forward in NC_001147 between 347694 and 348693 with 100% identity.
2627_at 1870.1 P
Saccharomyces cerevisiae chromosome XV, complete chromosome sequence. Found forward in NC_001147 between 348694 and 349693 with 100% identity.
2628_s_at 709.8 M
Saccharomyces cerevisiae chromosome XV, complete chromosome sequence. Found forward in NC_001147 between 349694 and 350693 with 100% identity.
2629_s_at 1438.8 P
Saccharomyces cerevisiae chromosome XV, complete chromosome sequence. Found forward in NC_001147 between 350694 and 351693 with 100% identity.
2630_s_at 975.2 P
Saccharomyces cerevisiae chromosome XV, complete chromosome sequence. Found forward in NC_001147 between 351694 and 352693 with 100% identity.
2631_s_at 1449.4 P
Saccharomyces cerevisiae chromosome XV, complete chromosome sequence. Found forward in NC_001147 between 352694 and 353362 with 100% identity.
2632_at 334.1 P
Saccharomyces cerevisiae chromosome XV, complete chromosome sequence. Found forward in NC_001147 between 540261 and 541260 with 100% identity.
2633_at 377.1 P
Saccharomyces cerevisiae chromosome XV, complete chromosome sequence. Found forward in NC_001147 between 541261 and 542260 with 100% identity.
2634_at 246.9 A
Saccharomyces cerevisiae chromosome XV, complete chromosome sequence. Found forward in NC_001147 between 542261 and 543260 with 100% identity.
2635_at 8.1 A
Saccharomyces cerevisiae chromosome XV, complete chromosome sequence. Found forward in NC_001147 between 543261 and 544260 with 100% identity.
2636_at 234.7 P
Saccharomyces cerevisiae chromosome XV, complete chromosome sequence. Found forward in NC_001147 between 544261 and 545260 with 100% identity.
2637_g_at 3123.9 P
Saccharomyces cerevisiae chromosome XV, complete chromosome sequence. Found forward in NC_001147 between 544261 and 545260 with 100% identity.
2638_s_at 6539.5 P
Saccharomyces cerevisiae chromosome XV, complete chromosome sequence. Found forward in NC_001147 between 545261 and 545831 with 100% identity.
2639_at -632.4 A
Saccharomyces cerevisiae chromosome XV, complete chromosome sequence. Found forward in NC_001147 between 618016 and 619015 with 100% identity.
2640_at 730.7 A
Saccharomyces cerevisiae chromosome XV, complete chromosome sequence. Found forward in NC_001147 between 619016 and 620015 with 100% identity.
2641_g_at 3132.3 P
Saccharomyces cerevisiae chromosome XV, complete chromosome sequence. Found forward in NC_001147 between 619016 and 620015 with 100% identity.
2642_s_at 1237.8 P
Saccharomyces cerevisiae chromosome XV, complete chromosome sequence. Found forward in NC_001147 between 620016 and 621015 with 100% identity.
2643_s_at 3155.2 P
Saccharomyces cerevisiae chromosome XV, complete chromosome sequence. Found forward in NC_001147 between 621016 and 622015 with 100% identity.
2644_s_at 2617.1 P

Saccharomyces cerevisiae chromosome XV, complete chromosome sequence. Found forward in NC_001147 between 622016 and 623015 with 100% identity.
2645_s_at 9860.6 P
Saccharomyces cerevisiae chromosome XV, complete chromosome sequence. Found forward in NC_001147 between 623016 and 623873 with 100% identity.
2646_at -1450.4 A
Saccharomyces cerevisiae chromosome XV, complete chromosome sequence. Found forward in NC_001147 between 730506 and 731505 with 100% identity.
2647_at -766.5 A
Saccharomyces cerevisiae chromosome XV, complete chromosome sequence. Found forward in NC_001147 between 731506 and 732505 with 100% identity.
2648_at 134.0 A
Saccharomyces cerevisiae chromosome XV, complete chromosome sequence. Found forward in NC_001147 between 732506 and 733505 with 100% identity.
2649_at -949.9 A
Saccharomyces cerevisiae chromosome XV, complete chromosome sequence. Found forward in NC_001147 between 733506 and 734505 with 100% identity.
2650_g_at 774.5 M
Saccharomyces cerevisiae chromosome XV, complete chromosome sequence. Found forward in NC_001147 between 733506 and 734505 with 100% identity.
2651_s_at 924.4 P
Saccharomyces cerevisiae chromosome XV, complete chromosome sequence. Found forward in NC_001147 between 734506 and 735505 with 100% identity.
2652_s_at 1948.5 P
Saccharomyces cerevisiae chromosome XV, complete chromosome sequence. Found forward in NC_001147 between 735506 and 735675 with 100% identity.
2653_at 413.7 A
Saccharomyces cerevisiae chromosome XV, complete chromosome sequence. Found forward in NC_001147 between 855642 and 856641 with 100% identity.
2654_at 114.2 A
Saccharomyces cerevisiae chromosome XV, complete chromosome sequence. Found forward in NC_001147 between 856642 and 857641 with 100% identity.
2655_at 1825.9 P
Saccharomyces cerevisiae chromosome XV, complete chromosome sequence. Found forward in NC_001147 between 857642 and 858641 with 100% identity.
2656_at 1303.0 P
Saccharomyces cerevisiae chromosome XV, complete chromosome sequence. Found forward in NC_001147 between 858642 and 859641 with 100% identity.
2657_at 100.7 A
Saccharomyces cerevisiae chromosome XV, complete chromosome sequence. Found forward in NC_001147 between 859642 and 860641 with 100% identity.
2658_at 31.9 A
Saccharomyces cerevisiae chromosome XV, complete chromosome sequence. Found forward in NC_001147 between 860642 and 861641 with 100% identity.
2659_g_at 233.6 A
Saccharomyces cerevisiae chromosome XV, complete chromosome sequence. Found forward in NC_001147 between 860642 and 861641 with 100% identity.
2575_s_at 1710.0 P
Saccharomyces cerevisiae chromosome XV, complete chromosome sequence. Found forward in NC_001147 between 861642 and 862641 with 100% identity.
2576_s_at 1155.7 P
Saccharomyces cerevisiae chromosome XV, complete chromosome sequence. Found forward in NC_001147 between 862642 and 863641 with 100% identity.
2577_s_at 1340.6 P
Saccharomyces cerevisiae chromosome XV, complete chromosome sequence. Found forward in NC_001147 between 863642 and 864641 with 100% identity.

2578_s_at 2934.4 P
Saccharomyces cerevisiae chromosome XV, complete chromosome sequence. Found forward in NC_001147 between 864642 and 865088 with 100% identity.
2579_at 1183.9 A
Saccharomyces cerevisiae chromosome XV, complete chromosome sequence. Found forward in NC_001147 between 946724 and 947723 with 100% identity.
2580_at 185.3 P
Saccharomyces cerevisiae chromosome XV, complete chromosome sequence. Found forward in NC_001147 between 947724 and 948723 with 100% identity.
2581_at 363.2 P
Saccharomyces cerevisiae chromosome XV, complete chromosome sequence. Found forward in NC_001147 between 948724 and 949723 with 100% identity.
2582_at -960.3 A
Saccharomyces cerevisiae chromosome XV, complete chromosome sequence. Found forward in NC_001147 between 949724 and 950723 with 100% identity.
2583_g_at 1352.6 P
Saccharomyces cerevisiae chromosome XV, complete chromosome sequence. Found forward in NC_001147 between 949724 and 950723 with 100% identity.
2584_s_at 1805.9 P
Saccharomyces cerevisiae chromosome XV, complete chromosome sequence. Found forward in NC_001147 between 950724 and 951723 with 100% identity.
2585_s_at 4335.9 P
Saccharomyces cerevisiae chromosome XV, complete chromosome sequence. Found forward in NC_001147 between 951724 and 952723 with 100% identity.
2586_s_at 2717.6 P
Saccharomyces cerevisiae chromosome XV, complete chromosome sequence. Found forward in NC_001147 between 952724 and 953361 with 100% identity.
2587_at 755.5 P
Saccharomyces cerevisiae chromosome XV, complete chromosome sequence. Found forward in NC_001147 between 959693 and 960692 with 100% identity.
2588_at 1523.4 P
Saccharomyces cerevisiae chromosome XV, complete chromosome sequence. Found forward in NC_001147 between 960693 and 961692 with 100% identity.
2589_g_at 3535.3 P
Saccharomyces cerevisiae chromosome XV, complete chromosome sequence. Found forward in NC_001147 between 960693 and 961692 with 100% identity.
2590_s_at 5792.2 P
Saccharomyces cerevisiae chromosome XV, complete chromosome sequence. Found forward in NC_001147 between 961693 and 962692 with 100% identity.
2591_s_at 3297.6 P
Saccharomyces cerevisiae chromosome XV, complete chromosome sequence. Found forward in NC_001147 between 962693 and 963692 with 100% identity.
2592_s_at 6892.8 P
Saccharomyces cerevisiae chromosome XV, complete chromosome sequence. Found forward in NC_001147 between 963693 and 964692 with 100% identity.
2593_s_at 9373.4 P
Saccharomyces cerevisiae chromosome XV, complete chromosome sequence. Found forward in NC_001147 between 964693 and 965472 with 100% identity.
2594_at 520.5 P
Saccharomyces cerevisiae chromosome XVI, complete chromosome sequence. Found forward in NC_001148 between 19079 and 20078 with 100% identity.
2595_at -34.8 P
Saccharomyces cerevisiae chromosome XVI, complete chromosome sequence. Found forward in NC_001148 between 20079 and 21078 with 100% identity.
2596_at -1758.8 A
Saccharomyces cerevisiae chromosome XVI, complete chromosome sequence. Found forward in

NC_001148 between 21079 and 22078 with 100% identity.

2597_at -52.6 A

Saccharomyces cerevisiae chromosome XVI, complete chromosome sequence. Found forward in NC_001148 between 22079 and 23078 with 100% identity.

2598_g_at 1349.5 P

Saccharomyces cerevisiae chromosome XVI, complete chromosome sequence. Found forward in NC_001148 between 22079 and 23078 with 100% identity.

2599_s_at 6564.8 P

Saccharomyces cerevisiae chromosome XVI, complete chromosome sequence. Found forward in NC_001148 between 23079 and 24078 with 100% identity.

2600_s_at 3110.1 P

Saccharomyces cerevisiae chromosome XVI, complete chromosome sequence. Found forward in NC_001148 between 24079 and 24201 with 100% identity.

2601_at 591.7 P

Saccharomyces cerevisiae chromosome XVI, complete chromosome sequence. Found forward in NC_001148 between 108147 and 109146 with 100% identity.

2602_g_at 4647.4 P

Saccharomyces cerevisiae chromosome XVI, complete chromosome sequence. Found forward in NC_001148 between 108147 and 109146 with 100% identity.

2603_s_at 3923.0 P

Saccharomyces cerevisiae chromosome XVI, complete chromosome sequence. Found forward in NC_001148 between 109147 and 110146 with 100% identity.

2604_s_at 8861.2 P

Saccharomyces cerevisiae chromosome XVI, complete chromosome sequence. Found forward in NC_001148 between 110147 and 111146 with 100% identity.

2605_s_at 11776.5 P

Saccharomyces cerevisiae chromosome XVI, complete chromosome sequence. Found forward in NC_001148 between 111147 and 112146 with 100% identity.

2606_s_at 10569.7 P

Saccharomyces cerevisiae chromosome XVI, complete chromosome sequence. Found forward in NC_001148 between 112147 and 113146 with 100% identity.

2607_s_at 12824.6 P

Saccharomyces cerevisiae chromosome XVI, complete chromosome sequence. Found forward in NC_001148 between 113147 and 113815 with 100% identity.

2608_at 459.4 P

Saccharomyces cerevisiae chromosome XVI, complete chromosome sequence. Found forward in NC_001148 between 140119 and 141118 with 100% identity.

2609_at 1883.7 P

Saccharomyces cerevisiae chromosome XVI, complete chromosome sequence. Found forward in NC_001148 between 141119 and 142118 with 100% identity.

2610_at 119.1 A

Saccharomyces cerevisiae chromosome XVI, complete chromosome sequence. Found forward in NC_001148 between 142119 and 143118 with 100% identity.

2611_at 535.1 P

Saccharomyces cerevisiae chromosome XVI, complete chromosome sequence. Found forward in NC_001148 between 143119 and 144118 with 100% identity.

2612_g_at 884.7 A

Saccharomyces cerevisiae chromosome XVI, complete chromosome sequence. Found forward in NC_001148 between 143119 and 144118 with 100% identity.

2613_s_at 748.4 A

Saccharomyces cerevisiae chromosome XVI, complete chromosome sequence. Found forward in NC_001148 between 144119 and 145118 with 100% identity.

2614_s_at 516.3 P

Saccharomyces cerevisiae chromosome XVI, complete chromosome sequence. Found forward in NC_001148 between 145119 and 146118 with 100% identity.

2615_s_at 341.6 P

Saccharomyces cerevisiae chromosome XVI, complete chromosome sequence. Found forward in NC_001148 between 146119 and 146628 with 100% identity.

2616_at -41.1 A

Saccharomyces cerevisiae chromosome XVI, complete chromosome sequence. Found forward in NC_001148 between 385268 and 386267 with 100% identity.

2617_at 639.7 P

Saccharomyces cerevisiae chromosome XVI, complete chromosome sequence. Found forward in NC_001148 between 386268 and 387267 with 100% identity.

2532_g_at 189.8 A

Saccharomyces cerevisiae chromosome XVI, complete chromosome sequence. Found forward in NC_001148 between 386268 and 387267 with 100% identity.

2533_s_at 458.9 P

Saccharomyces cerevisiae chromosome XVI, complete chromosome sequence. Found forward in NC_001148 between 387268 and 388267 with 100% identity.

2534_s_at 1820.4 P

Saccharomyces cerevisiae chromosome XVI, complete chromosome sequence. Found forward in NC_001148 between 388268 and 389267 with 100% identity.

2535_s_at 2088.1 P

Saccharomyces cerevisiae chromosome XVI, complete chromosome sequence. Found forward in NC_001148 between 389268 and 390267 with 100% identity.

2536_s_at 1677.2 P

Saccharomyces cerevisiae chromosome XVI, complete chromosome sequence. Found forward in NC_001148 between 390268 and 391267 with 100% identity.

2537_s_at 4533.7 P

Saccharomyces cerevisiae chromosome XVI, complete chromosome sequence. Found forward in NC_001148 between 391268 and 392267 with 100% identity.

2538_s_at 3835.4 P

Saccharomyces cerevisiae chromosome XVI, complete chromosome sequence. Found forward in NC_001148 between 392268 and 393149 with 100% identity.

2539_at 462.6 A

Saccharomyces cerevisiae chromosome XVI, complete chromosome sequence. Found forward in NC_001148 between 398975 and 399974 with 100% identity.

2540_at 227.8 A

Saccharomyces cerevisiae chromosome XVI, complete chromosome sequence. Found forward in NC_001148 between 399975 and 400974 with 100% identity.

2541_at -9.0 A

Saccharomyces cerevisiae chromosome XVI, complete chromosome sequence. Found forward in NC_001148 between 400975 and 401974 with 100% identity.

2542_at -207.4 A

Saccharomyces cerevisiae chromosome XVI, complete chromosome sequence. Found forward in NC_001148 between 401975 and 402974 with 100% identity.

2543_at -1124.1 A

Saccharomyces cerevisiae chromosome XVI, complete chromosome sequence. Found forward in NC_001148 between 402975 and 403974 with 100% identity.

2544_at -22.2 A

Saccharomyces cerevisiae chromosome XVI, complete chromosome sequence. Found forward in NC_001148 between 403975 and 404451 with 100% identity.

2545_at 198.7 A

Saccharomyces cerevisiae chromosome XVI, complete chromosome sequence. Found forward in NC_001148 between 435759 and 436758 with 100% identity.

2546_at 96.3 A

Saccharomyces cerevisiae chromosome XVI, complete chromosome sequence. Found forward in NC_001148 between 436759 and 437758 with 100% identity.

2547_at 322.8 A

Saccharomyces cerevisiae chromosome XVI, complete chromosome sequence. Found forward in NC_001148 between 437759 and 438758 with 100% identity.

2548_at 42.7 A
Saccharomyces cerevisiae chromosome XVI, complete chromosome sequence. Found forward in NC_001148 between 438759 and 439758 with 100% identity.
2549_at 10.8 P
Saccharomyces cerevisiae chromosome XVI, complete chromosome sequence. Found forward in NC_001148 between 439759 and 440758 with 100% identity.
2550_at -96.4 A
Saccharomyces cerevisiae chromosome XVI, complete chromosome sequence. Found forward in NC_001148 between 440759 and 441758 with 100% identity.
2551_at -310.0 A
Saccharomyces cerevisiae chromosome XVI, complete chromosome sequence. Found forward in NC_001148 between 441759 and 442758 with 100% identity.
2552_at -206.8 A
Saccharomyces cerevisiae chromosome XVI, complete chromosome sequence. Found forward in NC_001148 between 442759 and 443758 with 100% identity.
2553_at 357.7 P
Saccharomyces cerevisiae chromosome XVI, complete chromosome sequence. Found forward in NC_001148 between 443759 and 444574 with 100% identity.
2554_at 492.9 P
Saccharomyces cerevisiae chromosome XVI, complete chromosome sequence. Found forward in NC_001148 between 446337 and 447336 with 100% identity.
2555_at 2493.9 A
Saccharomyces cerevisiae chromosome XVI, complete chromosome sequence. Found forward in NC_001148 between 447337 and 448336 with 100% identity.
2556_at -141.8 A
Saccharomyces cerevisiae chromosome XVI, complete chromosome sequence. Found forward in NC_001148 between 448337 and 449336 with 100% identity.
2557_at 354.0 P
Saccharomyces cerevisiae chromosome XVI, complete chromosome sequence. Found forward in NC_001148 between 449337 and 450336 with 100% identity.
2558_at 290.1 A
Saccharomyces cerevisiae chromosome XVI, complete chromosome sequence. Found forward in NC_001148 between 450337 and 451336 with 100% identity.
2559_at 664.5 A
Saccharomyces cerevisiae chromosome XVI, complete chromosome sequence. Found forward in NC_001148 between 451337 and 451904 with 100% identity.
2560_at -353.2 A
Saccharomyces cerevisiae chromosome XVI, complete chromosome sequence. Found forward in NC_001148 between 519230 and 520229 with 100% identity.
2561_at 739.2 P
Saccharomyces cerevisiae chromosome XVI, complete chromosome sequence. Found forward in NC_001148 between 520230 and 521229 with 100% identity.
2562_g_at 18.8 P
Saccharomyces cerevisiae chromosome XVI, complete chromosome sequence. Found forward in NC_001148 between 520230 and 521229 with 100% identity.
2563_s_at 1951.6 P
Saccharomyces cerevisiae chromosome XVI, complete chromosome sequence. Found forward in NC_001148 between 521230 and 522229 with 100% identity.
2564_s_at 3223.0 P
Saccharomyces cerevisiae chromosome XVI, complete chromosome sequence. Found forward in NC_001148 between 522230 and 523229 with 100% identity.
2565_s_at 972.0 P
Saccharomyces cerevisiae chromosome XVI, complete chromosome sequence. Found forward in NC_001148 between 523230 and 524229 with 100% identity.
2566_s_at -819.5 P
Saccharomyces cerevisiae chromosome XVI, complete chromosome sequence. Found forward in

NC_001148 between 524230 and 524453 with 100% identity.
2567_at 640.8 P
Saccharomyces cerevisiae chromosome XVI, complete chromosome sequence. Found forward in NC_001148 between 536315 and 537314 with 100% identity.
2568_at 96.6 A
Saccharomyces cerevisiae chromosome XVI, complete chromosome sequence. Found forward in NC_001148 between 537315 and 538314 with 100% identity.
2569_at -899.9 A
Saccharomyces cerevisiae chromosome XVI, complete chromosome sequence. Found forward in NC_001148 between 538315 and 539314 with 100% identity.
2570_at 389.2 P
Saccharomyces cerevisiae chromosome XVI, complete chromosome sequence. Found forward in NC_001148 between 539315 and 540314 with 100% identity.
2571_s_at 896.5 P
Saccharomyces cerevisiae chromosome XVI, complete chromosome sequence. Found forward in NC_001148 between 540315 and 541314 with 100% identity.
2572_s_at 704.3 P
Saccharomyces cerevisiae chromosome XVI, complete chromosome sequence. Found forward in NC_001148 between 541315 and 541465 with 100% identity.
2573_at 8.2 A
Saccharomyces cerevisiae chromosome XVI, complete chromosome sequence. Found forward in NC_001148 between 542577 and 543576 with 100% identity.
2574_at 1018.1 P
Saccharomyces cerevisiae chromosome XVI, complete chromosome sequence. Found forward in NC_001148 between 543577 and 544576 with 100% identity.
2489_at 31.7 A
Saccharomyces cerevisiae chromosome XVI, complete chromosome sequence. Found forward in NC_001148 between 544577 and 545576 with 100% identity.
2490_s_at 3153.8 P
Saccharomyces cerevisiae chromosome XVI, complete chromosome sequence. Found forward in NC_001148 between 545577 and 546576 with 100% identity.
2491_s_at 3073.9 P
Saccharomyces cerevisiae chromosome XVI, complete chromosome sequence. Found forward in NC_001148 between 546577 and 547576 with 100% identity.
2492_f_at 856.2 P
Saccharomyces cerevisiae chromosome XVI, complete chromosome sequence. Found forward in NC_001148 between 547577 and 547638 with 100% identity.
2493_at -156.1 A
Saccharomyces cerevisiae chromosome XVI, complete chromosome sequence. Found forward in NC_001148 between 624964 and 625963 with 100% identity.
2494_at 501.4 A
Saccharomyces cerevisiae chromosome XVI, complete chromosome sequence. Found forward in NC_001148 between 625964 and 626963 with 100% identity.
2495_at 70.0 A
Saccharomyces cerevisiae chromosome XVI, complete chromosome sequence. Found forward in NC_001148 between 626964 and 627963 with 100% identity.
2496_g_at -890.1 A
Saccharomyces cerevisiae chromosome XVI, complete chromosome sequence. Found forward in NC_001148 between 626964 and 627963 with 100% identity.
2497_s_at 406.3 A
Saccharomyces cerevisiae chromosome XVI, complete chromosome sequence. Found forward in NC_001148 between 627964 and 628963 with 100% identity.
2498_s_at 632.7 A
Saccharomyces cerevisiae chromosome XVI, complete chromosome sequence. Found forward in NC_001148 between 628964 and 629963 with 100% identity.
2499_s_at -67.4 P

Saccharomyces cerevisiae chromosome XVI, complete chromosome sequence. Found forward in NC_001148 between 629964 and 630740 with 100% identity.
2500_at 1057.0 P
Saccharomyces cerevisiae chromosome XVI, complete chromosome sequence. Found forward in NC_001148 between 759478 and 760477 with 100% identity.
2501_g_at 994.1 A
Saccharomyces cerevisiae chromosome XVI, complete chromosome sequence. Found forward in NC_001148 between 759478 and 760477 with 100% identity.
2502_s_at -145.8 P
Saccharomyces cerevisiae chromosome XVI, complete chromosome sequence. Found forward in NC_001148 between 760478 and 761477 with 100% identity.
2503_s_at 90.9 P
Saccharomyces cerevisiae chromosome XVI, complete chromosome sequence. Found forward in NC_001148 between 761478 and 762477 with 100% identity.
2504_s_at 432.1 P
Saccharomyces cerevisiae chromosome XVI, complete chromosome sequence. Found forward in NC_001148 between 762478 and 763477 with 100% identity.
2505_s_at 941.2 P
Saccharomyces cerevisiae chromosome XVI, complete chromosome sequence. Found forward in NC_001148 between 763478 and 764477 with 100% identity.
2506_s_at 1310.7 P
Saccharomyces cerevisiae chromosome XVI, complete chromosome sequence. Found forward in NC_001148 between 764478 and 765477 with 100% identity.
2507_s_at 459.8 P
Saccharomyces cerevisiae chromosome XVI, complete chromosome sequence. Found forward in NC_001148 between 765478 and 766477 with 100% identity.
2508_s_at 2229.9 P
Saccharomyces cerevisiae chromosome XVI, complete chromosome sequence. Found forward in NC_001148 between 766478 and 766991 with 100% identity.
2509_at 1056.5 P
Saccharomyces cerevisiae chromosome XVI, complete chromosome sequence. Found forward in NC_001148 between 869140 and 870139 with 100% identity.
2510_at 165.2 A
Saccharomyces cerevisiae chromosome XVI, complete chromosome sequence. Found forward in NC_001148 between 870140 and 871139 with 100% identity.
2511_g_at 904.2 P
Saccharomyces cerevisiae chromosome XVI, complete chromosome sequence. Found forward in NC_001148 between 870140 and 871139 with 100% identity.
2512_s_at 29.0 A
Saccharomyces cerevisiae chromosome XVI, complete chromosome sequence. Found forward in NC_001148 between 871140 and 872139 with 100% identity.
2513_s_at 505.9 M
Saccharomyces cerevisiae chromosome XVI, complete chromosome sequence. Found forward in NC_001148 between 872140 and 873139 with 100% identity.
2514_s_at 842.2 P
Saccharomyces cerevisiae chromosome XVI, complete chromosome sequence. Found forward in NC_001148 between 873140 and 874139 with 100% identity.
2515_s_at 912.5 A
Saccharomyces cerevisiae chromosome XVI, complete chromosome sequence. Found forward in NC_001148 between 874140 and 874421 with 100% identity.
2516_at 309.2 A
Saccharomyces cerevisiae chromosome II, complete chromosome sequence. Found forward in NC_001134 between 25441 and 26440 with 100% identity.
2517_at 1049.4 M
Saccharomyces cerevisiae chromosome II, complete chromosome sequence. Found forward in NC_001134 between 26441 and 27440 with 100% identity.

2518_at 591.9 A
Saccharomyces cerevisiae chromosome II, complete chromosome sequence. Found forward in NC_001134 between 27441 and 28440 with 100% identity.
2519_at -2484.3 A
Saccharomyces cerevisiae chromosome II, complete chromosome sequence. Found forward in NC_001134 between 28441 and 29440 with 100% identity.
2520_at -377.3 A
Saccharomyces cerevisiae chromosome II, complete chromosome sequence. Found forward in NC_001134 between 29441 and 30440 with 100% identity.
2521_f_at 444.9 P
Saccharomyces cerevisiae chromosome II, complete chromosome sequence. Found forward in NC_001134 between 35441 and 35606 with 100% identity.
2522_at -480.7 A
Saccharomyces cerevisiae chromosome II, complete chromosome sequence. Found forward in NC_001134 between 51513 and 52512 with 100% identity.
2523_at 84.6 A
Saccharomyces cerevisiae chromosome II, complete chromosome sequence. Found forward in NC_001134 between 52513 and 53512 with 100% identity.
2524_at 62.8 A
Saccharomyces cerevisiae chromosome II, complete chromosome sequence. Found forward in NC_001134 between 53513 and 54512 with 100% identity.
2525_at 316.7 P
Saccharomyces cerevisiae chromosome II, complete chromosome sequence. Found forward in NC_001134 between 54513 and 55512 with 100% identity.
2526_at 45.4 A
Saccharomyces cerevisiae chromosome II, complete chromosome sequence. Found forward in NC_001134 between 55513 and 56512 with 100% identity.
2527_at 18.2 A
Saccharomyces cerevisiae chromosome II, complete chromosome sequence. Found forward in NC_001134 between 56513 and 57512 with 100% identity.
2528_at 468.6 P
Saccharomyces cerevisiae chromosome II, complete chromosome sequence. Found forward in NC_001134 between 57513 and 58512 with 100% identity.
2529_at -1465.5 A
Saccharomyces cerevisiae chromosome II, complete chromosome sequence. Found forward in NC_001134 between 58513 and 59512 with 100% identity.
2530_at 215.2 P
Saccharomyces cerevisiae chromosome II, complete chromosome sequence. Found forward in NC_001134 between 59513 and 59815 with 100% identity.
2531_at 934.8 P
Saccharomyces cerevisiae chromosome II, complete chromosome sequence. Found forward in NC_001134 between 73564 and 74563 with 100% identity.
2446_at -265.3 A
Saccharomyces cerevisiae chromosome II, complete chromosome sequence. Found forward in NC_001134 between 74564 and 75563 with 100% identity.
2447_g_at 353.4 P
Saccharomyces cerevisiae chromosome II, complete chromosome sequence. Found forward in NC_001134 between 74564 and 75563 with 100% identity.
2448_s_at 1220.4 P
Saccharomyces cerevisiae chromosome II, complete chromosome sequence. Found forward in NC_001134 between 75564 and 76563 with 100% identity.
2449_s_at 2209.7 P
Saccharomyces cerevisiae chromosome II, complete chromosome sequence. Found forward in NC_001134 between 76564 and 77563 with 100% identity.
2450_s_at 1408.9 P
Saccharomyces cerevisiae chromosome II, complete chromosome sequence. Found forward in

NC_001134 between 77564 and 78563 with 100% identity.
2451_s_at 5674.3 P
Saccharomyces cerevisiae chromosome II, complete chromosome sequence. Found forward in NC_001134 between 78564 and 79261 with 100% identity.
2452_at 174.9 P
Saccharomyces cerevisiae chromosome II, complete chromosome sequence. Found forward in NC_001134 between 187307 and 188306 with 100% identity.
2453_at 13.2 A
Saccharomyces cerevisiae chromosome II, complete chromosome sequence. Found forward in NC_001134 between 188307 and 189306 with 100% identity.
2454_at -244.5 A
Saccharomyces cerevisiae chromosome II, complete chromosome sequence. Found forward in NC_001134 between 189307 and 190306 with 100% identity.
2455_at 1126.3 A
Saccharomyces cerevisiae chromosome II, complete chromosome sequence. Found forward in NC_001134 between 190307 and 191306 with 100% identity.
2456_at 93.1 A
Saccharomyces cerevisiae chromosome II, complete chromosome sequence. Found forward in NC_001134 between 191307 and 192306 with 100% identity.
2457_at 118.8 A
Saccharomyces cerevisiae chromosome II, complete chromosome sequence. Found forward in NC_001134 between 192307 and 192975 with 100% identity.
2458_g_at 6313.0 P
Saccharomyces cerevisiae chromosome II, complete chromosome sequence. Found forward in NC_001134 between 192307 and 192975 with 100% identity.
2459_at 630.1 A
Saccharomyces cerevisiae chromosome II, complete chromosome sequence. Found forward in NC_001134 between 220363 and 221362 with 100% identity.
2460_at 26.7 A
Saccharomyces cerevisiae chromosome II, complete chromosome sequence. Found forward in NC_001134 between 226363 and 227362 with 100% identity.
2461_at 745.4 P
Saccharomyces cerevisiae chromosome II, complete chromosome sequence. Found forward in NC_001134 between 227363 and 228362 with 100% identity.
2462_g_at 1316.3 P
Saccharomyces cerevisiae chromosome II, complete chromosome sequence. Found forward in NC_001134 between 227363 and 228362 with 100% identity.
2463_s_at 1362.4 A
Saccharomyces cerevisiae chromosome II, complete chromosome sequence. Found forward in NC_001134 between 228363 and 229362 with 100% identity.
2464_s_at 3418.4 P
Saccharomyces cerevisiae chromosome II, complete chromosome sequence. Found forward in NC_001134 between 229363 and 230362 with 100% identity.
2465_s_at 2918.1 P
Saccharomyces cerevisiae chromosome II, complete chromosome sequence. Found forward in NC_001134 between 230363 and 231362 with 100% identity.
2466_s_at 1353.3 P
Saccharomyces cerevisiae chromosome II, complete chromosome sequence. Found forward in NC_001134 between 231363 and 232362 with 100% identity.
2467_s_at 2933.2 P
Saccharomyces cerevisiae chromosome II, complete chromosome sequence. Found forward in NC_001134 between 232363 and 233362 with 100% identity.
2468_s_at 3705.6 P
Saccharomyces cerevisiae chromosome II, complete chromosome sequence. Found forward in NC_001134 between 233363 and 234362 with 100% identity.
2469_s_at 4393.1 P

Saccharomyces cerevisiae chromosome II, complete chromosome sequence. Found forward in NC_001134 between 234363 and 234580 with 100% identity.
2470_at 1753.2 P
Saccharomyces cerevisiae chromosome II, complete chromosome sequence. Found forward in NC_001134 between 505265 and 506264 with 100% identity.
2471_g_at -350.6 A
Saccharomyces cerevisiae chromosome II, complete chromosome sequence. Found forward in NC_001134 between 505265 and 506264 with 100% identity.
2472_s_at -647.0 A
Saccharomyces cerevisiae chromosome II, complete chromosome sequence. Found forward in NC_001134 between 506265 and 507264 with 100% identity.
2473_s_at 344.1 P
Saccharomyces cerevisiae chromosome II, complete chromosome sequence. Found forward in NC_001134 between 507265 and 508264 with 100% identity.
2474_s_at 169.1 P
Saccharomyces cerevisiae chromosome II, complete chromosome sequence. Found forward in NC_001134 between 508265 and 509264 with 100% identity.
2475_s_at 357.3 P
Saccharomyces cerevisiae chromosome II, complete chromosome sequence. Found forward in NC_001134 between 509265 and 510264 with 100% identity.
2476_s_at 741.8 P
Saccharomyces cerevisiae chromosome II, complete chromosome sequence. Found forward in NC_001134 between 510265 and 511264 with 100% identity.
2477_s_at 788.8 P
Saccharomyces cerevisiae chromosome II, complete chromosome sequence. Found forward in NC_001134 between 511265 and 512233 with 100% identity.
2478_at -148.9 A
Saccharomyces cerevisiae chromosome II, complete chromosome sequence. Found forward in NC_001134 between 517809 and 518808 with 100% identity.
2479_at -5.5 A
Saccharomyces cerevisiae chromosome II, complete chromosome sequence. Found forward in NC_001134 between 518809 and 519808 with 100% identity.
2480_at 288.9 A
Saccharomyces cerevisiae chromosome II, complete chromosome sequence. Found forward in NC_001134 between 519809 and 520808 with 100% identity.
2481_at 14.0 M
Saccharomyces cerevisiae chromosome II, complete chromosome sequence. Found forward in NC_001134 between 520809 and 521808 with 100% identity.
2482_at 286.2 A
Saccharomyces cerevisiae chromosome II, complete chromosome sequence. Found forward in NC_001134 between 521809 and 522808 with 100% identity.
2483_at -35.8 P
Saccharomyces cerevisiae chromosome II, complete chromosome sequence. Found forward in NC_001134 between 522809 and 523808 with 100% identity.
2484_at -245.4 A
Saccharomyces cerevisiae chromosome II, complete chromosome sequence. Found forward in NC_001134 between 523809 and 524808 with 100% identity.
2485_at -476.6 A
Saccharomyces cerevisiae chromosome II, complete chromosome sequence. Found forward in NC_001134 between 524809 and 525808 with 100% identity.
2486_at -35.5 A
Saccharomyces cerevisiae chromosome II, complete chromosome sequence. Found forward in NC_001134 between 525809 and 526808 with 100% identity.
2487_at 565.7 P
Saccharomyces cerevisiae chromosome II, complete chromosome sequence. Found forward in NC_001134 between 526809 and 526984 with 100% identity.

2488_at 287.7 A
Saccharomyces cerevisiae chromosome II, complete chromosome sequence. Found forward in NC_001134 between 637162 and 638161 with 100% identity.
2421_at 264.0 A
Saccharomyces cerevisiae chromosome II, complete chromosome sequence. Found forward in NC_001134 between 638162 and 639161 with 100% identity.
2422_at 274.7 A
Saccharomyces cerevisiae chromosome II, complete chromosome sequence. Found forward in NC_001134 between 639162 and 640161 with 100% identity.
2423_at -13.6 A
Saccharomyces cerevisiae chromosome II, complete chromosome sequence. Found forward in NC_001134 between 640162 and 641161 with 100% identity.
2424_at 354.7 P
Saccharomyces cerevisiae chromosome II, complete chromosome sequence. Found forward in NC_001134 between 641162 and 642161 with 100% identity.
2425_at 333.3 A
Saccharomyces cerevisiae chromosome II, complete chromosome sequence. Found forward in NC_001134 between 642162 and 642542 with 100% identity.
2426_at 525.0 P
Saccharomyces cerevisiae chromosome II, complete chromosome sequence. Found forward in NC_001134 between 751813 and 752812 with 100% identity.
2427_at 528.4 P
Saccharomyces cerevisiae chromosome II, complete chromosome sequence. Found forward in NC_001134 between 752813 and 753812 with 100% identity.
2428_at -262.9 A
Saccharomyces cerevisiae chromosome II, complete chromosome sequence. Found forward in NC_001134 between 753813 and 754812 with 100% identity.
2429_at -815.5 A
Saccharomyces cerevisiae chromosome II, complete chromosome sequence. Found forward in NC_001134 between 754813 and 755812 with 100% identity.
2430_at 659.2 A
Saccharomyces cerevisiae chromosome II, complete chromosome sequence. Found forward in NC_001134 between 755813 and 756812 with 100% identity.
2431_at 52.6 A
Saccharomyces cerevisiae chromosome II, complete chromosome sequence. Found forward in NC_001134 between 756813 and 757578 with 100% identity.
2432_at 5971.2 P
Saccharomyces cerevisiae chromosome III, complete chromosome sequence. Found forward in NC_001135 between 82220 and 83219 with 100% identity.
2433_at 5309.1 P
Saccharomyces cerevisiae chromosome III, complete chromosome sequence. Found forward in NC_001135 between 83220 and 84219 with 100% identity.
2434_at 1932.8 A
Saccharomyces cerevisiae chromosome III, complete chromosome sequence. Found forward in NC_001135 between 84220 and 85219 with 100% identity.
2435_at 713.0 A
Saccharomyces cerevisiae chromosome III, complete chromosome sequence. Found forward in NC_001135 between 90220 and 91219 with 100% identity.
2436_g_at 2028.7 P
Saccharomyces cerevisiae chromosome III, complete chromosome sequence. Found forward in NC_001135 between 90220 and 91219 with 100% identity.
2437_s_at 6781.5 P
Saccharomyces cerevisiae chromosome III, complete chromosome sequence. Found forward in NC_001135 between 91220 and 91533 with 100% identity.
2438_at -234.2 A
Saccharomyces cerevisiae chromosome III, complete chromosome sequence. Found forward in

NC_001135 between 177526 and 178525 with 100% identity.
2439_g_at 116.8 M
Saccharomyces cerevisiae chromosome III, complete chromosome sequence. Found forward in NC_001135 between 177526 and 178525 with 100% identity.
2440_s_at 308.1 A
Saccharomyces cerevisiae chromosome III, complete chromosome sequence. Found forward in NC_001135 between 178526 and 179525 with 100% identity.
2441_s_at 258.7 P
Saccharomyces cerevisiae chromosome III, complete chromosome sequence. Found forward in NC_001135 between 179526 and 180525 with 100% identity.
2442_s_at 1610.0 P
Saccharomyces cerevisiae chromosome III, complete chromosome sequence. Found forward in NC_001135 between 180526 and 181525 with 100% identity.
2443_s_at 582.8 P
Saccharomyces cerevisiae chromosome III, complete chromosome sequence. Found forward in NC_001135 between 181526 and 182525 with 100% identity.
2444_s_at -1118.1 A
Saccharomyces cerevisiae chromosome III, complete chromosome sequence. Found forward in NC_001135 between 182526 and 183525 with 100% identity.
2445_s_at 1589.3 P
Saccharomyces cerevisiae chromosome III, complete chromosome sequence. Found forward in NC_001135 between 183526 and 184252 with 100% identity.
2395_at 437.3 A
Saccharomyces cerevisiae chromosome III, complete chromosome sequence. Found forward in NC_001135 between 275986 and 276985 with 100% identity.
2396_at 157.1 P
Saccharomyces cerevisiae chromosome III, complete chromosome sequence. Found forward in NC_001135 between 276986 and 277985 with 100% identity.
2397_at -683.9 A
Saccharomyces cerevisiae chromosome III, complete chromosome sequence. Found forward in NC_001135 between 277986 and 278985 with 100% identity.
2398_g_at 1239.9 P
Saccharomyces cerevisiae chromosome III, complete chromosome sequence. Found forward in NC_001135 between 277986 and 278985 with 100% identity.
2399_s_at 806.3 P
Saccharomyces cerevisiae chromosome III, complete chromosome sequence. Found forward in NC_001135 between 278986 and 279985 with 100% identity.
2400_s_at 1758.7 P
Saccharomyces cerevisiae chromosome III, complete chromosome sequence. Found forward in NC_001135 between 279986 and 280985 with 100% identity.
2401_s_at 1491.1 P
Saccharomyces cerevisiae chromosome III, complete chromosome sequence. Found forward in NC_001135 between 280986 and 281985 with 100% identity.
2402_s_at 1982.7 P
Saccharomyces cerevisiae chromosome III, complete chromosome sequence. Found forward in NC_001135 between 281986 and 282985 with 100% identity.
2403_s_at 5348.0 P
Saccharomyces cerevisiae chromosome III, complete chromosome sequence. Found forward in NC_001135 between 282986 and 283985 with 100% identity.
2404_s_at 3579.0 P
Saccharomyces cerevisiae chromosome III, complete chromosome sequence. Found forward in NC_001135 between 283986 and 284665 with 100% identity.
2405_at 1179.4 A
Saccharomyces cerevisiae chromosome IV, complete chromosome sequence. Found forward in NC_001136 between 79795 and 80794 with 100% identity.
2406_at 38.5 A

Saccharomyces cerevisiae chromosome IV, complete chromosome sequence. Found forward in NC_001136 between 80795 and 81794 with 100% identity.
2407_at 869.1 P
Saccharomyces cerevisiae chromosome IV, complete chromosome sequence. Found forward in NC_001136 between 81795 and 82794 with 100% identity.
2408_at 330.4 P
Saccharomyces cerevisiae chromosome IV, complete chromosome sequence. Found forward in NC_001136 between 82795 and 83794 with 100% identity.
2409_at -123.8 A
Saccharomyces cerevisiae chromosome IV, complete chromosome sequence. Found forward in NC_001136 between 83795 and 84794 with 100% identity.
2410_g_at 833.9 A
Saccharomyces cerevisiae chromosome IV, complete chromosome sequence. Found forward in NC_001136 between 83795 and 84794 with 100% identity.
2411_s_at 768.5 P
Saccharomyces cerevisiae chromosome IV, complete chromosome sequence. Found forward in NC_001136 between 84795 and 85486 with 100% identity.
2412_at 210.8 A
Saccharomyces cerevisiae chromosome IV, complete chromosome sequence. Found forward in NC_001136 between 149704 and 150703 with 100% identity.
2413_at 107.2 A
Saccharomyces cerevisiae chromosome IV, complete chromosome sequence. Found forward in NC_001136 between 150704 and 151703 with 100% identity.
2414_at 136.8 A
Saccharomyces cerevisiae chromosome IV, complete chromosome sequence. Found forward in NC_001136 between 151704 and 152703 with 100% identity.
2415_at -118.2 A
Saccharomyces cerevisiae chromosome IV, complete chromosome sequence. Found forward in NC_001136 between 152704 and 153703 with 100% identity.
2416_at 253.4 P
Saccharomyces cerevisiae chromosome IV, complete chromosome sequence. Found forward in NC_001136 between 153704 and 154703 with 100% identity.
2417_at 319.6 A
Saccharomyces cerevisiae chromosome IV, complete chromosome sequence. Found forward in NC_001136 between 154704 and 155703 with 100% identity.
2418_at 37.8 A
Saccharomyces cerevisiae chromosome IV, complete chromosome sequence. Found forward in NC_001136 between 155704 and 156703 with 100% identity.
2419_g_at 1020.3 P
Saccharomyces cerevisiae chromosome IV, complete chromosome sequence. Found forward in NC_001136 between 155704 and 156703 with 100% identity.
2420_s_at 1525.7 P
Saccharomyces cerevisiae chromosome IV, complete chromosome sequence. Found forward in NC_001136 between 156704 and 157405 with 100% identity.
2352_at 566.7 A
Saccharomyces cerevisiae chromosome IV, complete chromosome sequence. Found forward in NC_001136 between 205861 and 206860 with 100% identity.
2353_at 540.2 A
Saccharomyces cerevisiae chromosome IV, complete chromosome sequence. Found forward in NC_001136 between 206861 and 207860 with 100% identity.
2354_at -524.8 A
Saccharomyces cerevisiae chromosome IV, complete chromosome sequence. Found forward in NC_001136 between 207861 and 208860 with 100% identity.
2355_at -155.9 A
Saccharomyces cerevisiae chromosome IV, complete chromosome sequence. Found forward in NC_001136 between 208861 and 209860 with 100% identity.

2356_at 369.4 P
Saccharomyces cerevisiae chromosome IV, complete chromosome sequence. Found forward in NC_001136 between 209861 and 210860 with 100% identity.
2357_at 908.7 A
Saccharomyces cerevisiae chromosome IV, complete chromosome sequence. Found forward in NC_001136 between 210861 and 211376 with 100% identity.
2358_at 28.1 A
Saccharomyces cerevisiae chromosome IV, complete chromosome sequence. Found forward in NC_001136 between 257132 and 258131 with 100% identity.
2359_at -159.1 A
Saccharomyces cerevisiae chromosome IV, complete chromosome sequence. Found forward in NC_001136 between 258132 and 259131 with 100% identity.
2360_g_at 2618.2 P
Saccharomyces cerevisiae chromosome IV, complete chromosome sequence. Found forward in NC_001136 between 258132 and 259131 with 100% identity.
2361_s_at 3625.3 P
Saccharomyces cerevisiae chromosome IV, complete chromosome sequence. Found forward in NC_001136 between 259132 and 260131 with 100% identity.
2362_s_at 3666.7 P
Saccharomyces cerevisiae chromosome IV, complete chromosome sequence. Found forward in NC_001136 between 260132 and 261131 with 100% identity.
2363_s_at 2937.0 P
Saccharomyces cerevisiae chromosome IV, complete chromosome sequence. Found forward in NC_001136 between 261132 and 262131 with 100% identity.
2364_s_at 3049.7 P
Saccharomyces cerevisiae chromosome IV, complete chromosome sequence. Found forward in NC_001136 between 262132 and 262724 with 100% identity.
2365_at 532.8 A
Saccharomyces cerevisiae chromosome IV, complete chromosome sequence. Found forward in NC_001136 between 344736 and 345735 with 100% identity.
2366_s_at -313.6 A
Saccharomyces cerevisiae chromosome IV, complete chromosome sequence. Found forward in NC_001136 between 345736 and 346735 with 100% identity.
2367_s_at 3093.1 P
Saccharomyces cerevisiae chromosome IV, complete chromosome sequence. Found forward in NC_001136 between 346736 and 347735 with 100% identity.
2368_s_at 512.0 P
Saccharomyces cerevisiae chromosome IV, complete chromosome sequence. Found forward in NC_001136 between 347736 and 348735 with 100% identity.
2369_s_at 438.9 P
Saccharomyces cerevisiae chromosome IV, complete chromosome sequence. Found forward in NC_001136 between 348736 and 349735 with 100% identity.
2370_s_at 1181.1 P
Saccharomyces cerevisiae chromosome IV, complete chromosome sequence. Found forward in NC_001136 between 349736 and 350536 with 100% identity.
2371_at 84.4 A
Saccharomyces cerevisiae chromosome IV, complete chromosome sequence. Found forward in NC_001136 between 618990 and 619989 with 100% identity.
2372_at 1309.6 P
Saccharomyces cerevisiae chromosome IV, complete chromosome sequence. Found forward in NC_001136 between 619990 and 620989 with 100% identity.
2373_at -1291.6 A
Saccharomyces cerevisiae chromosome IV, complete chromosome sequence. Found forward in NC_001136 between 620990 and 621989 with 100% identity.
2374_at 1697.8 P
Saccharomyces cerevisiae chromosome IV, complete chromosome sequence. Found forward in

NC_001136 between 621990 and 622989 with 100% identity.
2375_s_at 244.3 P
Saccharomyces cerevisiae chromosome IV, complete chromosome sequence. Found forward in NC_001136 between 622990 and 623989 with 100% identity.
2376_s_at 1565.1 P
Saccharomyces cerevisiae chromosome IV, complete chromosome sequence. Found forward in NC_001136 between 623990 and 624214 with 100% identity.
2377_at 1003.0 P
Saccharomyces cerevisiae chromosome IV, complete chromosome sequence. Found forward in NC_001136 between 630598 and 631597 with 100% identity.
2378_g_at 3426.6 P
Saccharomyces cerevisiae chromosome IV, complete chromosome sequence. Found forward in NC_001136 between 630598 and 631597 with 100% identity.
2379_s_at 1396.7 P
Saccharomyces cerevisiae chromosome IV, complete chromosome sequence. Found forward in NC_001136 between 631598 and 632597 with 100% identity.
2380_s_at 2945.1 P
Saccharomyces cerevisiae chromosome IV, complete chromosome sequence. Found forward in NC_001136 between 632598 and 633597 with 100% identity.
2381_s_at 2543.7 P
Saccharomyces cerevisiae chromosome IV, complete chromosome sequence. Found forward in NC_001136 between 633598 and 634597 with 100% identity.
2382_s_at 3099.0 P
Saccharomyces cerevisiae chromosome IV, complete chromosome sequence. Found forward in NC_001136 between 634598 and 635597 with 100% identity.
2383_at 572.4 A
Saccharomyces cerevisiae chromosome IV, complete chromosome sequence. Found forward in NC_001136 between 735394 and 736393 with 100% identity.
2384_at 349.5 P
Saccharomyces cerevisiae chromosome IV, complete chromosome sequence. Found forward in NC_001136 between 736394 and 737393 with 100% identity.
2385_at -391.0 A
Saccharomyces cerevisiae chromosome IV, complete chromosome sequence. Found forward in NC_001136 between 737394 and 738393 with 100% identity.
2386_at 248.8 P
Saccharomyces cerevisiae chromosome IV, complete chromosome sequence. Found forward in NC_001136 between 738394 and 739393 with 100% identity.
2387_at -72.8 A
Saccharomyces cerevisiae chromosome IV, complete chromosome sequence. Found forward in NC_001136 between 739394 and 740393 with 100% identity.
2388_s_at 153.1 P
Saccharomyces cerevisiae chromosome IV, complete chromosome sequence. Found forward in NC_001136 between 756048 and 757047 with 100% identity.
2389_s_at -12.9 A
Saccharomyces cerevisiae chromosome IV, complete chromosome sequence. Found forward in NC_001136 between 757048 and 758047 with 100% identity.
2390_s_at 224.6 A
Saccharomyces cerevisiae chromosome IV, complete chromosome sequence. Found forward in NC_001136 between 759048 and 760047 with 100% identity.
2391_s_at 267.6 A
Saccharomyces cerevisiae chromosome IV, complete chromosome sequence. Found forward in NC_001136 between 760048 and 761047 with 100% identity.
2392_s_at 697.2 P
Saccharomyces cerevisiae chromosome IV, complete chromosome sequence. Found forward in NC_001136 between 761048 and 762047 with 100% identity.
2393_s_at 1902.2 P

Saccharomyces cerevisiae chromosome IV, complete chromosome sequence. Found forward in NC_001136 between 762048 and 763047 with 100% identity.
2394_s_at 1464.7 P
Saccharomyces cerevisiae chromosome IV, complete chromosome sequence. Found forward in NC_001136 between 763048 and 763367 with 100% identity.
2309_at 275.6 A
Saccharomyces cerevisiae chromosome IV, complete chromosome sequence. Found forward in NC_001136 between 796686 and 797685 with 100% identity.
2310_at -320.1 A
Saccharomyces cerevisiae chromosome IV, complete chromosome sequence. Found forward in NC_001136 between 797686 and 798685 with 100% identity.
2311_at 942.5 P
Saccharomyces cerevisiae chromosome IV, complete chromosome sequence. Found forward in NC_001136 between 798686 and 799685 with 100% identity.
2312_at 650.0 A
Saccharomyces cerevisiae chromosome IV, complete chromosome sequence. Found forward in NC_001136 between 799686 and 800685 with 100% identity.
2313_at 775.1 P
Saccharomyces cerevisiae chromosome IV, complete chromosome sequence. Found forward in NC_001136 between 800686 and 801685 with 100% identity.
2314_at 1079.1 A
Saccharomyces cerevisiae chromosome IV, complete chromosome sequence. Found forward in NC_001136 between 801686 and 802685 with 100% identity.
2315_at 632.4 P
Saccharomyces cerevisiae chromosome IV, complete chromosome sequence. Found forward in NC_001136 between 802686 and 803685 with 100% identity.
2316_at 220.7 A
Saccharomyces cerevisiae chromosome IV, complete chromosome sequence. Found forward in NC_001136 between 877250 and 878249 with 100% identity.
2317_at 142.7 P
Saccharomyces cerevisiae chromosome IV, complete chromosome sequence. Found forward in NC_001136 between 878250 and 879249 with 100% identity.
2319_f_at -442.8 A
Saccharomyces cerevisiae chromosome IV, complete chromosome sequence. Found forward in NC_001136 between 647450 and 647656 with 100% identity.
2320_at -6.3 A
Saccharomyces cerevisiae chromosome IV, complete chromosome sequence. Found forward in NC_001136 between 1133751 and 1134750 with 100% identity.
2321_at 328.1 A
Saccharomyces cerevisiae chromosome IV, complete chromosome sequence. Found forward in NC_001136 between 1134751 and 1135750 with 100% identity.
2322_at 1067.2 P
Saccharomyces cerevisiae chromosome IV, complete chromosome sequence. Found forward in NC_001136 between 1135751 and 1136750 with 100% identity.
2323_g_at 692.1 P
Saccharomyces cerevisiae chromosome IV, complete chromosome sequence. Found forward in NC_001136 between 1135751 and 1136750 with 100% identity.
2324_s_at -83.5 P
Saccharomyces cerevisiae chromosome IV, complete chromosome sequence. Found forward in NC_001136 between 1136751 and 1137750 with 100% identity.
2325_s_at 891.8 P
Saccharomyces cerevisiae chromosome IV, complete chromosome sequence. Found forward in NC_001136 between 1137751 and 1138750 with 100% identity.
2326_s_at 869.1 P
Saccharomyces cerevisiae chromosome IV, complete chromosome sequence. Found forward in NC_001136 between 1138751 and 1139750 with 100% identity.

2327_s_at 682.8 P
Saccharomyces cerevisiae chromosome IV, complete chromosome sequence. Found forward in NC_001136 between 1139751 and 1139967 with 100% identity.
2328_at 66.4 A
Saccharomyces cerevisiae chromosome IV, complete chromosome sequence. Found forward in NC_001136 between 1305061 and 1306060 with 100% identity.
2329_at 581.4 P
Saccharomyces cerevisiae chromosome IV, complete chromosome sequence. Found forward in NC_001136 between 1306061 and 1307060 with 100% identity.
2330_g_at 312.1 P
Saccharomyces cerevisiae chromosome IV, complete chromosome sequence. Found forward in NC_001136 between 1306061 and 1307060 with 100% identity.
2331_s_at 1341.6 P
Saccharomyces cerevisiae chromosome IV, complete chromosome sequence. Found forward in NC_001136 between 1307061 and 1308060 with 100% identity.
2332_s_at 2684.0 P
Saccharomyces cerevisiae chromosome IV, complete chromosome sequence. Found forward in NC_001136 between 1308061 and 1309060 with 100% identity.
2333_s_at 1902.5 P
Saccharomyces cerevisiae chromosome IV, complete chromosome sequence. Found forward in NC_001136 between 1309061 and 1310060 with 100% identity.
2334_s_at 1142.4 P
Saccharomyces cerevisiae chromosome IV, complete chromosome sequence. Found forward in NC_001136 between 1310061 and 1311060 with 100% identity.
2335_s_at 1253.9 P
Saccharomyces cerevisiae chromosome IV, complete chromosome sequence. Found forward in NC_001136 between 1311061 and 1311164 with 100% identity.
2336_at 1341.0 P
Saccharomyces cerevisiae chromosome IV, complete chromosome sequence. Found forward in NC_001136 between 1346165 and 1347164 with 100% identity.
2337_at -299.0 A
Saccharomyces cerevisiae chromosome IV, complete chromosome sequence. Found forward in NC_001136 between 1347165 and 1348164 with 100% identity.
2338_at -267.8 A
Saccharomyces cerevisiae chromosome IV, complete chromosome sequence. Found forward in NC_001136 between 1348165 and 1349164 with 100% identity.
2339_at 714.3 A
Saccharomyces cerevisiae chromosome IV, complete chromosome sequence. Found forward in NC_001136 between 1349165 and 1350164 with 100% identity.
2340_at 298.6 P
Saccharomyces cerevisiae chromosome IV, complete chromosome sequence. Found forward in NC_001136 between 1350165 and 1351164 with 100% identity.
2341_g_at 1335.1 P
Saccharomyces cerevisiae chromosome IV, complete chromosome sequence. Found forward in NC_001136 between 1350165 and 1351164 with 100% identity.
2342_s_at 1691.3 P
Saccharomyces cerevisiae chromosome IV, complete chromosome sequence. Found forward in NC_001136 between 1351165 and 1351842 with 100% identity.
2343_at 2200.3 P
Saccharomyces cerevisiae chromosome IV, complete chromosome sequence. Found forward in NC_001136 between 1369375 and 1370374 with 100% identity.
2344_g_at 3534.7 P
Saccharomyces cerevisiae chromosome IV, complete chromosome sequence. Found forward in NC_001136 between 1369375 and 1370374 with 100% identity.
2345_s_at 464.6 P
Saccharomyces cerevisiae chromosome IV, complete chromosome sequence. Found forward in

NC_001136 between 1370375 and 1371374 with 100% identity.

2346_s_at 91.1 A

Saccharomyces cerevisiae chromosome IV, complete chromosome sequence. Found forward in NC_001136 between 1371375 and 1372374 with 100% identity.

2347_s_at -105.1 A

Saccharomyces cerevisiae chromosome IV, complete chromosome sequence. Found forward in NC_001136 between 1372375 and 1373374 with 100% identity.

2348_s_at 1960.6 P

Saccharomyces cerevisiae chromosome IV, complete chromosome sequence. Found forward in NC_001136 between 1373375 and 1374374 with 100% identity.

2349_s_at -130.7 P

Saccharomyces cerevisiae chromosome IV, complete chromosome sequence. Found forward in NC_001136 between 1374375 and 1375374 with 100% identity.

2350_s_at 2409.7 P

Saccharomyces cerevisiae chromosome IV, complete chromosome sequence. Found forward in NC_001136 between 1375375 and 1376374 with 100% identity.

2351_s_at 1219.1 P

Saccharomyces cerevisiae chromosome IV, complete chromosome sequence. Found forward in NC_001136 between 1376375 and 1377374 with 100% identity.

2266_s_at 4134.2 P

Saccharomyces cerevisiae chromosome IV, complete chromosome sequence. Found forward in NC_001136 between 1377375 and 1378374 with 100% identity.

2267_s_at 2220.1 P

Saccharomyces cerevisiae chromosome IV, complete chromosome sequence. Found forward in NC_001136 between 1378375 and 1379085 with 100% identity.

2268_at 240.0 P

Saccharomyces cerevisiae chromosome V, complete chromosome sequence. Found forward in NC_001137 between 7553 and 8552 with 100% identity.

2269_at 420.0 A

Saccharomyces cerevisiae chromosome V, complete chromosome sequence. Found forward in NC_001137 between 8553 and 9552 with 100% identity.

2270_at 273.3 P

Saccharomyces cerevisiae chromosome V, complete chromosome sequence. Found forward in NC_001137 between 9553 and 10552 with 100% identity.

2271_at -444.8 A

Saccharomyces cerevisiae chromosome V, complete chromosome sequence. Found forward in NC_001137 between 10553 and 11552 with 100% identity.

2272_at 247.8 P

Saccharomyces cerevisiae chromosome V, complete chromosome sequence. Found forward in NC_001137 between 11553 and 12552 with 100% identity.

2273_at -207.9 A

Saccharomyces cerevisiae chromosome V, complete chromosome sequence. Found forward in NC_001137 between 12553 and 13552 with 100% identity.

2274_at -82.0 A

Saccharomyces cerevisiae chromosome V, complete chromosome sequence. Found forward in NC_001137 between 13553 and 13915 with 100% identity.

2275_g_at -1239.0 A

Saccharomyces cerevisiae chromosome V, complete chromosome sequence. Found forward in NC_001137 between 13553 and 13915 with 100% identity.

2276_at -111.1 A

Saccharomyces cerevisiae chromosome V, complete chromosome sequence. Found forward in NC_001137 between 109004 and 110003 with 100% identity.

2277_at 8.0 P

Saccharomyces cerevisiae chromosome V, complete chromosome sequence. Found forward in NC_001137 between 110004 and 111003 with 100% identity.

2278_at 474.4 P

Saccharomyces cerevisiae chromosome V, complete chromosome sequence. Found forward in NC_001137 between 111004 and 112003 with 100% identity.
2279_g_at 1792.2 P
Saccharomyces cerevisiae chromosome V, complete chromosome sequence. Found forward in NC_001137 between 111004 and 112003 with 100% identity.
2280_s_at 1888.7 P
Saccharomyces cerevisiae chromosome V, complete chromosome sequence. Found forward in NC_001137 between 112004 and 113003 with 100% identity.
2281_s_at 1821.9 P
Saccharomyces cerevisiae chromosome V, complete chromosome sequence. Found forward in NC_001137 between 113004 and 114003 with 100% identity.
2282_s_at 4966.9 P
Saccharomyces cerevisiae chromosome V, complete chromosome sequence. Found forward in NC_001137 between 114004 and 115003 with 100% identity.
2283_s_at 3150.9 P
Saccharomyces cerevisiae chromosome V, complete chromosome sequence. Found forward in NC_001137 between 115004 and 115300 with 100% identity.
2284_at 58.8 A
Saccharomyces cerevisiae chromosome V, complete chromosome sequence. Found forward in NC_001137 between 425685 and 426684 with 100% identity.
2285_at -133.0 A
Saccharomyces cerevisiae chromosome V, complete chromosome sequence. Found forward in NC_001137 between 426685 and 427684 with 100% identity.
2286_at 675.7 A
Saccharomyces cerevisiae chromosome V, complete chromosome sequence. Found forward in NC_001137 between 427685 and 428684 with 100% identity.
2287_at 265.5 A
Saccharomyces cerevisiae chromosome V, complete chromosome sequence. Found forward in NC_001137 between 428685 and 429684 with 100% identity.
2288_at 1945.3 A
Saccharomyces cerevisiae chromosome V, complete chromosome sequence. Found forward in NC_001137 between 429685 and 430684 with 100% identity.
2289_at -421.2 A
Saccharomyces cerevisiae chromosome V, complete chromosome sequence. Found forward in NC_001137 between 430685 and 431126 with 100% identity.
2290_at 2560.2 P
Saccharomyces cerevisiae chromosome V, complete chromosome sequence. Found forward in NC_001137 between 442412 and 443411 with 100% identity.
2291_g_at 2932.3 P
Saccharomyces cerevisiae chromosome V, complete chromosome sequence. Found forward in NC_001137 between 442412 and 443411 with 100% identity.
2294_f_at 1688.8 P
Saccharomyces cerevisiae chromosome V, complete chromosome sequence. Found forward in NC_001137 between 446412 and 447411 with 100% identity.
2295_at 408.2 A
Saccharomyces cerevisiae chromosome V, complete chromosome sequence. Found forward in NC_001137 between 476841 and 477840 with 100% identity.
2296_at 992.0 P
Saccharomyces cerevisiae chromosome V, complete chromosome sequence. Found forward in NC_001137 between 477841 and 478840 with 100% identity.
2297_at 31.7 A
Saccharomyces cerevisiae chromosome V, complete chromosome sequence. Found forward in NC_001137 between 478841 and 479840 with 100% identity.
2298_at -58.3 A
Saccharomyces cerevisiae chromosome V, complete chromosome sequence. Found forward in NC_001137 between 479841 and 480840 with 100% identity.

2299_at -72.0 A
Saccharomyces cerevisiae chromosome V, complete chromosome sequence. Found forward in NC_001137 between 480841 and 481840 with 100% identity.

2300_at 1093.1 A
Saccharomyces cerevisiae chromosome V, complete chromosome sequence. Found forward in NC_001137 between 481841 and 482840 with 100% identity.

2301_at 40.5 A
Saccharomyces cerevisiae chromosome V, complete chromosome sequence. Found forward in NC_001137 between 482841 and 483321 with 100% identity.

2302_at 154.2 A
Saccharomyces cerevisiae chromosome V, complete chromosome sequence. Found forward in NC_001137 between 491954 and 492953 with 100% identity.

2303_f_at 800.7 P
Saccharomyces cerevisiae chromosome V, complete chromosome sequence. Found forward in NC_001137 between 492954 and 493953 with 100% identity.

2306_at 670.6 P
Saccharomyces cerevisiae chromosome V, complete chromosome sequence. Found forward in NC_001137 between 497954 and 498953 with 100% identity.

2307_at 120.2 M
Saccharomyces cerevisiae chromosome V, complete chromosome sequence. Found forward in NC_001137 between 498954 and 499172 with 100% identity.

2308_at -387.7 A
Saccharomyces cerevisiae chromosome V, complete chromosome sequence. Found forward in NC_001137 between 530026 and 531025 with 100% identity.

2223_at 54.3 P
Saccharomyces cerevisiae chromosome V, complete chromosome sequence. Found forward in NC_001137 between 531026 and 532025 with 100% identity.

2224_at 347.7 A
Saccharomyces cerevisiae chromosome V, complete chromosome sequence. Found forward in NC_001137 between 532026 and 533025 with 100% identity.

2225_at 401.3 M
Saccharomyces cerevisiae chromosome V, complete chromosome sequence. Found forward in NC_001137 between 533026 and 534025 with 100% identity.

2226_at 1190.7 P
Saccharomyces cerevisiae chromosome V, complete chromosome sequence. Found forward in NC_001137 between 534026 and 535025 with 100% identity.

2227_at -276.9 A
Saccharomyces cerevisiae chromosome V, complete chromosome sequence. Found forward in NC_001137 between 535026 and 536025 with 100% identity.

2228_at 81.8 A
Saccharomyces cerevisiae chromosome V, complete chromosome sequence. Found forward in NC_001137 between 536026 and 536271 with 100% identity.

2229_at 153.0 A
Saccharomyces cerevisiae chromosome VI, complete chromosome sequence. Found forward in NC_001138 between 69614 and 70613 with 100% identity.

2230_at 526.7 P
Saccharomyces cerevisiae chromosome VI, complete chromosome sequence. Found forward in NC_001138 between 70614 and 71613 with 100% identity.

2231_at -371.1 A
Saccharomyces cerevisiae chromosome VI, complete chromosome sequence. Found forward in NC_001138 between 71614 and 72613 with 100% identity.

2232_at 311.1 A
Saccharomyces cerevisiae chromosome VI, complete chromosome sequence. Found forward in NC_001138 between 72614 and 73613 with 100% identity.

2233_at 442.0 M
Saccharomyces cerevisiae chromosome VI, complete chromosome sequence. Found forward in

NC_001138 between 73614 and 74613 with 100% identity.

2234_at 286.8 A

Saccharomyces cerevisiae chromosome VI, complete chromosome sequence. Found forward in NC_001138 between 74614 and 74871 with 100% identity.

2235_at 1222.7 P

Saccharomyces cerevisiae chromosome VI, complete chromosome sequence. Found forward in NC_001138 between 136029 and 137028 with 100% identity.

2236_at -226.1 A

Saccharomyces cerevisiae chromosome VI, complete chromosome sequence. Found forward in NC_001138 between 137029 and 138028 with 100% identity.

2237_at 36.4 A

Saccharomyces cerevisiae chromosome VI, complete chromosome sequence. Found forward in NC_001138 between 143029 and 144028 with 100% identity.

2238_at -85.8 A

Saccharomyces cerevisiae chromosome VI, complete chromosome sequence. Found forward in NC_001138 between 144029 and 145028 with 100% identity.

2239_at 1188.8 P

Saccharomyces cerevisiae chromosome VI, complete chromosome sequence. Found forward in NC_001138 between 145029 and 145108 with 100% identity.

2240_at -631.4 A

Saccharomyces cerevisiae chromosome VI, complete chromosome sequence. Found forward in NC_001138 between 184470 and 185469 with 100% identity.

2241_s_at 762.4 P

Saccharomyces cerevisiae chromosome VI, complete chromosome sequence. Found forward in NC_001138 between 185470 and 186469 with 100% identity.

2242_s_at 652.4 P

Saccharomyces cerevisiae chromosome VI, complete chromosome sequence. Found forward in NC_001138 between 186470 and 187469 with 100% identity.

2243_s_at 480.8 P

Saccharomyces cerevisiae chromosome VI, complete chromosome sequence. Found forward in NC_001138 between 187470 and 188469 with 100% identity.

2244_s_at 747.6 P

Saccharomyces cerevisiae chromosome VI, complete chromosome sequence. Found forward in NC_001138 between 188470 and 189469 with 100% identity.

2245_s_at 1355.4 A

Saccharomyces cerevisiae chromosome VI, complete chromosome sequence. Found forward in NC_001138 between 189470 and 190469 with 100% identity.

2246_s_at 2225.7 P

Saccharomyces cerevisiae chromosome VI, complete chromosome sequence. Found forward in NC_001138 between 190470 and 190825 with 100% identity.

2247_at 836.9 P

Saccharomyces cerevisiae chromosome VII, complete chromosome sequence. Found forward in NC_001139 between 16307 and 17306 with 100% identity.

2248_at 219.7 A

Saccharomyces cerevisiae chromosome VII, complete chromosome sequence. Found forward in NC_001139 between 17307 and 18306 with 100% identity.

2249_at -133.2 A

Saccharomyces cerevisiae chromosome VII, complete chromosome sequence. Found forward in NC_001139 between 18307 and 19306 with 100% identity.

2250_at 2578.9 P

Saccharomyces cerevisiae chromosome VII, complete chromosome sequence. Found forward in NC_001139 between 19307 and 20306 with 100% identity.

2251_at 333.3 P

Saccharomyces cerevisiae chromosome VII, complete chromosome sequence. Found forward in NC_001139 between 20307 and 21306 with 100% identity.

2252_g_at 2544.5 P

Saccharomyces cerevisiae chromosome VII, complete chromosome sequence. Found forward in NC_001139 between 20307 and 21306 with 100% identity.

2253_s_at 152.6 P

Saccharomyces cerevisiae chromosome VII, complete chromosome sequence. Found forward in NC_001139 between 21307 and 21608 with 100% identity.

2254_at 1.9 A

Saccharomyces cerevisiae chromosome VII, complete chromosome sequence. Found forward in NC_001139 between 103045 and 104044 with 100% identity.

2255_at 179.4 P

Saccharomyces cerevisiae chromosome VII, complete chromosome sequence. Found forward in NC_001139 between 104045 and 105044 with 100% identity.

2256_at -268.9 A

Saccharomyces cerevisiae chromosome VII, complete chromosome sequence. Found forward in NC_001139 between 105045 and 106044 with 100% identity.

2257_at 1231.9 A

Saccharomyces cerevisiae chromosome VII, complete chromosome sequence. Found forward in NC_001139 between 106045 and 107044 with 100% identity.

2258_at 154.4 P

Saccharomyces cerevisiae chromosome VII, complete chromosome sequence. Found forward in NC_001139 between 107045 and 108044 with 100% identity.

2259_at 736.3 P

Saccharomyces cerevisiae chromosome VII, complete chromosome sequence. Found forward in NC_001139 between 108045 and 109044 with 100% identity.

2260_g_at 322.5 P

Saccharomyces cerevisiae chromosome VII, complete chromosome sequence. Found forward in NC_001139 between 108045 and 109044 with 100% identity.

2261_s_at 921.9 A

Saccharomyces cerevisiae chromosome VII, complete chromosome sequence. Found forward in NC_001139 between 109045 and 109906 with 100% identity.

2262_at 1370.6 P

Saccharomyces cerevisiae chromosome VII, complete chromosome sequence. Found forward in NC_001139 between 131050 and 132049 with 100% identity.

2263_g_at 1805.5 P

Saccharomyces cerevisiae chromosome VII, complete chromosome sequence. Found forward in NC_001139 between 131050 and 132049 with 100% identity.

2264_s_at 2157.8 P

Saccharomyces cerevisiae chromosome VII, complete chromosome sequence. Found forward in NC_001139 between 132050 and 133049 with 100% identity.

2265_s_at 1442.9 P

Saccharomyces cerevisiae chromosome VII, complete chromosome sequence. Found forward in NC_001139 between 133050 and 134049 with 100% identity.

2180_s_at 4223.5 P

Saccharomyces cerevisiae chromosome VII, complete chromosome sequence. Found forward in NC_001139 between 134050 and 135049 with 100% identity.

2181_s_at 5949.0 P

Saccharomyces cerevisiae chromosome VII, complete chromosome sequence. Found forward in NC_001139 between 135050 and 136049 with 100% identity.

2182_s_at 7537.5 P

Saccharomyces cerevisiae chromosome VII, complete chromosome sequence. Found forward in NC_001139 between 136050 and 137049 with 100% identity.

2183_s_at 9492.7 P

Saccharomyces cerevisiae chromosome VII, complete chromosome sequence. Found forward in NC_001139 between 137050 and 138049 with 100% identity.

2184_s_at 6965.1 P

Saccharomyces cerevisiae chromosome VII, complete chromosome sequence. Found forward in NC_001139 between 138050 and 139047 with 100% identity.

2185_at 677.0 P
Saccharomyces cerevisiae chromosome VII, complete chromosome sequence. Found forward in NC_001139 between 176031 and 177030 with 100% identity.
2186_at 784.7 A
Saccharomyces cerevisiae chromosome VII, complete chromosome sequence. Found forward in NC_001139 between 177031 and 178030 with 100% identity.
2187_at 444.1 A
Saccharomyces cerevisiae chromosome VII, complete chromosome sequence. Found forward in NC_001139 between 178031 and 179030 with 100% identity.
2188_at 250.2 M
Saccharomyces cerevisiae chromosome VII, complete chromosome sequence. Found forward in NC_001139 between 179031 and 180030 with 100% identity.
2189_at 262.0 P
Saccharomyces cerevisiae chromosome VII, complete chromosome sequence. Found forward in NC_001139 between 180031 and 181030 with 100% identity.
2190_g_at 2126.3 P
Saccharomyces cerevisiae chromosome VII, complete chromosome sequence. Found forward in NC_001139 between 180031 and 181030 with 100% identity.
2191_s_at 2486.0 P
Saccharomyces cerevisiae chromosome VII, complete chromosome sequence. Found forward in NC_001139 between 181031 and 181622 with 100% identity.
2192_at -392.3 A
Saccharomyces cerevisiae chromosome VII, complete chromosome sequence. Found forward in NC_001139 between 241856 and 242855 with 100% identity.
2193_at 207.6 P
Saccharomyces cerevisiae chromosome VII, complete chromosome sequence. Found forward in NC_001139 between 242856 and 243855 with 100% identity.
2194_at 3438.3 A
Saccharomyces cerevisiae chromosome VII, complete chromosome sequence. Found forward in NC_001139 between 243856 and 244855 with 100% identity.
2195_at 865.8 P
Saccharomyces cerevisiae chromosome VII, complete chromosome sequence. Found forward in NC_001139 between 244856 and 245855 with 100% identity.
2196_s_at 2475.8 P
Saccharomyces cerevisiae chromosome VII, complete chromosome sequence. Found forward in NC_001139 between 245856 and 246855 with 100% identity.
2197_s_at 3512.0 P
Saccharomyces cerevisiae chromosome VII, complete chromosome sequence. Found forward in NC_001139 between 246856 and 247627 with 100% identity.
2198_at 190.0 A
Saccharomyces cerevisiae chromosome VII, complete chromosome sequence. Found forward in NC_001139 between 331616 and 332615 with 100% identity.
2199_at -115.7 A
Saccharomyces cerevisiae chromosome VII, complete chromosome sequence. Found forward in NC_001139 between 332616 and 333615 with 100% identity.
2200_at -166.7 A
Saccharomyces cerevisiae chromosome VII, complete chromosome sequence. Found forward in NC_001139 between 333616 and 334615 with 100% identity.
2201_at -2845.8 A
Saccharomyces cerevisiae chromosome VII, complete chromosome sequence. Found forward in NC_001139 between 334616 and 335615 with 100% identity.
2202_g_at 622.7 A
Saccharomyces cerevisiae chromosome VII, complete chromosome sequence. Found forward in NC_001139 between 334616 and 335615 with 100% identity.
2203_s_at 1684.4 P
Saccharomyces cerevisiae chromosome VII, complete chromosome sequence. Found forward in

NC_001139 between 335616 and 336615 with 100% identity.
2204_s_at 2365.6 P
Saccharomyces cerevisiae chromosome VII, complete chromosome sequence. Found forward in NC_001139 between 336616 and 337137 with 100% identity.
2205_at 2645.0 P
Saccharomyces cerevisiae chromosome VII, complete chromosome sequence. Found forward in NC_001139 between 547463 and 548462 with 100% identity.
2206_g_at 193.9 A
Saccharomyces cerevisiae chromosome VII, complete chromosome sequence. Found forward in NC_001139 between 547463 and 548462 with 100% identity.
2207_s_at 627.1 P
Saccharomyces cerevisiae chromosome VII, complete chromosome sequence. Found forward in NC_001139 between 548463 and 549462 with 100% identity.
2208_s_at 933.1 P
Saccharomyces cerevisiae chromosome VII, complete chromosome sequence. Found forward in NC_001139 between 549463 and 550462 with 100% identity.
2209_s_at 1343.4 P
Saccharomyces cerevisiae chromosome VII, complete chromosome sequence. Found forward in NC_001139 between 550463 and 551462 with 100% identity.
2210_s_at 3073.9 P
Saccharomyces cerevisiae chromosome VII, complete chromosome sequence. Found forward in NC_001139 between 551463 and 552462 with 100% identity.
2211_s_at 2737.0 P
Saccharomyces cerevisiae chromosome VII, complete chromosome sequence. Found forward in NC_001139 between 552463 and 553445 with 100% identity.
2212_at 854.9 P
Saccharomyces cerevisiae chromosome VII, complete chromosome sequence. Found forward in NC_001139 between 659764 and 660763 with 100% identity.
2213_at -1465.3 A
Saccharomyces cerevisiae chromosome VII, complete chromosome sequence. Found forward in NC_001139 between 660764 and 661763 with 100% identity.
2214_at -781.3 P
Saccharomyces cerevisiae chromosome VII, complete chromosome sequence. Found forward in NC_001139 between 661764 and 662763 with 100% identity.
2215_g_at 4238.8 P
Saccharomyces cerevisiae chromosome VII, complete chromosome sequence. Found forward in NC_001139 between 661764 and 662763 with 100% identity.
2216_s_at 4734.3 P
Saccharomyces cerevisiae chromosome VII, complete chromosome sequence. Found forward in NC_001139 between 662764 and 663763 with 100% identity.
2217_s_at 4422.2 P
Saccharomyces cerevisiae chromosome VII, complete chromosome sequence. Found forward in NC_001139 between 663764 and 664763 with 100% identity.
2218_s_at 4327.3 P
Saccharomyces cerevisiae chromosome VII, complete chromosome sequence. Found forward in NC_001139 between 664764 and 665565 with 100% identity.
2219_at -442.0 A
Saccharomyces cerevisiae chromosome VII, complete chromosome sequence. Found forward in NC_001139 between 683060 and 684059 with 100% identity.
2220_at -137.2 A
Saccharomyces cerevisiae chromosome VII, complete chromosome sequence. Found forward in NC_001139 between 684060 and 685059 with 100% identity.
2221_at -233.6 A
Saccharomyces cerevisiae chromosome VII, complete chromosome sequence. Found forward in NC_001139 between 685060 and 686059 with 100% identity.
2222_at 355.1 A

Saccharomyces cerevisiae chromosome VII, complete chromosome sequence. Found forward in NC_001139 between 686060 and 687059 with 100% identity.
2138_at 384.2 P
Saccharomyces cerevisiae chromosome VII, complete chromosome sequence. Found forward in NC_001139 between 687060 and 688059 with 100% identity.
2139_g_at 701.1 A
Saccharomyces cerevisiae chromosome VII, complete chromosome sequence. Found forward in NC_001139 between 687060 and 688059 with 100% identity.
2140_s_at 459.1 P
Saccharomyces cerevisiae chromosome VII, complete chromosome sequence. Found forward in NC_001139 between 688060 and 689059 with 100% identity.
2141_s_at 2022.4 P
Saccharomyces cerevisiae chromosome VII, complete chromosome sequence. Found forward in NC_001139 between 689060 and 689459 with 100% identity.
2142_at 1642.7 P
Saccharomyces cerevisiae chromosome VII, complete chromosome sequence. Found forward in NC_001139 between 860395 and 861394 with 100% identity.
2143_at 67.2 A
Saccharomyces cerevisiae chromosome VII, complete chromosome sequence. Found forward in NC_001139 between 861395 and 862394 with 100% identity.
2144_at 973.7 A
Saccharomyces cerevisiae chromosome VII, complete chromosome sequence. Found forward in NC_001139 between 862395 and 863394 with 100% identity.
2145_at -179.4 A
Saccharomyces cerevisiae chromosome VII, complete chromosome sequence. Found forward in NC_001139 between 863395 and 864394 with 100% identity.
2146_at 537.9 P
Saccharomyces cerevisiae chromosome VII, complete chromosome sequence. Found forward in NC_001139 between 864395 and 865394 with 100% identity.
2147_at 623.9 A
Saccharomyces cerevisiae chromosome VII, complete chromosome sequence. Found forward in NC_001139 between 865395 and 866330 with 100% identity.
2148_at 53.5 A
Saccharomyces cerevisiae chromosome VII, complete chromosome sequence. Found forward in NC_001139 between 923127 and 924126 with 100% identity.
2149_at -103.6 A
Saccharomyces cerevisiae chromosome VII, complete chromosome sequence. Found forward in NC_001139 between 924127 and 925126 with 100% identity.
2150_g_at 1026.1 A
Saccharomyces cerevisiae chromosome VII, complete chromosome sequence. Found forward in NC_001139 between 924127 and 925126 with 100% identity.
2151_s_at -51.2 P
Saccharomyces cerevisiae chromosome VII, complete chromosome sequence. Found forward in NC_001139 between 925127 and 926126 with 100% identity.
2152_s_at 258.5 P
Saccharomyces cerevisiae chromosome VII, complete chromosome sequence. Found forward in NC_001139 between 926127 and 927126 with 100% identity.
2153_s_at 1006.0 P
Saccharomyces cerevisiae chromosome VII, complete chromosome sequence. Found forward in NC_001139 between 927127 and 928126 with 100% identity.
2154_s_at 978.9 P
Saccharomyces cerevisiae chromosome VII, complete chromosome sequence. Found forward in NC_001139 between 928127 and 929126 with 100% identity.
2155_s_at 1122.1 P
Saccharomyces cerevisiae chromosome VII, complete chromosome sequence. Found forward in NC_001139 between 929127 and 930126 with 100% identity.

2156_s_at 882.8 P
Saccharomyces cerevisiae chromosome VII, complete chromosome sequence. Found forward in NC_001139 between 930127 and 930307 with 100% identity.
2157_at 154.6 P
Saccharomyces cerevisiae chromosome VII, complete chromosome sequence. Found forward in NC_001139 between 955166 and 956165 with 100% identity.
2158_at 567.0 A
Saccharomyces cerevisiae chromosome VII, complete chromosome sequence. Found forward in NC_001139 between 956166 and 957165 with 100% identity.
2159_at -1271.9 A
Saccharomyces cerevisiae chromosome VII, complete chromosome sequence. Found forward in NC_001139 between 957166 and 958165 with 100% identity.
2160_at 488.8 P
Saccharomyces cerevisiae chromosome VII, complete chromosome sequence. Found forward in NC_001139 between 958166 and 959165 with 100% identity.
2161_at 23.7 A
Saccharomyces cerevisiae chromosome VII, complete chromosome sequence. Found forward in NC_001139 between 959166 and 960165 with 100% identity.
2162_g_at 10260.4 P
Saccharomyces cerevisiae chromosome VII, complete chromosome sequence. Found forward in NC_001139 between 959166 and 960165 with 100% identity.
2163_s_at 13745.8 P
Saccharomyces cerevisiae chromosome VII, complete chromosome sequence. Found forward in NC_001139 between 960166 and 960596 with 100% identity.
2164_at 265.6 P
Saccharomyces cerevisiae chromosome VII, complete chromosome sequence. Found forward in NC_001139 between 1031505 and 1032504 with 100% identity.
2165_g_at 203.2 A
Saccharomyces cerevisiae chromosome VII, complete chromosome sequence. Found forward in NC_001139 between 1031505 and 1032504 with 100% identity.
2166_s_at 489.8 P
Saccharomyces cerevisiae chromosome VII, complete chromosome sequence. Found forward in NC_001139 between 1032505 and 1033504 with 100% identity.
2167_s_at 526.3 P
Saccharomyces cerevisiae chromosome VII, complete chromosome sequence. Found forward in NC_001139 between 1033505 and 1034504 with 100% identity.
2168_s_at 351.7 P
Saccharomyces cerevisiae chromosome VII, complete chromosome sequence. Found forward in NC_001139 between 1034505 and 1035504 with 100% identity.
2169_s_at 2135.6 P
Saccharomyces cerevisiae chromosome VII, complete chromosome sequence. Found forward in NC_001139 between 1035505 and 1036504 with 100% identity.
2170_s_at 1494.0 P
Saccharomyces cerevisiae chromosome VII, complete chromosome sequence. Found forward in NC_001139 between 1036505 and 1037190 with 100% identity.
2171_at 21.2 A
Saccharomyces cerevisiae chromosome VII, complete chromosome sequence. Found forward in NC_001139 between 1051406 and 1052405 with 100% identity.
2172_at 1713.5 P
Saccharomyces cerevisiae chromosome VII, complete chromosome sequence. Found forward in NC_001139 between 1052406 and 1053405 with 100% identity.
2173_g_at 945.2 P
Saccharomyces cerevisiae chromosome VII, complete chromosome sequence. Found forward in NC_001139 between 1052406 and 1053405 with 100% identity.
2174_s_at 1673.1 P
Saccharomyces cerevisiae chromosome VII, complete chromosome sequence. Found forward in

NC_001139 between 1053406 and 1054405 with 100% identity.
2175_s_at 1501.3 P
Saccharomyces cerevisiae chromosome VII, complete chromosome sequence. Found forward in NC_001139 between 1054406 and 1055405 with 100% identity.
2176_s_at 1929.7 P
Saccharomyces cerevisiae chromosome VII, complete chromosome sequence. Found forward in NC_001139 between 1055406 and 1056405 with 100% identity.
2177_s_at 5327.2 P
Saccharomyces cerevisiae chromosome VII, complete chromosome sequence. Found forward in NC_001139 between 1056406 and 1056753 with 100% identity.
2178_at 579.2 P
Saccharomyces cerevisiae chromosome VII, complete chromosome sequence. Found forward in NC_001139 between 1084878 and 1085877 with 100% identity.
2179_at -253.9 A
Saccharomyces cerevisiae chromosome VIII, complete chromosome sequence. Found forward in NC_001140 between 39533 and 40532 with 100% identity.
2100_g_at 2144.7 P
Saccharomyces cerevisiae chromosome VIII, complete chromosome sequence. Found forward in NC_001140 between 39533 and 40532 with 100% identity.
2101_s_at 163.3 A
Saccharomyces cerevisiae chromosome VIII, complete chromosome sequence. Found forward in NC_001140 between 40533 and 41532 with 100% identity.
2102_s_at 1466.4 P
Saccharomyces cerevisiae chromosome VIII, complete chromosome sequence. Found forward in NC_001140 between 41533 and 42532 with 100% identity.
2103_s_at 3305.5 P
Saccharomyces cerevisiae chromosome VIII, complete chromosome sequence. Found forward in NC_001140 between 42533 and 43532 with 100% identity.
2104_s_at 6863.9 P
Saccharomyces cerevisiae chromosome VIII, complete chromosome sequence. Found forward in NC_001140 between 43533 and 44532 with 100% identity.
2105_s_at 2302.3 P
Saccharomyces cerevisiae chromosome VIII, complete chromosome sequence. Found forward in NC_001140 between 44533 and 45188 with 100% identity.
2106_at 1102.8 A
Saccharomyces cerevisiae chromosome VIII, complete chromosome sequence. Found forward in NC_001140 between 84563 and 85562 with 100% identity.
2107_at 94.1 P
Saccharomyces cerevisiae chromosome VIII, complete chromosome sequence. Found forward in NC_001140 between 150066 and 151065 with 100% identity.
2108_at -94.4 A
Saccharomyces cerevisiae chromosome VIII, complete chromosome sequence. Found forward in NC_001140 between 151066 and 152065 with 100% identity.
2109_g_at 371.2 P
Saccharomyces cerevisiae chromosome VIII, complete chromosome sequence. Found forward in NC_001140 between 151066 and 152065 with 100% identity.
2110_s_at 145.0 M
Saccharomyces cerevisiae chromosome VIII, complete chromosome sequence. Found forward in NC_001140 between 152066 and 153065 with 100% identity.
2111_s_at 497.8 P
Saccharomyces cerevisiae chromosome VIII, complete chromosome sequence. Found forward in NC_001140 between 153066 and 154065 with 100% identity.
2112_s_at 425.9 P
Saccharomyces cerevisiae chromosome VIII, complete chromosome sequence. Found forward in NC_001140 between 154066 and 155065 with 100% identity.
2113_s_at 237.0 P

Saccharomyces cerevisiae chromosome VIII, complete chromosome sequence. Found forward in NC_001140 between 155066 and 156065 with 100% identity.

2114_s_at 1453.3 P

Saccharomyces cerevisiae chromosome VIII, complete chromosome sequence. Found forward in NC_001140 between 156066 and 156943 with 100% identity.

2115_at 85.9 A

Saccharomyces cerevisiae chromosome VIII, complete chromosome sequence. Found forward in NC_001140 between 299647 and 300646 with 100% identity.

2116_at 489.6 P

Saccharomyces cerevisiae chromosome VIII, complete chromosome sequence. Found forward in NC_001140 between 300647 and 301646 with 100% identity.

2117_at -700.4 A

Saccharomyces cerevisiae chromosome VIII, complete chromosome sequence. Found forward in NC_001140 between 301647 and 302646 with 100% identity.

2118_at 1592.4 P

Saccharomyces cerevisiae chromosome VIII, complete chromosome sequence. Found forward in NC_001140 between 302647 and 303646 with 100% identity.

2119_g_at 534.2 P

Saccharomyces cerevisiae chromosome VIII, complete chromosome sequence. Found forward in NC_001140 between 302647 and 303646 with 100% identity.

2120_s_at 88.7 P

Saccharomyces cerevisiae chromosome VIII, complete chromosome sequence. Found forward in NC_001140 between 303647 and 304646 with 100% identity.

2121_s_at -1770.8 P

Saccharomyces cerevisiae chromosome VIII, complete chromosome sequence. Found forward in NC_001140 between 304647 and 305646 with 100% identity.

2122_s_at 382.8 P

Saccharomyces cerevisiae chromosome VIII, complete chromosome sequence. Found forward in NC_001140 between 305647 and 306646 with 100% identity.

2123_s_at 491.8 P

Saccharomyces cerevisiae chromosome VIII, complete chromosome sequence. Found forward in NC_001140 between 306647 and 307646 with 100% identity.

2124_s_at 647.9 A

Saccharomyces cerevisiae chromosome VIII, complete chromosome sequence. Found forward in NC_001140 between 307647 and 308646 with 100% identity.

2125_s_at 773.7 P

Saccharomyces cerevisiae chromosome VIII, complete chromosome sequence. Found forward in NC_001140 between 308647 and 309646 with 100% identity.

2126_s_at 2536.7 P

Saccharomyces cerevisiae chromosome VIII, complete chromosome sequence. Found forward in NC_001140 between 309647 and 310646 with 100% identity.

2127_s_at 675.6 P

Saccharomyces cerevisiae chromosome VIII, complete chromosome sequence. Found forward in NC_001140 between 310647 and 311646 with 100% identity.

2128_s_at 1103.4 P

Saccharomyces cerevisiae chromosome VIII, complete chromosome sequence. Found forward in NC_001140 between 311647 and 312646 with 100% identity.

2129_s_at 3826.1 P

Saccharomyces cerevisiae chromosome VIII, complete chromosome sequence. Found forward in NC_001140 between 312647 and 313497 with 100% identity.

2130_at -360.3 A

Saccharomyces cerevisiae chromosome VIII, complete chromosome sequence. Found forward in NC_001140 between 430206 and 431205 with 100% identity.

2131_at -681.6 A

Saccharomyces cerevisiae chromosome VIII, complete chromosome sequence. Found forward in NC_001140 between 431206 and 432205 with 100% identity.

2132_at	-542.9	A	Saccharomyces cerevisiae chromosome VIII, complete chromosome sequence. Found forward in NC_001140 between 432206 and 433205 with 100% identity.
2133_at	-15.0	A	Saccharomyces cerevisiae chromosome VIII, complete chromosome sequence. Found forward in NC_001140 between 433206 and 434205 with 100% identity.
2134_at	143.7	P	Saccharomyces cerevisiae chromosome VIII, complete chromosome sequence. Found forward in NC_001140 between 434206 and 435205 with 100% identity.
2135_at	-1102.9	A	Saccharomyces cerevisiae chromosome VIII, complete chromosome sequence. Found forward in NC_001140 between 435206 and 436205 with 100% identity.
2136_at	2305.6	A	Saccharomyces cerevisiae chromosome VIII, complete chromosome sequence. Found forward in NC_001140 between 436206 and 437169 with 100% identity.
2137_at	586.7	A	Saccharomyces cerevisiae chromosome VIII, complete chromosome sequence. Found forward in NC_001140 between 522872 and 523871 with 100% identity.
11394_at	536.7	P	Saccharomyces cerevisiae chromosome VIII, complete chromosome sequence. Found forward in NC_001140 between 523872 and 524871 with 100% identity.
11395_at	100.4	A	Saccharomyces cerevisiae chromosome VIII, complete chromosome sequence. Found forward in NC_001140 between 524872 and 525871 with 100% identity.
11396_g_at	378.0	P	Saccharomyces cerevisiae chromosome VIII, complete chromosome sequence. Found forward in NC_001140 between 524872 and 525871 with 100% identity.
11397_f_at	1011.1	P	Saccharomyces cerevisiae chromosome VIII, complete chromosome sequence. Found forward in NC_001140 between 525872 and 526871 with 100% identity.
11398_s_at	274.2	A	Saccharomyces cerevisiae chromosome VIII, complete chromosome sequence. Found forward in NC_001140 between 526872 and 527871 with 100% identity.
11399_s_at	4918.7	P	Saccharomyces cerevisiae chromosome VIII, complete chromosome sequence. Found forward in NC_001140 between 527872 and 528114 with 100% identity.
11400_s_at	202.9	P	Saccharomyces cerevisiae chromosome VIII, complete chromosome sequence. Found forward in NC_001140 between 532177 and 533176 with 100% identity.
11401_at	-388.1	A	Saccharomyces cerevisiae chromosome VIII, complete chromosome sequence. Found forward in NC_001140 between 533177 and 534176 with 100% identity.
11402_at	135.0	A	Saccharomyces cerevisiae chromosome VIII, complete chromosome sequence. Found forward in NC_001140 between 534177 and 535176 with 100% identity.
11403_at	373.1	P	Saccharomyces cerevisiae chromosome VIII, complete chromosome sequence. Found forward in NC_001140 between 535177 and 536176 with 100% identity.
11404_at	10.3	A	Saccharomyces cerevisiae chromosome VIII, complete chromosome sequence. Found forward in NC_001140 between 537177 and 537754 with 100% identity.
11405_at	2222.7	P	Saccharomyces cerevisiae chromosome VIII, complete chromosome sequence. Found forward in NC_001140 between 543488 and 544487 with 100% identity.
11406_f_at	56.5	A	Saccharomyces cerevisiae chromosome VIII, complete chromosome sequence. Found forward in

NC_001140 between 544488 and 545487 with 100% identity.

11407_f_at -63.0 A

Saccharomyces cerevisiae chromosome VIII, complete chromosome sequence. Found forward in NC_001140 between 546488 and 547487 with 100% identity.

11408_f_at 2377.9 P

Saccharomyces cerevisiae chromosome VIII, complete chromosome sequence. Found forward in NC_001140 between 547488 and 548487 with 100% identity.

11409_f_at 43.4 A

Saccharomyces cerevisiae chromosome VIII, complete chromosome sequence. Found forward in NC_001140 between 548488 and 549487 with 100% identity.

11410_at -82.1 A

Saccharomyces cerevisiae chromosome VIII, complete chromosome sequence. Found forward in NC_001140 between 549488 and 549898 with 100% identity.

11411_at -29.3 A

Saccharomyces cerevisiae chromosome IX, complete chromosome sequence. Found forward in NC_001141 between 9696 and 10695 with 100% identity.

11412_at -173.0 A

Saccharomyces cerevisiae chromosome IX, complete chromosome sequence. Found forward in NC_001141 between 10696 and 11695 with 100% identity.

11413_s_at 668.1 P

Saccharomyces cerevisiae chromosome IX, complete chromosome sequence. Found forward in NC_001141 between 11696 and 12695 with 100% identity.

11414_s_at 13.5 A

Saccharomyces cerevisiae chromosome IX, complete chromosome sequence. Found forward in NC_001141 between 12696 and 13695 with 100% identity.

11415_f_at 1103.9 P

Saccharomyces cerevisiae chromosome IX, complete chromosome sequence. Found forward in NC_001141 between 13696 and 14695 with 100% identity.

11416_at 1864.8 P

Saccharomyces cerevisiae chromosome IX, complete chromosome sequence. Found forward in NC_001141 between 106607 and 107606 with 100% identity.

11417_at -324.6 A

Saccharomyces cerevisiae chromosome IX, complete chromosome sequence. Found forward in NC_001141 between 107607 and 108606 with 100% identity.

11418_at 183.5 A

Saccharomyces cerevisiae chromosome IX, complete chromosome sequence. Found forward in NC_001141 between 108607 and 109606 with 100% identity.

11419_at 167.4 A

Saccharomyces cerevisiae chromosome IX, complete chromosome sequence. Found forward in NC_001141 between 109607 and 110606 with 100% identity.

11420_at -831.8 A

Saccharomyces cerevisiae chromosome IX, complete chromosome sequence. Found forward in NC_001141 between 110607 and 111606 with 100% identity.

11421_at 0.9 A

Saccharomyces cerevisiae chromosome IX, complete chromosome sequence. Found forward in NC_001141 between 111607 and 112606 with 100% identity.

11422_at -360.3 A

Saccharomyces cerevisiae chromosome IX, complete chromosome sequence. Found forward in NC_001141 between 112607 and 113606 with 100% identity.

11423_at 66.6 A

Saccharomyces cerevisiae chromosome IX, complete chromosome sequence. Found forward in NC_001141 between 113607 and 114606 with 100% identity.

11424_g_at 2209.7 P

Saccharomyces cerevisiae chromosome IX, complete chromosome sequence. Found forward in NC_001141 between 113607 and 114606 with 100% identity.

11425_s_at 1599.4 A

Saccharomyces cerevisiae chromosome IX, complete chromosome sequence. Found forward in NC_001141 between 114607 and 115606 with 100% identity.
11426_s_at 1235.1 P
Saccharomyces cerevisiae chromosome IX, complete chromosome sequence. Found forward in NC_001141 between 115607 and 116404 with 100% identity.
11427_at -1867.0 A
Saccharomyces cerevisiae chromosome IX, complete chromosome sequence. Found forward in NC_001141 between 204053 and 205052 with 100% identity.
11428_at 217.0 P
Saccharomyces cerevisiae chromosome IX, complete chromosome sequence. Found forward in NC_001141 between 205053 and 206052 with 100% identity.
11429_at -89.5 A
Saccharomyces cerevisiae chromosome IX, complete chromosome sequence. Found forward in NC_001141 between 365963 and 366962 with 100% identity.
11430_at 52.1 A
Saccharomyces cerevisiae chromosome IX, complete chromosome sequence. Found forward in NC_001141 between 366963 and 367962 with 100% identity.
11431_at -366.6 A
Saccharomyces cerevisiae chromosome IX, complete chromosome sequence. Found forward in NC_001141 between 367963 and 368962 with 100% identity.
11432_at 3923.4 A
Saccharomyces cerevisiae chromosome IX, complete chromosome sequence. Found forward in NC_001141 between 368963 and 369962 with 100% identity.
11433_at -305.2 A
Saccharomyces cerevisiae chromosome IX, complete chromosome sequence. Found forward in NC_001141 between 369963 and 370962 with 100% identity.
11434_g_at 361.5 A
Saccharomyces cerevisiae chromosome IX, complete chromosome sequence. Found forward in NC_001141 between 369963 and 370962 with 100% identity.
11435_s_at 1173.1 P
Saccharomyces cerevisiae chromosome IX, complete chromosome sequence. Found forward in NC_001141 between 370963 and 371962 with 100% identity.
11436_s_at 451.8 A
Saccharomyces cerevisiae chromosome IX, complete chromosome sequence. Found forward in NC_001141 between 371963 and 372495 with 100% identity.