Expression Analysis: Pivot Tab

	JJ52 total	JJ52 total	JJ52 total	JJ52 total	JJ52 total	JJ52 total	JJ52 total	Descriptions
	Avg Diff	Abs Call	Diff Call	Avg Diff Change	B=A	Fold Change	Sort Score	
AFFX-MurIL2_at	-128.8	A						M16762 Mouse interleukin 2 (IL-2) gene, exon 4
AFFX-MurIL10_at	92.2	A						M37897 Mouse interleukin 10 mRNA, complete cds
AFFX-MurIL4_at	11.4	A						M25892 Mus musculus interleukin 4 (Il-4) mRNA, complete cds
AFFX-MurFAS_at	127.1	A						M83649 Mus musculus Fas antigen mRNA, complete cds
AFFX-BioB-5_at	2478.8	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	3233.3	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	3699.8	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	7834.7	P						J04423 E coli bioC protein (-5 and -3 represent transcript regions 5 prime and 3 prime respectively)
AFFX-BioC-3_at	7359.1	P						J04423 E coli bioC protein (-5 and -3 represent transcript regions 5 prime and 3 prime respectively)
AFFX-BioDn-5_at	2883.0	P						J04423 E coli bioD gene dethiobiotin synthetase (-5 and -3 represent transcript regions 5 prime and 3 prime respectively)
AFFX-BioDn-3_at	8369.9	P						J04423 E coli bioD gene dethiobiotin synthetase (-5 and -3 represent transcript regions 5 prime and 3 prime respectively)
AFFX-CreX-5_at	4794.8	P						X03453 Bacteriophage P1 cre recombinase protein (-5 and -3 represent transcript regions 5 prime and 3 prime respectively)
AFFX-CreX-3_at	7212.0	P						X03453 Bacteriophage P1 cre recombinase protein (-5 and -3 represent transcript regions 5 prime and 3 prime respectively)
AFFX-BioB-5_st	-5.6	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	-526.7	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	-516.4	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	-429.1	A						J04423 E coli bioC protein (-5 and -3 represent transcript regions 5 prime and 3 prime respectively)
AFFX-BioC-3_st	172.3	A						J04423 E coli bioC protein (-5 and -3 represent transcript regions 5 prime and 3 prime respectively)
AFFX-BioDn-5_st	-189.3	A						J04423 E coli bioD gene dethiobiotin synthetase (-5 and -3 represent transcript regions 5 prime and 3 prime respectively)
AFFX-BioDn-3_st	511.6	A						

J04423 E coli bioD gene dethiobiotin synthetase (-5 and -3 represent transcript regions 5 prime and 3 prime respectively)

AFFX-CreX-5_st 153.7 A

X03453 Bacteriophage P1 cre recombinase protein (-5 and -3 represent transcript regions 5 prime and 3 prime respectively)

AFFX-CreX-3_st -701.5 A

X03453 Bacteriophage P1 cre recombinase protein (-5 and -3 represent transcript regions 5 prime and 3 prime respectively)

AFFX-DapX-5_at 69.8 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 310.9 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 -174.2 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 -59.9 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 -441.6 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 595.4 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 -270.2 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 -259.7 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 278.6 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 249.3 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-M_at 38.1 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-3_at 123.5 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 22.3 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 25.3 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 8.6 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 12601.9 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	10338.2	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	9205.5	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	5811.0	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-YER148wM_at	6903.0	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	10325.6	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	469.2	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	1163.6	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	1181.4	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	1576.4	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	528.9	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-18srRnac_at	443.1	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	253.8	A	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	48.1	A	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	6233.4	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-25srRnab_at	141.5	A	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	18.1	A	

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 127.1 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-25srRnae_at 2362.9 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 9010.5 P
X61388 SGD: YEL002C Yeast S.cerevisiae WBP1 Oligosaccharyltransferase beta subunit
AFFX-YEL018w/_at 2350.9 P
U18530 SGD:YEL018W Yeast S. cerevisiae Protein of unknown function
AFFX-YEL024w/RIP1_at 7073.1 P
M23316 SGD:YEL024C Yeast S.cerevisiae RIP1 Rieske iron-sulfur protein of the mitochondrial cytochrome bc1 complex .
AFFX-YEL021w/URA3_at 885.5 P
K02207 SGD:YEL021W Yeast S.cerevisiae URA3 gene coding for OMP decarboxylase
11378_at 393.3 A
Aldehyde dehydrogenase 1, mitochondrial
11379_at 909.3 P
Suppressor of Sulfoxyde Ethionine resistance
11380_at 581.6 P
hypothetical protein
11381_at -74.2 A
putative pseudogene
11382_at 276.5 A
putative pseudogene
11383_at 49.6 A
putative pseudogene
11384_at 154.3 P
hypothetical protein
11385_s_at 1399.2 P
putative Flo1p homolog
11386_at 509.7 A
NADP-linked glutamate dehydrogenase
11387_at 570.0 P
similarity to alcohol/sorbitol dehydrogenase
11388_at 6552.6 P
similarity to alcohol/sorbitol dehydrogenase
11389_at 3003.0 P
ExtraCellular Mutant
11390_at 1230.1 P
Calnexin and calreticulin homolog
11391_at 491.6 A
questionable ORF
11392_at 853.7 P
similarity to hypothetical protein YOR371c
11393_at 2691.4 P
hypothetical protein
11356_at 2441.0 P
inducible acetyl-coenzyme A synthetase
11357_at 6501.7 P
strong similarity to hypothetical proteins YOR365c,YGL139w,YPL221w

11358_at 813.6 P
peroxisome proliferating transcription factor
11359_at 8344.6 P
weak similarity to Legionella small basic protein sbpA
11360_at 563.4 P
weak similarity to GTP-binding proteins
11361_at 480.7 P
Spc72p interacts with Stu2p in the two-hybrid assay\; Spc72p localizes to the spindle pole bodies. Molecular weight is 72 kD
11362_at 2021.3 P
hypothetical protein
11363_at 412.8 A
hypothetical protein
11364_at 10063.8 P
H-protein subunit of the glycine cleavage system
11365_at 2557.6 P
pre-tRNA processing
11366_at 5.2 A
questionable ORF
11367_at 9827.6 P
Function unknown now
11368_at 1625.3 P
Guanine nucleotide exchange factor (a.k.a. GDP-release factor) for cdc42
11369_at 4748.3 P
G(sub)1 cyclin
11370_at 7930.2 P
cytochrome c heme lyase (CCHL)
11371_at 6912.7 P
Pyruvate kinase
11372_at 441.0 P
strong similarity to GTP-binding proteins
11373_at 8639.2 P
Function unknown now
11374_at 9908.4 P
97 kDa protein
11375_at 29.9 A
questionable ORF
11376_at 483.3 P
hypothetical protein
11377_at 1339.8 P
Function unknown now
11333_at 3689.2 P
An integral subunit of RNase P and apparent subunit of RNase MRP
11334_at 575.7 A
Function unknown now
11335_at 2267.8 P
FUN21
11336_at 3260.3 P
homolog of Snc2p, vesicle-associated membrane protein (synaptobrevin) homolog, forms a complex with Snc2p and Sec9p
11337_at 6092.1 P
homolog of Snc2p, vesicle-associated membrane protein (synaptobrevin) homolog, forms a complex with Snc2p and Sec9p
11338_at 4300.1 P
myosin
11339_at 238.3 P

similarity to hypothetical protein YOR324c
11340_at 660.0 P
hypothetical protein
11341_at 1418.3 P
Membrane-spanning Ca-ATPase (P-type),member of the cation transport (E1-E2) ATPases
11342_at 2392.5 P
putative nuclear protein
11343_at 979.9 P
putative GTP-exchange protein
11344_at 11270.6 P
dolichyl phosphate-D-mannose:protein O-D-mannosyltransferase
11345_at 4012.2 P
predicted membrane protein
11346_at 5589.9 P
95 kDa containg leucine rich tandem repeats
11347_at 2416.9 P
Protein with similarity to human RCC1 protein
11348_at 2037.4 P
Shows homology to SNF2 transcriptional regulator
11349_at 433.9 P 3
transmembrane domains
11350_at 2016.3 P
Serine\/threonine kinase
11351_at 8370.7 P
protein phosphatase 2A regulatory subunit A
11352_at 1098.3 P
DNA glycosylase
11353_at 4578.6 P
protein of unknown function
11354_at 3742.5 P
regulation of phospholipid metabolism
11355_at 9878.9 P
cystathionine gamma-lyase
11310_at 590.1 P
possible mitochondrial transit peptide
11311_at 843.3 P
Mitochondrial outer membrane protein involved in mitochondrial morphology and inheritance
11312_at 2557.2 P
sporulation protein
11313_at 2441.5 P
protein of unknown function
11314_at 6404.0 P
p24 protein involved in membrane trafficking
11315_i_at 4727.5 P
Heat shock protein of HSP70 family, cytoplasmic
11316_r_at 0.0 A
Heat shock protein of HSP70 family, cytoplasmic
11317_s_at 15631.8 P
Heat shock protein of HSP70 family, cytoplasmic
11318_at 416.0 P
strong similarity to A.klebsiana glutamate dehydrogenase
11319_at 8847.5 P
Translation elongation factor EF-1beta, GDP\/GTP exchange factor for Tef1p\/Tef2p
11320_at 8646.7 P
Translation elongation factor EF-1beta, GDP\/GTP exchange factor for Tef1p\/Tef2p
11321_at 1003.0 P

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	2167.8	P
transcription factor tau (TFIIIC) subunit 138
11323_at	621.0	P
transcription factor tau (TFIIIC) subunit 138
11324_at	4581.1	P
protein of unknown function
11325_at	11116.3	P
p24 protein involved in membrane trafficking
11326_at	2918.0	P
beta transducin domain
11327_at	8049.6	P
69 kDa subunit of the heterotrimeric RPA (RF-A) single-stranded DNA binding protein, binds URS1 and CAR1
11328_at	1858.4	P
34kDa subunit of the tetrameric tRNA splicing endonuclease
11329_at	3556.8	P
maximal growth
11330_at	9204.1	P
phosphoribosyl amino imidazolesuccinocarbozamide synthetase
11331_at	503.1	P
protein kinase
11332_at	787.6	P
protein kinase domain
11287_f_at	717.4	P
strong similarity to members of the srp1p/Tip1p family
11288_at	409.8	P
membrane protein
11289_at	1138.1	P
membrane protein
11290_at	2501.5	P
membrane protein
11291_at	266.6	P
membrane protein
11292_at	23.0	P
hypothetical protein
11293_at	2051.2	P
membrane protein
11294_g_at	3359.1	P
membrane protein
11295_r_at	1617.4	P
membrane protein
11296_s_at	949.5	P
membrane protein
11297_at	3216.4	P
Outer carnitine acetyltransferase, mitochondrial
11298_at	2116.3	P
ankyrin repeat
11299_at	1603.5	P
Shows homology to the human oxysterol binding protein (OSBP)
11300_at	-12.4	P
predicted nuclear targeting signal
11301_i_at	-346.3	A
FLO1 putative cell wall glycoprotein
11302_at	641.8	P

predicted membrane protein
11303_s_at 609.7 P
strong similarity to hypothetical protein YHR212c
11304_at 344.2 P
putative pseudogene
11305_s_at 85.6 A
putative pseudogene
11306_at 509.7 P
Potential membrane protein
11307_s_at 6445.4 P
identical to YHR214w hypothetical protein, similarity to Sta1p
11308_s_at 6792.8 P
Potential membrane protein
11309_at 218.1 M
Potential membrane protein
11261_at -35.1 A
potential mitochondrial transit peptide
11262_s_at 16492.1 P
Acid phosphatase, secreted
11263_f_at 7531.1 P
strong similarity to IMP dehydrogenases
11264_f_at 8206.8 P
strong similarity to IMP dehydrogenases
11265_i_at 595.9 P
hypothetical protein
11266_f_at 3585.5 P
hypothetical protein
11267_at 196.7 P
identified by SAGE
11268_at -2.3 A
hypothetical protein
11269_at 385.8 M
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 37.8 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 144.1 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 457.5 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 261.7 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 767.3 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 802.6 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 104.1 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 -23.5 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 1150.4 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 764.0 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 107.2 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 181.1 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 -62.1 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 327.3 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 5789.7 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 7.5 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 74.0 P
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 -29.8 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 -278.6 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 401.7 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 419.6 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 162.2 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 507.4 A
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 479.7 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 -212.0 A
Centromere
11246_r_at 45.1 A
Centromere
11247_s_at 12341.9 P
strong similarity to members of the Sir1p/Tip1p family

11248_s_at 1621.2 P
strong similarity to members of the Sir1p/Tip1p family
11249_f_at 2057.5 P
strong similarity to members of the Srp1p/Tip1p family
11250_s_at 1029.2 P
strong similarity to Pep1p
11251_s_at 389.8 P
homology to maltase(alpha-D-glucosidase)
11252_s_at -65.3 A
questionable ORF
11253_s_at -11.1 A
High-affinity hexose transporter
11254_at 152.2 M
strong similarity to E.coli galactoside O-acetyltransferase
11255_at 257.3 A
hypothetical protein
11256_at 2.6 A
strong similarity to Mal62p
11257_at 75.0 A
hypothetical protein
11258_at 79.4 A
High-affinity hexose transporter
11259_at 1513.1 P
similarity to Methanobacterium aryldialkylphosphatase related protein
11260_at 2573.4 P
strong similarity to S.pombe isp4 protein
11215_at 169.5 A
questionable ORF
11216_at 4587.5 P
CH3HC4 zinc-binding integral peroxisomal membrane protein
11217_at 1173.3 P
Protein required for COB mRNA stability or 5 processing
11218_at 2633.1 P
mitochondrial nuclease
11219_at 1580.7 P
weak similarity to rat omega-conotoxin-sensitive calcium channel alpha-1 subunit rbB-I
11220_at 726.5 P
similarity to YIL130p and Put3p
11221_at 5525.3 P
involved in secretion of proteins that lack classical secretory signal sequences
11222_at 2028.3 P
weak similarity to Tor2p
11223_at 764.6 P
RNA splicing factor
11224_at 132.5 A
questionable ORF
11225_at 720.7 P
ExtraCellular Mutant
11226_at 9195.2 P
strong similarity to aconitate hydratase
11227_at 1318.9 P
hypothetical protein
11228_at 8991.2 P
strong similarity to Pho87p
11229_at 1293.7 P
ubiquitin carboxyl-terminal hydrolase

11230_at 12708.9 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 -23.0 A
questionable ORF
11232_at 1536.5 P
Protein involved in initiation of DNA replication
11233_at 3804.3 P
similarity to Sly41p
11234_at 3174.1 P
hypothetical protein
11235_at 8375.6 P
Ribosomal protein S14B (rp59B)
11236_at 4471.1 P
Ribosomal protein S22A (S24A) (rp50) (YS22)
11237_at 11435.1 P
Ribosomal protein L39 (L46) (YL40)
11192_at 855.2 A
questionable ORF
11193_at 2081.2 P
protein kinase homolog
11194_at 1577.8 P
putative mannosyltransferase
11195_at 300.8 P
hypothetical protein
11196_at 2929.7 P
hypothetical protein
11197_at 5610.4 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 -73.4 A
questionable ORF
11199_at 1715.6 P
similarity to hypothetical protein YJR030c
11200_at 1034.9 P
essential for assembly of a functional F1-ATPase
11201_at 1125.7 P
Putative homolog of subunit 1 of bovine prefoldin, a chaperone comprised of six subunits
11202_at 6823.6 P
hypothetical protein
11203_i_at 12262.6 P
Ribosomal protein L17B (L20B) (YL17)
11204_s_at 8391.5 P
Ribosomal protein L17B (L20B) (YL17)
11205_i_at 7433.2 P
Ribosomal protein L17B (L20B) (YL17)
11206_f_at 13162.8 P
Ribosomal protein L17B (L20B) (YL17)
11207_at 781.1 P
transcription factor
11208_at 291.7 A
questionable ORF
11209_at 8930.2 P
Cell wall beta-glucan assembly
11210_at 9445.6 P
subunit 3 of replication factor-A

11211_at 5211.5 P
carboxypeptidase yscS
11212_at 7260.8 P
similarity to YBR162c
11213_at 2.7 A
An a-specific gene that is induced to a higher expression level by alpha factor
11214_at 133.1 A
questionable ORF
11170_at 629.6 A
transcription factor containing a SET domain
11171_at 8561.7 P
Farnesyl diphosphate synthetase (FPP synthetase)
11172_at 7292.5 P
Ubiquinol cytochrome-c reductase subunit 8 (11 kDa protein)
11173_at 2931.1 P
Protein kinase homolog, mutant is salt and pH sensitive
11174_at 2946.4 P
putative catalytic subunit of cAMP-dependent protein kinase
11175_at 485.3 P
hypothetical protein
11176_at 471.2 A
weak similarity to dnaJ proteins
11177_at 362.1 A
hypothetical protein
11178_at 670.1 P
member of the Pir1p/Hsp150p/Pir3p family
11179_at 8128.8 P
Heat shock protein, secretory glycoprotein
11180_at 8433.7 P
Protein with homology to Hsp150p and Pir1p, Pir2p, and Pir3p
11181_at 8102.7 P
Factor arrest protein
11182_at 1574.8 P
sensitive to sulfonylurea herbicides on complex media (YPD)
11183_at 1578.0 P
Fructose-2,6-bisphosphatase
11184_at 1616.4 P
Protein involved in vacuolar sorting
11185_at 509.7 P
L-myo-inositol-1-phosphate synthase
11186_at 1176.5 A
questionable ORF
11187_at 10491.6 P
similarity to hypothetical protein YDL123w
11188_at 465.6 P
questionable ORF
11189_at 938.4 P
similarity to hypothetical protein YDR131c
11190_at 7669.1 P
RNA polymerase I subunit, not shared (A34.5)
11191_at 950.2 P
weak similarity to C.elegans hypothetical protein C43G2.4
11147_at 875.6 P
IME2-Dependent Signalling
11148_at 4842.1 P
weak similarity to T.pacificus retinal-binding protein

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11149_at     303.6        P
hypothetical protein
11150_at     9643.0       P
16.5 kDa inner membrane protein required for import of mitochondrial precursor proteins
11151_at     895.8        P
questionable ORF
11152_g_at   2198.2       P
questionable ORF
11153_at     1109.7       P
Serine-threonine protein kinase
11154_at     2245.7       P
fourth-largest subunit of RNA polymerase II
11155_at     2629.0       P
Probable glycosyltransferase of KRE2\/KTR1\/YUR1 family\; located in the Golgi
11156_s_at   11027.1      P
translation initiation factor eIF4A
11157_at     525.2        P
self-glucosylating initiator of glycogen synthesis\; similar to mammalian glycogenin
11158_i_at   3080.7       A
Ribosomal protein S21B (S26B) (YS25)
11159_s_at   10251.7      P
Ribosomal protein S21B (S26B) (YS25)
11160_at     270.6        P
questionable ORF
11161_at     4995.3       P
putative plasma membrane transporter capable of transporting sphingoid long chain bases into cells
11162_at     1378.4       P
mitochondrial carrier protein
11163_at     294.2        P
weak similarity to human phospholipase D
11164_at     1281.3       P
weak similarity to nonepidermal Xenopus keratin, type I
11165_at     10790.5      P
carbamoyl-phophate synthetase, aspartate transcarbamylase, and glutamine amidotransferase
11166_at     1897.9       P
180 kDa high affinity potassium transporter
11167_at     2328.8       P
MAP kinase kinase (MEK), may act as a scaffolding protein for Sho1p, Ste11p, and Hog1p
11168_at     329.0        P
negative transcriptional regulator
11169_at     1192.7       P
Nit2 nitrilase
11124_at     3254.5       P
translational repressor of GCN4
11125_at     2911.6       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     6736.9       P
weak similarity to D.melanogaster troponin T and human nucleolin
11127_at     5317.0       P
weak similarity to dog-fish transition protein S2
11128_at     11049.9      P
D-ribulose-5-Phosphate 3-epimerase
11129_at     342.4        M
questionable ORF
11130_at     85.6         A
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questionable ORF
11131_at 2784.6 P
hypothetical protein
11132_at 8770.6 P
Putative inorganic phosphate transporter
11133_at 3369.2 P
With NCA2, regulates proper expression of subunits 6 (Atp6p) and 8 (Atp8p) of the Fo-F1 ATP synthase
11134_at 4004.0 P
Anti-silencing protein that causes depression of silent loci when overexpressed
11135_at 1564.0 P
similarity to Met30p and N.crassa sulfur controller-2
11136_at 3835.0 P
Component of Chaperonin Containing T-complex subunit seven
11137_at 1238.6 P
GATA zinc finger protein 3 homologous to Dal80 in structure and function
11138_at 6403.3 P
weak similarity to ATPase Drs2p
11139_at 4051.8 P
strong similarity to hypothetical S. pombe protein
11140_at 473.9 P
similarity to hypothetical S. pombe protein
11141_at 505.4 P
Serine\/Threonine protein kinase, positively regulated by IME1
11142_at 50.8 A
similarity to hypothetical protein YKR029c
11143_at 928.5 P
weak similarity to C.elegans hypothetical protein F45G2.c
11144_at 610.8 P
putative regulatory protein
11145_at 2897.0 P
mitochondrial elongation factor G-like protein
11146_at 2281.8 P
gamma-glutamylcysteine synthetase
11102_at 2867.1 P
similarity to hypothetical C. elegans protein C56A3.8
11103_at 1858.7 P
Involved in chitin biosynthesis and\/or its regulation
11104_at 2916.6 P
SIT4 associated protein, MW of 185 kDa
11105_at 9148.8 P
similarity to hypothetical C. elegans protein T15B7.2
11106_at 3840.1 P
ribosomal protein YmL49, mitochondrial
11107_at 1575.2 P
putative 163 kDa protein kinase
11108_at 1905.9 P
similarity to E.hirae NaH-antiporter NapA
11109_at 1636.7 P
outward-rectifier potassium channel
11110_at 1678.9 P
DNA helicase
11111_at 4791.6 P
weak similarity to human G protein-coupled receptor
11112_at 1308.6 P
Part of the DNA polymerase II complex, acts in a checkpoiint pathway during S-phase
11113_at 194.5 A

shows homology to DNA binding domain of Gal4p, has a leucine zipper motif and acidic region\; lexA-Sip4p activates transcription

11114_at 1498.4 P

Ornithine carbamoyltransferase

11115_at 1053.8 P

tRNA ligase

11116_at -15.9 A

questionable ORF

11117_at 278.4 A

70 kD component of the Exocyst complex\; required for exocytosis

11118_at 1451.3 P

similarity to hypothetical protein YKR021w

11119_at 1061.4 P

similarity to hypothetical protein YKR019c

11120_at 4412.1 P

strong similarity to hypothetical protein YKR018c

11121_at 4264.9 P

54.8 kDa actin-related protein

11122_at 9941.6 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 4595.0 P

Similar to plant PR-1 class of pathogen related proteins

11079_at 6420.4 P

Similar to plant PR-1 class of pathogen related proteins

11080_at 462.4 A

hypothetical protein

11081_at 6603.3 P

Establishes Silent omatin\; homolog of TOF2

11082_at 430.3 P

questionable ORF

11083_at 2150.3 P

required for structural maintenance of chromosomes

11084_at 1988.8 P

DnaJ-like protein of the endoplasmic reticulum membrane

11085_at 1720.0 P

hypothetical protein

11086_at 1132.8 P

Acetylglutamate Synthase

11087_at 681.2 P

similarity to AMP deaminases

11088_at 4066.8 P

similarity to C.elegans hypothetical protein

11089_at 4483.2 P

strong similarity to human esterase D

11090_at 992.9 A

questionable ORF

11091_at 1183.1 P

hypothetical protein

11092_at 5514.3 P

weak similarity to DNA-directed DNA polymerase II chain C

11093_at 193.4 A

hypothetical protein

11094_at 5149.7 P

Mitochondrial ribosomal protein MRPL8 (YmL8) (E. coli L17)

11095_at 2435.5 P

similarity to S.pombe SPAC13G6.3 protein
11096_at	741.8	P
82-kDa protein, with putative coiled-coil domain, has carboxy-terminal domain, containing heptad repeats, that binds Nsp1p\; nucleoporin
11097_at	3446.2	P
similarity to kynurenine aminotransferase and glutamine-phenylpyruvate transaminase
11098_at	687.6	P
Homolog of human CLN3
11099_at	282.0	P
strong similarity to hypothetical protein YBR270c
11100_at	362.5	P
probable serine\/threonine kinase
11101_at	1327.2	P
Metalloregulatory protein involved in zinc-responsive transcriptional regulation
11057_at	10486.9	P
similarity to R.fascians hypothetical protein 6
11058_at	3790.0	P
Translocase for the insertion of proteins into the mitochondrial inner membrane.
11059_at	1921.6	P
Vacuolar protein similar to mouse gene H<beta>58
11060_at	14014.3	P
Glyceraldehyde-3-phosphate dehydrogenase 1
11061_g_at	6777.4	A
Glyceraldehyde-3-phosphate dehydrogenase 1
11062_at	763.3	P
hypothetical protein
11063_at	3167.2	P
DEAD-box family helicase required for mRNA export from nucleus
11064_at	710.8	P
hypothetical protein
11065_at	4087.4	P
similarity to hypothetical protein YBR273c
11066_at	568.7	P
Regulator of Ty1 Transposition
11067_at	1169.8	P
similarity to E.coli lipoate-protein ligase A
11068_at	392.1	P
strong similarity to succinate dehydrogenase flavoprotein
11069_at	879.8	P
GTPase-activating protein for Ypt6
11070_at	-1840.6	A
similarity to hypothetical protein YKR015c
11071_at	7058.1	P
Putative microtubule-associated protein (MAP)
11072_at	7701.9	P
Nucleoskeletal protein found in nuclear pores and spindle pole body
11073_at	1838.4	P
similarity to human protein interacting with human nuclearpore protein Nup93
11074_at	49.3	A
strong similarity to hypothetical protein YJL037w
11075_at	1849.4	P
strong similarity to hypothetical protein YJL038c
11076_at	621.3	P
weak similarity to Mvp1p
11077_at	1511.5	P
weak similarity to P.gingivalis PgaA and B.japonicum nitrogen fixation protein

11078_at 10325.9 P
Homologue of mammalian BiP (GPR78) protein\; member of the HSP70 gene family
11034_at 3215.6 P
putative RNA helicase
11035_at 829.8 P
questionable ORF
11036_at 1618.2 P
Geranylgeranyltransferase Type II alpha subunit (PGGTase-II, alpha subunit)
11037_at 1548.8 P
spindle-assembly checkpoint protein
11038_at 1893.6 P
similarity to C.elegans hypothetical protein T05G5.8
11039_at 254.9 A
hypothetical protein
11040_at 905.7 P
hypothetical protein
11041_at 10607.1 P
small subunit of ribonucleotide reductase
11042_at 599.1 P
member of yeast Pol I core factor (CF) also composed of Rrn11p, Rrn6p and TATA-binding protein
11043_at 669.7 P
similar to Aps1p and mammalian small subunit (sigma-2 adaptin) of plasma membrane-associated clathrin assembly complex (AP-2)
11044_at 366.8 P
Nuclear gene encoding mitochondrial protein
11045_at -9.2 A
questionable ORF
11046_at 2661.7 P
weak similarity to S.pombe hypothetical protein SPAC23A1.16
11047_at 4740.5 P
similarity to P.falciparum glutamic acid-rich protein
11048_at 345.3 P
hypothetical protein
11049_g_at 696.5 P
hypothetical protein
11050_at 1773.0 P
questionable ORF
11051_at 1111.8 P
hypothetical protein
11052_at 4252.5 P
weak similarity to hypothetical protein YNL278w and YLR187w
11053_at 156.4 P
questionable ORF
11054_at 7107.6 P
Cytoplasmic chaperonin subunit gamma
11055_at 941.6 P
Checkpoint protein required for cell cycle arrest in response to loss of microtubule function
11056_at 8559.8 P
weak similarity to regulatory protein PHO81
11010_at 4380.6 P
weak similarity to chicken hypothetical protein
11011_at 2853.8 P
weak similarity to C.elegans hypothetical protei ZK792.5
11012_at 1260.5 P
questionable ORF
11013_at 10554.7 P

Component of Chaperonin Containing T-complex subunit eight
11014_at 11.9 A
hypothetical protein
11015_at 2607.9 P
cyclin-related subunit of the kinase complex that phosphorylates the RPO21 CTD (carboxy-terminal domain)\; also called CTDK-I beta subunit
11016_at 1852.5 P
adenylate cyclase
11017_at 2751.0 P
Multicopy suppressor of ypt6 null mutation
11018_at 1248.5 P
hypothetical protein
11019_at 12411.5 P
64-kDa, alpha subunit of oligosaccharyltransferase complex\; homologous to mammalian ribophorin I
11020_i_at 3814.9 P
Subunit of 20S proteasome
11021_f_at 5165.2 P
Subunit of 20S proteasome
11022_at 11212.6 P
Subunit of 20S proteasome
11023_at 8686.7 P
weak similarity to A.thaliana aminoacid permease AAP4
11024_at 3948.0 P
Protein component of the U3 small nucleolar ribonucleoprotein (snoRNP)
11025_at 1410.1 P
hypothetical protein
11026_at 10447.3 P
alpha-agglutinin
11027_at 1284.5 P
beta-adaptin, large subunit of the clathrin-associated protein complex
11028_at 1576.9 P
DNA-directed DNA polymerase delta, 55 KD subunit
11029_at 4168.6 P
Translation initiation factor eIF-2 alpha subunit
11030_at 285.3 P
similarity to S.pombe hypothetical protein
11031_s_at 14239.0 P
glyceraldehyde 3-phosphate dehydrogenase
11032_at 2062.5 P
ATP sulfurylase
11033_at 3483.3 P
Homologue of the SPC12 subunit of mammalian signal peptidase complex. Protein is important for efficient signal peptidase activity.
10988_at 401.4 P
hypothetical protein
10989_at 905.0 P
hypothetical protein
10990_at 2881.9 P
similarity to C.elegans B0491.1 protein
10991_at 5508.8 P
strong similarity to S.pombe hypothetical protein SPBC16C6.05
10992_at 2931.2 P
strong similarity to Sng1p
10993_at 11517.2 P
dihydroxyacid dehydratase
10994_at 10914.8 P

Peptidyl-prolyl cis\/trans isomerase (PPIase)
10995_at 1167.2 P
questionable ORF
10996_at 1853.3 P
peroxisomal acyl-CoA thioesterase
10997_at 179.7 P
questionable ORF
10998_at 617.9 P
meiotic recombination protein
10999_at 75.4 A
meiotic recombination protein
11000_at 1000.5 P
Sm-like protein
11001_at -47.3 A
hypothetical protein
11002_at 5875.9 P
weak similarity to C.elegans Z49131_E ZC373.5 protein
11003_at 8282.2 P
3-hydroxyanthranilic acid dioxygenase
11004_at 751.0 P
similarity to hypothetical protein YJL181w
11005_at 2418.6 P
Component of a complex guanine nucleotide exchange activity for the ADP-ribosylation factor ARF
11006_at 968.0 P a
cyclophilin related to the mammalian CyP-40\; physically interacts with RPD3 gene product
11007_at 900.8 P
similarity to Drosophila DmX gene
11008_at 1231.7 P
Required for assembly of active cytochrome c oxidase
11009_at 333.9 P
DNA-dependent ATPase, homologous to human Cockayne syndrome B gene ERCC6, that is a putative helicase
10965_at 779.5 P
similarity to human E6-associated protein
10966_at 116.8 A
questionable ORF
10967_at 88.4 A
questionable ORF
10968_at 560.7 P
hypothetical protein
10969_at 1262.7 P
putative transport protein involved in intracellular iron metabolism
10970_at 3346.1 P
hypothetical protein
10971_at 4432.4 P
Protein in nuclear pore complex\; may function in nuclear envelope integrity\; may also be involved in tRNA biogenesis
10972_at 204.9 A
third (55 kDa) subunit of DNA polymerase delta
10973_at 9875.7 P
weak similarity to putative transport protein YKR103w
10974_at 3575.3 P
Mitochondrial matrix protein involved in protein import\; subunit of SceI endonuclease
10975_at 2158.7 P
weak similarity to Xenopus vimentin 4
10976_at 3617.1 P

anaerobically expressed form of translation initiation factor eIF-5A
10977_at 12542.6 P
iso-1-cytochrome c
10978_at 1834.8 P
Associated with ferric reductase
10979_at 464.2 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 1917.7 P
osmotic growth protein
10981_at 4183.6 P
Nucleotide excision repair protein involved in G(sub)2 repair of inactive genes
10982_at 286.3 P
hypothetical protein
10983_at 1588.8 P
similarity to hypothetical protein YML047c
10984_at 623.2 P
Protein required for growth at high temperature
10985_at 1389.1 P
hypothetical protein
10986_at 1499.0 P
thymidylate kinase
10987_at 5437.7 P
Clathrin-associated protein, small subunit
10943_at 2251.4 P
Putative serine\/threonine protein kinase that enhances spermine uptake
10944_at 83.7 A
basic helix-loop-helix protein
10945_at 23.3 A
similarity to Mnn4p
10946_at 1181.7 P
52-kDa amidase specific for N-terminal asparagine and glutamine
10947_at 4652.0 P
A12.2 subunit of RNA polymerase I
10948_at 11003.2 P
subunit of chaperonin subunit epsilon
10949_at 7574.1 P
actin-related gene
10950_at 2086.6 P
phosphatidylinositol kinase homolog
10951_at 1647.0 P
Essential protein of unknown function
10952_at 2328.2 P
Subunit 2 of Replication Factor C\; homologous to human RFC 37 kDa subunit
10953_at 4344.3 P
controls 6-N-hydroxylaminopurine sensitivity and mutagenesis
10954_at 12346.8 P
similarity to C.elegans hypothetical protein C14A4.1
10955_at 8.6 A
questionable ORF
10956_at 5603.4 P
strong similarity to C.elegans hypothetical protein and similarity to YLR243w
10957_at 7340.4 P

Methylene-fatty-acyl-phospholipid synthase (unsaturated phospholipid N-methyltransferase)
10958_at 5499.8 P
Protein interacts with Gsp1p
10959_at 2408.5 P
putative mannosyltransferase
10960_at 4184.9 P
Component of 10 nm filaments of mother-bud neck
10961_at 10032.2 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 4476.9 P
similarity to mammalian indoleamine 2,3-dioxygenase
10963_at 4389.4 P
questionable ORF
10964_at 4550.8 P
hypothetical protein
10920_at 128.5 P
questionable ORF
10921_at 525.7 P
hypothetical protein
10922_at 610.7 P
hypothetical protein
10923_at 1503.3 P
weak similarity to S.pombe hypothetical protein SPAC1B3.08
10924_at 12046.7 P
hypothetical protein
10925_at 1708.2 P
gamma subunit of G protein coupled to mating factor receptors
10926_at 917.0 P
questionable ORF
10927_at 3308.4 P
weak similarity to S.pombe hypothetical protein SPBC14C8.18c
10928_at 1026.0 P
hypothetical protein
10929_at 1508.9 P F
box protein with several leucine rich repeats
10930_at 3746.6 P
Benomyl dependent tubulin mutant
10931_at 1439.8 P
Component of a pre-mRNA polyadenylation factor that interacts with poly(A) polymerase
10932_at 536.5 P
meiotic gene expression\; meiosis inducing protein
10933_at 6772.6 P
Ribosomal protein L43B
10934_at 192.0 A
protein related to mitochondrial carriers
10935_at 2143.5 P
similarity to Corynebacterium 2,5-diketo-D-gluconic acid reductase and aldehyde reductases
10936_at 553.7 P
weak similarity to Caj1p
10937_at 808.4 P
weak similarity to Bacillus licheniformis esterase
10938_at 480.8 P
ubiquitin hydrolase
10939_at 2031.7 P

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weak similarity to Bud3p
10940_at	2201.8		P
weak similarity to superoxide dismutases
10941_at	1284.7		P
hypothetical protein
10942_at	7677.9		P
CTP synthase
10897_at	7002.6		P
Cu, Zn superoxide dismutase
10898_at	10310.2		P
strong similarity to human adenosine kinase
10899_at	525.4		P
ExtraCellular Mutant
10900_at	1529.4		P
weak similarity to acylglycerol lipase
10901_at	389.3		P
similarity to hypothetical protein YIL014c-a
10902_at	5072.6		P
carbamyl phosphate synthetase
10903_at	740.3		P
similarity to human myotubularin
10904_at	1689.7		P
weak similarity to E.coli colanic acid biosynthesis positive regulator RcsB
10905_at	900.3		P
involved in nuclear function
10906_at	5973.3		P
similarity to bacterial, chloroplast and mitochondrial ribosomal protein S7
10907_at	945.6		P
questionable ORF
10908_at	1032.1		P
similarity to hypothetical protein YBL043w
10909_at	4973.0		P
similarity to hypothetical protein YPR114w
10910_at	7170.9		P
zinc metallo-protease that catalyzes the first step of N-terminal processing of the yeast a-factor precursor
10911_at	3685.7		P
weak similarity to Helicobacter pylori UreD protein
10912_at	172.8		P
similarity to human retinoblastoma binding protein 2
10913_at	-353.5		A
hypothetical protein
10914_at	8156.7		P
F(1)F(0)-ATPase complex beta subunit, mitochondrial
10915_at	623.1		P
CCR4 associated factor
10916_at	10008.7		P
Ribosomal protein S5 (S2) (rp14) (YS8)
10917_at	2323.2		P
weak similarity to Staphylococcus multidrug resistance protein
10918_at	2200.9		P
similarity to human KIAA0171 protein
10919_at	2116.5		P
similarity to human  prostate-specific membrane antigen and transferrin receptor protein
10875_at	3164.1		P
similarity to regulatory protein Ard1p
10876_at	-283.3		A
```

questionable ORF
10877_at 826.0 P
weak similarity to hypothetical protein YNL024c
10878_at 2387.5 P
similarity to O-succinylhomoserine (thiol)-lyase
10879_at 625.7 P
specific alpha-mannosidase
10880_at 1978.1 P
Putative Upf1p interacting protein
10881_at 10355.0 P
strong similarity to hypothetical protein YDR399w
10882_at 448.9 P
similarity to paramyosin, myosin
10883_at 313.0 P
Required for maintenance of chromosomes and minichromosomes
10884_at 1409.2 P
weak similarity to human 3 ,5 -cyclic-GMP phosphodiesterase
10885_at 7763.2 P
ExtraCellular Mutant
10886_at 987.8 P
similarity to C.elegans hypothetical protein T08A11.1
10887_at 11280.2 P
Homoserine dehydrogenase (L-homoserine:NADP oxidoreductase)
10888_at 1669.4 P
involved in cell-cycle regulation of histone transcription
10889_at 933.9 P
hypothetical protein
10890_at 1395.4 P
similarity to thiamin pyrophosphokinase
10891_at 8457.6 P
dolichyl phosphate-D-mannose:protein O-D-mannosyltransferase
10892_at 2124.3 P
involved in mitochondrial genome maintenance
10893_s_at 11117.4 P
Ribosomal protein S4A (YS6) (rp5) (S7A)
10894_at 281.1 P
questionable ORF
10895_at 1253.3 P
heat shock transcription factor homolog
10896_at 7214.8 P
Branched-Chain Amino Acid Transaminase
10851_at 885.1 P
similarity to 2-nitropropane dioxygenase
10852_at 108.1 A
Protein induced during anaerobic growth
10853_at 1281.4 P
similarity to mucin proteins, YKL224c, Sta1p
10854_at 1508.1 P
allantoate permease
10855_at 301.5 P
Endo-polygalacturonase
10856_at 371.1 P
hypothetical protein
10857_at 1187.5 P
Hypothetical aryl-alcohol dehydrogenase (AAD)
10858_s_at 1572.5 P

Thiamine biosynthetic enzyme

10859_at	95.0	A	hypothetical protein
10860_s_at	448.5	P	hexose transporter
10861_s_at	2586.1	P	sorbitol-induced sorbitol dehydrogenase
10862_s_at	8.7	A	strong similarity to Mal31p
10863_i_at	844.6	P	identified by SAGE
10864_r_at	1590.2	P	identified by SAGE
10865_at	1302.8	P	C-terminal part of YJR030c
10866_at	2377.2	P	similarity to human DDP gene, hypothetical protein of S.pombe (YA94_SCHPO) and Mrs11p (YHR005c-a)
10867_s_at	2170.2	P	Co-assembles with Bud3p at bud sites
10868_at	6166.3	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	3557.7	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	50.9	A	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	1595.1	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	4715.3	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	413.9	P	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	6139.6	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	370.9	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	688.0	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	218.6	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	969.5	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	342.4	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 906.2 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 177.5 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 1540.7 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 3718.7 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 290.9 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 12039.8 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 318.9 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 -4.2 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 913.8 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 4081.4 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 35.5 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 205.9 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 284.5 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 648.5 A
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 2620.6 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 657.1 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 603.2 P
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 249.2 P
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 -11.3 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 711.5 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 113.7 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 275.7 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 180.2 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 463.8 P
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 496.8 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 -107.3 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 2220.6 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 3348.7 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 -5.8 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 911.8 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 858.3 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 956.6 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 2488.9 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
10821_g_at 65.2 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 -4.4 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 1037.7 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 418.8 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 425.8 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 16.7 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 548.6 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 3866.3 P

small nuclear RNA128

10783_at 79.6 A

small nuclear RNA190

10784_at 2058.6 P

small nuclear RNA37

10785_at 876.3 P

snRNA

10786_i_at -132.0 A

Centromere

10787_at 2470.3 P

small nuclear RNA3

10788_at 48.3 A

ARS121 Found forward in NC_001142 between 683650 and 683699 with 100% identity.

10789_f_at 1262.4 P

strong similarity to members of the Srp1p/Tip1p family

10790_at 343.0 P

weak similarity to transcription factors, similarity to finger proteins YOR162c, YOR172w and YLR266c

10791_at 115.8 A

weak similarity to human X-linked PEST-containing transporter

10792_at 251.1 P

Ferric reductase, similar to Fre1p

10793_at 2545.0 P

Protein with similarity to subtelomerically-encoded proteins such as Cos5p, Ybr302p, Cos3p, Cos1p, Cos4p, Cos8p, Cos6p, Cos9p

10794_at 1874.7 P

threonine dehydratase

10795_at -90.4 A

carboxylic acid transporter protein homolog

10796_at 12217.6 P

dihydroorotate dehydrogenase

10797_at 3509.5 P

similarity to P. aeruginosa hyuA and hyuB

10798_at 5111.0 P

weak similarity to mouse transcriptional coactivator ALY

10799_at 4953.9 P

phospholipase A2-activating protein

10800_at 9339.0 P

integral membrane protein localizing to the ER and Golgi

10801_at 3918.5 P

anthranilate synthase Component II and indole-3-phosphate (multifunctional enzyme)

10802_at 8316.4 P

ubiquitin activating enzyme, similar to Uba2p

10803_at 385.4 P

ABC transporter, glycoprotein, component of a-factor secretory pathway

10804_at 1107.9 P

Subunit of complex involved in processing of the 3 end of cytochrome b pre-mRNA

10805_at 3951.9 P

hypothetical protein
10760_at 1521.9 P
hypothetical protein
10761_at 2188.0 P
nuclear protein LOS1
10762_at 5243.3 P
probable purine nucleotide-binding protein
10763_at 1880.5 P
phosphatidylinositol kinase homolg
10764_at 335.9 P
questionable ORF
10765_at 2379.7 P
member of the AAA-protein family
10766_at 8157.2 P
v-SNARE
10767_at 3796.4 P
similarity to rabbit histidine-rich calcium-binding protein
10768_at 875.7 P
mitochondrial threonine-tRNA synthetase
10769_at 1892.0 P
Interacts with and may be a positive regulator of GLC7 which encodes type1 protein phosphatase
10770_at 9756.8 P
acyl carrier protein
10771_at 7391.3 P
diphthamide synthesis protein
10772_at 1645.7 P
Type 2B protein phosphatase\; regulatory B subunit of calcineurin
10773_at 3906.3 P
Type 2B protein phosphatase\; regulatory B subunit of calcineurin
10774_at 925.4 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 271.0 P
peroxisomal ABC transporter 2
10776_at 467.6 P
strong similarity to hypothetical protein YLR413w
10777_at 2789.8 P
mRNA transport regulator
10778_at 1772.7 P
probable purine nucleotide-binding protein
10779_at 5899.9 P
Ornithine decarboxylase
10780_at 1018.4 P
hypothetical protein
10781_at 8973.8 P
pentafunctional enzyme consisting of the following domains : acetyl transferase, enoyl reductase, dehydratase and malonyl\/palmityl transferase
10737_at 12337.9 P
ribose-phosphate pyrophosphokinase
10738_i_at 73.8 A
Ribosomal protein L17A (L20A) (YL17)
10739_f_at 12963.4 P
Ribosomal protein L17A (L20A) (YL17)
10740_at 4009.3 P
kinesin-like protein

10741_at	8273.5	P	a factor recptor
10742_at	604.3	A	questionable ORF
10743_at	2477.4	P	hypothetical protein
10744_at	6536.6	P	weak similarity to E.coli hypothetical protein
10745_at	1450.3	P	probable transport protein
10746_at	2381.1	P	U5 snRNP-specific protein related to EF-2
10747_at	6249.8	P	Nucleolar protein
10748_at	715.7	P	probable serine\/threonine-specific protein kinase (EC 2.7.1.-)
10749_at	2029.0	P	mitochondrial ribosomal protein L14
10750_at	611.4	P	questionable ORF
10751_at	1119.0	P	probable serine\/threonine-specific protein kinase (EC 2.7.1.-)
10752_at	3789.2	P	16 kDa mitochondrial ribosomal large subunit protein
10753_at	1012.2	P	cAMP-dependent protein kinase catalytic subunit
10754_at	6384.1	P	Morphogenesis Checkpoint Dependent
10755_at	11366.9	P	Protein containing tandem internal repeats
10756_at	1939.2	P	Protein containing tandem internal repeats
10757_at	218.4	P	hypothetical protein
10758_at	412.9	P	probable serine\/threonine-specific protein kinase (EC 2.7.1.-)
10759_at	8994.8	P	similarity to hypothetical S. pombe protein
10714_at	1063.9	P	hypothetical protein
10715_at	2478.9	P	hypothetical protein
10716_at	6123.0	P	aminopeptidase yscII
10717_at	11448.3	P	40S ribosomal protein S27A (rp61) (YS20)
10718_at	555.8	P	hypothetical protein
10719_at	1365.5	P	signal recognition particle receptor, beta chain
10720_at	191.0	P	questionable ORF
10721_at	10603.1	P	Phosphoglycerate mutase
10722_at	2178.3	P	similarity to C.elegans hypothetical protein R107.2

10723_at	4214.4	P	NADH-cytochrome b5 reductase
10724_at	712.7	P	debranching enzyme
10725_at	3266.4	P	flavoprotein subunit of succinate dehydrogenase
10726_at	402.9	A	questionable ORF
10727_at	8735.8	P	strong similarity to S.pombe hypothetical protein C3H1.09C
10728_at	11183.8	P	putative ATPase, 26S protease subunit component
10729_at	2103.2	P	Subunit of RNA polymerase III
10730_at	3058.6	P	low temperature viability protein
10731_at	6401.7	P	mitochondrial ribosomal protein
10732_at	7842.4	P	succinate dehydrogenase cytochrome b
10733_at	2379.5	P	triglyceride lipase-cholesterol esterase
10734_at	1389.4	P	alpha subunit of the kinase which phosphorylates the RNA polymerase largest subunit CTD (carboxyl-terminal domain)
10735_at	2081.4	P	15.5 kDa mitochondrial ribosomal protein YmL31
10736_at	1016.5	P	hypothetical protein
10692_at	961.9	P	questionable ORF
10693_at	2801.6	P	Beta-adaptin, large subunit of the clathrin-associated protein (AP-1) complex
10694_at	525.9	P	probable neutral zinc metalloproteinase
10695_at	354.7	P	probable purine nucleotide-binding protein
10696_at	1503.2	P	probable folyl-polyglutamate synthetase
10697_at	829.6	A	questionable ORF
10698_at	1391.9	P	Required for mother cell-specific HO expression
10699_at	1022.3	P	myosin I
10700_at	8047.7	P	Phospo-mutase homolog
10701_at	5843.4	P	phosphoglucomutase, minor isoform
10702_at	4183.7	P	76.5 kDa Serine\/threonine protein kinase with similarity to protein kinase C, is 90\% identical to Ypk2p
10703_at	2153.0	P	DNA-independent RNA Polymerase I transcription factor
10704_at	530.9	A	suppressor of SHR3\; confers leflunomide resistance when overexpressed
10705_g_at	-24.8	A	

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suppressor of SHR3\; confers leflunomide resistance when overexpressed
10706_at     915.9        P
questionable ORF
10707_at     5745.9       P
component of signal recognition particle
10708_at     1066.0       P
strong similarity to YMR102c
10709_at     10316.8      P
similarity to mitochondrial uncoupling proteins (MCF)
10710_at     2052.6       P
25.2 kDa protein involved in assembly of vacuolar H(+) ATPase
10711_at     213.2        P
questionable ORF
10712_at     9669.8       P
Hsp90 (Ninety) Associated Co-chaperone
10713_at     2898.3       P
probable serine\/threonine-specific protein kinase (EC 2.7.1.-)
10669_at     1331.0       A
questionable ORF
10670_at     3184.2       P
major apurinic\/apyrimidinic endonuclease\/3 -repair diesterase
10671_at     2995.0       P
42 kDa 5  to 3  exonuclease required for Okazaki fragment processing
10672_at     2678.8       P
transcriptional activator and ARS1 binding protein
10673_at     613.9        P
questionable ORF
10674_at     6418.2       P
Protein involved in resistance to K. lactis killer toxin
10675_at     4602.5       P
transcriptional activator protein of CYC1 (component of HAP2\/HAP3 heteromer)
10676_at     40.8         A
DNA replication and checkpoint protein 1
10677_at     -22.2        A
weak similarity to S.antibioticus probable oxidoreductase
10678_at     2708.6       P
aspartate aminotransferase, mitochondrial
10679_at     1143.0       P
similarity to YMR086w
10680_at     7948.7       P
Glutamine_fructose-6-phosphate amidotransferase (glucoseamine-6-phosphate synthase)
10681_at     3453.0       P
vacuolar aminopeptidase ysc1
10682_at     -253.8       A
hypothetical protein
10683_at     756.6        P
Putative protein kinase homologous to S. pombe cdr1\/nim1
10684_at     4047.1       P
similarity to C.elegans hypothetical protein
10685_at     843.3        P
similarity to C.elegans hypothetical proteins C18G6.06 and C16C10.2
10686_at     2966.3       P
hypothetical protein
10687_at     -175.4       A
hypothetical protein
10688_at     8348.2       P
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cell wall mannoprotein
10689_at 3480.1 P
cell wall mannoprotein
10690_at 430.0 P
similarity to C.elegans hypothetical proteins
10691_at 5963.1 P
weak similarity to E.coli hypothetical protein
10646_at 227.0 A
MBR1 protein precursor
10647_at 630.7 P
GTPase-activating protein (GAP) for Rsr1p\/Bud1p
10648_at 1044.1 P
strong similarity to Sec14p
10649_at 795.8 P
hypothetical protein
10650_at 377.6 P
Centromere protein required for normal chromosome segregation and spindle integrity
10651_at 1016.4 P
similarity to C.tropicalis hal3 protein, to C-term. of Sis2p and to hypothetical protein YOR054c
10652_at 2918.5 P
cytochrome c1 heme lyase
10653_at 704.1 P
hypothetical protein
10654_at 9795.6 P
mitochondrial malate dehydrogenase
10655_at 5089.1 P
strong similarity to S.pombe hypothetical protein SPAC29B12
10656_at 6400.5 P
weak similarity to C.elegans hypothetical protein
10657_at 435.0 P
questionable ORF
10658_at 8637.3 P
Translation elongation factor EF-1gamma
10659_at 11983.8 P
Translation elongation factor EF-1gamma
10660_at 8571.1 P
Vacuolar H-ATPas hydrophilic subunit C of V1 sector
10661_at 1349.0 P
kinesin heavy chain homolog, but is not believed to act as a kinesin, colocalizes with Myo2p
10662_at 2567.5 P
probable ATP-dependent RNA helicase
10663_at 7576.3 P
hypothetical protein
10664_at 647.1 P
questionable ORF
10665_g_at 977.7 P
questionable ORF
10666_at 1093.9 P
hypothetical protein
10667_at 1675.6 P
involved in early pre-mRNA splicing
10668_at 1834.4 P
novel member of the Hsp70 family of molecular chaperones that localizes to the lumen of the endoplasmic reticulum:
10624_at 416.8 P
Binds Sin3p in two-hybrid assay

10625_at 3105.1 P
weak similarity to A.parasiticus nor-1 protein
10626_at 392.4 P
similarity to B.subtilis transcriptional regulatory protein
10627_at 5410.9 P
strong similarity to hypothetical E.coli protein b1832
10628_at 4326.1 P
Nuclear pore complex protein homologous to Nup116p
10629_at 7576.5 P
Nucleoside diphosphate kinase
10630_at 4013.7 P
hypothetical protein
10631_at 8428.3 P
Yeast endoplasmic reticulum 25 kDa transmembrane protein
10632_at 3674.4 P
overexpression overcomes manganese toxicity
10633_at 2460.7 P
weak similarity to mammalian microtubule-associated protein MAP 1B
10634_at 2783.7 P
zinc finger protein
10635_at 623.1 P
hypothetical protein
10636_at 8956.9 P
aldolase
10637_at 2653.8 P
similarity to C.elegans hypothetical protein
10638_at 3727.1 P
Transcription factor IIA, small chain
10639_at 1435.2 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 9824.1 P
strong similarity to human IgE-dependent histamine-releasing factor
10641_at 705.5 P
probable acetoacetyl-CoA reductase
10642_at 10722.8 P
similarity to glutenin, high molecular weight chain proteins and Snf5p
10643_at 8062.3 P
similarity to C.elegans hypothetical protein T09A5.7 (12.5 kD)
10644_at 954.9 P
questionable ORF
10645_at 1411.8 P
hypothetical protein
10601_at 2760.3 P
hypothetical protein
10602_at 408.6 P
similarity to YMR031c
10603_at 760.5 P
high similarity to histone H3 and to human centromere protein CENP-A
10604_at 540.5 P
protein kinase
10605_at 1778.8 P
hypothetical protein
10606_at 6892.1 P
strong similarity to YMR238w
10607_at 1500.8 P

p58 polypeptide of DNA primase
10608_at 4462.4 P
hypothetical protein
10609_at 4497.6 P
putative transcription factor
10610_at 1502.9 P
component of the spindle pole body
10611_at 1835.3 P
endosomal Vps protein complex subunit
10612_at 2342.5 P
NifU-like protein B
10613_at 6670.9 P
Putative membrane protein
10614_at 3015.4 P
transcriptional repressor and activator
10615_at 358.2 A
weak similarity to C.elegans ubc-2 protein
10616_at -38.6 A
questionable ORF
10617_at 10820.9 P
Uridinephosphoglucose pyrophosphorylase
10618_at 2840.2 P
weak similarity to YOL013c
10619_at 1325.9 P
hypothetical protein
10620_at 7342.0 P
intrastrand crosslink recognition protein
10621_at 667.4 A
hypothetical protein
10622_at 84.5 A
questionable ORF
10623_at 8274.5 P
mitochondrial malic enzyme
10579_at 4779.8 P
Large subunit of transcription factor tfIIE
10580_at 2431.2 P
similarity to E.coli molybdopterin-converting factor chlN
10581_at 1629.3 P
strong similarity to glutathione peroxidase
10582_at 2972.7 P
76-kDa subunit of Pab1p-dependent poly(A) ribonuclease (PAN)
10583_at 10318.5 P
uridine-monophosphate kinase (uridylate kinase)
10584_at 1181.5 P
weak similarity to human cylicin II
10585_at 1155.1 P
putative metal-binding nucleic acid-binding protein, interacts with Cdc23p and Cdc27p to catalyze the conjugation of ubiquitin to cyclin B
10586_at 3227.4 P
contains four beta-transducin repeats
10587_at 1755.9 P
suppressor protein
10588_at 3074.5 P
CAAX farnesyltransferase alpha subunit
10589_at 2486.2 P
similarity to C.elegans hypothetical protein

10590_at 1084.5 P
DNA helicase A
10591_at 5664.0 P
ATP synthase d subunit
10592_at 1113.5 P
zinc-finger transcription factor of the Zn(2)-Cys(6) binuclear cluster domain type
10593_at 3553.3 P
hypothetical protein
10594_at 5146.0 P
Arp Complex Subunit
10595_at 1415.3 P
Splicing component that associates with the yeast U1 small nuclear ribonucleoprotein particle
10596_at 1121.7 P
cruciform cutting endonuclease
10597_at 3095.9 P
Ubiquitin Fusion Degradation
10598_at 9814.2 P
mRNA turnover 4
10599_at 7092.2 P
strong similarity to Lag1p
10600_at 4684.0 P
alpha subunit of capping protein
10555_at 1890.5 P
required for transport of proteins between an early and a later golgi compartment. possible NSF attachment protein receptor (V-SNARE)
10556_i_at 18865.1 P
Ribosomal protein L14A
10557_f_at 10023.0 P
Ribosomal protein L14A
10558_s_at 11416.7 P
Ribosomal protein L14A
10559_at 2373.9 P
weak similarity to YKR029c and D.melanogaster transcription elongation factor DmS-II
10560_at 8716.5 P
aureobasidin-resistance protein
10561_at 3573.3 P
Mitochondrial ribosomal protein MRP17
10562_at 2975.7 P
similarity to hypothetical protein YKL041w
10563_at 5011.7 P
adenylylsulfate kinase
10564_at 3529.1 P
putative GTP-binding protein\; similar to mammalian Mx proteins
10565_at 2406.9 P
poly(A) polymerase
10566_at 2602.0 P
similarity to Kes1p, Hes1p and Osh1p
10567_at 1411.9 P
ExtraCellular Mutant
10568_at 592.3 P
hypothetical protein
10569_at 4228.1 P
mitochondrial ribosomal protein YmL13
10570_at 1805.7 P
weak similarity to Streptococcus protein M5 precursor
10571_at 1375.5 P

Member of RSC complex.
10572_at 1000.9 P
peroxisomal multifunctional beta-oxidation protein
10573_at 201.7 A
topoisomerase I interacting factor 2
10574_at 1703.4 P
hypothetical protein
10575_at 31.4 A
questionable ORF
10576_at 13913.1 P
Similar to plant PR-1 class of pathogen related proteins
10577_at 2169.6 P
probable purine nucleotide-binding protein
10578_at -14.2 A
similarity to hypothetical protein YJL043w
10533_at 1786.7 P
weak similarity to mysoin heavy chain proteins
10534_at 105.3 A
similarity to human hypothetical KIAA0161 protein
10535_at 5475.9 P
strong similarity to hypothetical protein YJL082w
10536_at 298.8 P
Increased rDNA silencing
10537_at 116.1 A
hypothetical protein
10538_at 775.5 P
strong similarity to hypothetical protein YJL084c
10539_at 915.0 P
hypothetical protein
10540_at 351.3 P
similarity to S.pombe hypothetical protein SPAC23C4
10541_at 2971.1 P
putative RNA helicase
10542_at 1322.1 P
hypothetical protein
10543_at 5348.0 P
translation initiation factor eIF2B, 34 KD, alpha subunit\; negative regulator of GCD12, thereby serving indirectly as a positive regulator of GCN4
10544_at 1414.1 P
strong similarity to Chs6p
10545_at 3193.1 P
Type 2A-related protein phosphatase
10546_at 944.5 P
similarity to YJL105w and Lentinula MFBA protein
10547_at 4309.9 P
weak similarity to NADH dehydrogenases
10548_at 2390.9 P
Phospholipase D
10549_at -36.8 A
hypothetical protein
10550_at 208.6 A
questionable ORF
10551_at -45.1 A
negative regulator of multiple nitrogen catabolic genes
10552_at 4163.5 P
RAD52 Inhibitor (Fifty Two Inhibitor)

10553_at 899.4 P
CCR4 associated factor
10554_at 854.2 P
component of spindle pole
10510_at 1998.0 P
probable calcium-binding protein
10511_at 548.3 P
general amino acid permease
10512_at 997.0 P
questionable ORF
10513_at 19.5 A
hypothetical protein
10514_at 10735.5 P
YOUTH, involved in determining yeast longevity
10515_at 9606.2 P
weak similarity to phosphoglycerate mutase
10516_at 819.5 P
hypothetical protein
10517_at 891.2 P
hypothetical protein
10518_at 13071.7 P
hypothetical protein
10519_at 1738.4 P
questionable ORF
10520_at 9837.0 P
nucleosome assembly protein I
10521_at 1966.9 P
hypothetical protein
10522_at 2001.4 P
membrane protein\; low affinity potassium transport
10523_at 764.8 P
similarity to C.elegans hypothetical protein
10524_at 1346.0 P
mitochondrial carrier protein, highly homologous to Mrs3p
10525_at 704.2 P
DHS-1-P phosphatase
10526_at 3267.6 P
heavy chain of cytoplasmic dynein
10527_at 1187.3 P
ras homolog--GTP binding protein
10528_at 2633.8 P
endo-exonuclease yNucR
10529_i_at 1035.4 A
Ribosomal protein S21A (S26A) (YS25)
10530_at 149.4 P
self-glucosylating initiator of glycogen synthesis\; similar to mammalian glycogenin
10531_at 2052.1 P
hypothetical protein
10532_at 1620.9 P
putative mannosyltransferase\; type 2 membrane protein
10487_at 1233.8 P
Small subunit of TFIIE transcription factor
10488_at 1043.9 P
May regulate expression of genes involved in bud formation and morphogenesis
10489_at 709.3 P
weak similarity to transcription factors

10490_at	7123.5	P	hypothetical protein
10491_at	6497.4	P	Cytochrome-c peroxidase
10492_at	2852.0	P	strong similarity to Sct1p
10493_at	7505.1	P	Hydrophilic protein that acts in conjunction with SNARE proteins in targeting and fusion of ER to Golgi transport vesicles
10494_at	2546.2	P	siroheme synthase
10495_at	2110.9	P	strong similarity to S. pombe phosphatidyl synthase
10496_at	3120.4	P	weak similarity to C.elegans hypothetical protein
10497_at	3937.7	P	sit4 suppressor
10498_at	611.4	P	hypothetical protein
10499_at	4976.9	P	strong similarity to hypothetical S. pombe protein
10500_at	1100.6	P	weak similarity to negative regulator Reg1p
10501_at	1155.6	P	ExtraCellular Mutant
10502_at	890.3	P	hypothetical protein
10503_at	386.0	P	similarity to Vps5p
10504_at	1371.0	P	similarity to S.pombe hypothetical protein SPAC1D4.10
10505_at	6258.6	P	NAD-dependent 5,10-methylenetetrahydrafolate dehydrogenase
10506_at	8909.2	P	hypothetical protein
10507_at	3471.2	P	Nuclear pore complex protein involved in poly(A)+ RNA transport, nuclear pore distribution, and possibly in the biogenesis of functional tRNA
10508_at	327.1	P	weak similarity to S.japonicum paramyosin
10509_at	3044.6	P	Protein related to translation elongation factor EF-1alpha and to Suf12p\/Sup2p\/Gst1p\/Sup35p
10464_at	2474.4	P	22.3 kDa mitochondrial ribosomal large subunit protein YmL20\; homologous to L17 of E. coli
10465_at	1188.0	P	putative ATP-binding protein
10466_at	2459.7	P	similarity to hypothetical Myxococcus xanthus protein
10467_at	4195.4	P	weak similarity to b.subtilis spore germination protein II
10468_at	1910.5	P	strong similarity to YOR081c
10469_at	1715.8	P	similarity to chicken Lim protein kinase and Islet proteins
10470_at	4388.6	P	Suppressor of rad53 lethality

10471_at 10790.2 P
nucleolar protein that is immunologically and structurally related to rat Nopp140, a nonribosomal protein of the nucleolus and coiled bodies.
10472_at 9315.6 P
Peptide transporter
10473_i_at 15952.8 P
Ribosomal protein L40B
10474_s_at 8972.7 P
Ribosomal protein L40B
10475_at 1623.0 P
myosin-like protein
10476_at 2468.2 P
similarity to mitochondrial aldehyde dehydrogenase Ald1p
10477_g_at 364.4 P
similarity to mitochondrial aldehyde dehydrogenase Ald1p
10478_at 579.2 P
phosphoenolpyruvate carboxylkinase
10479_at 1264.0 P
Ubiquitin-specific protease
10480_at 632.2 P
Transcription factor regulating basal and induced activity of histidine and adenine biosynthesis genes
10481_at 2394.0 P
cause growth inhibition when overexpressed
10482_at 381.6 P
repressor of silent mating loci
10483_at 437.0 P
Protein with similarity to flocculation protein Flo1p
10484_at 257.7 P
similarity to multidrug resistance proteins
10485_at 377.0 P
similarity to multidrug resistance proteins
10486_s_at -101.7 A
strong similarity to Sge1p and hypothetical protein YCL069w
10442_s_at 1067.8 P
regulates the mannosylphosphorylation
10443_at 158.0 P
hypothetical protein identified by SAGE
10444_at 762.5 A
hypothetical protein
10445_s_at 4828.5 P
regulates the mannosylphosphorylation
10446_s_at 1706.4 P
Protein of unknown function
10447_s_at 3192.6 P
probable serine\/threonine-specific protein kinase (EC 2.7.1.-)
10448_s_at 3581.3 P
strong similarity to holacid-halidohydrolase
10449_at -86.3 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 176.0 P
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 149.5 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 822.0 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 114.2 A
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 91.0 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 371.5 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 6550.8 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 193.7 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 775.7 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 1040.3 A
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 794.6 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 193.0 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 3397.5 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 118.6 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 1375.2 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 1755.5 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 2041.4 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 715.4 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 188.7 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 -371.6 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 3523.0 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	332.2	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	1415.3	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	-43.6	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	647.4	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	335.0	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	-86.8	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	762.8	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	247.8	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	2618.2	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	1609.4	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	-145.1	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	1354.7	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	303.5	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	1172.2	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	819.2	A
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	181.7	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	268.4	P
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	-135.1	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	-14.6	A

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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	32.0		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	-12.3		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	239.3		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	563.3		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	26.1		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	580.3		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	342.3		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	1592.6		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	242.3		P
snRNA
10408_at	1498.5		P
snRNA
10409_at	2779.3		P
snRNA
10410_at	528.0		P
snRNA
10411_f_at	736.0		P
Growth INhibitory protein
10412_f_at	1707.6		P
strong similarity to members of the Srp1/Tip1p family
10413_at	791.6		P
transacetylase
10414_at	221.5		P
weak similarity to M.leprae metH2 protein
10415_at	118.6		P
strong similarity to amino acid transport protein Gap1p
10416_at	884.9		P
Glutathione transferase
10417_at	7.3		A
hypothetical protein
10418_at	1819.9		P
similarity to N.crassa O-succinylhomoserine (thiol)-lyase
10373_at	135.4		A
similarity to E.coli dioxygenase
10374_at	1435.7		P
weak similarity to Y.pseudotuberculosis CDP-3,6-dideoxy-D-glycero-L-glycero-4-hexulose-5-epimerase
10375_at	766.6		P
similarity to Dal5p
```

10376_at 1198.9 P
similarity to transcription factor Pip2p
10377_at 3857.3 P
similarity to water channel proteins
10378_at 2099.5 P
member of mip family transmembrane channels
10379_at 1300.8 P
similar to FRE2
10380_at 12532.2 P
Cofilin, actin binding and severing protein
10381_at 564.9 P
hypothetical protein
10382_at 9919.5 P
yeast bile transporter, similar to mammalian bile transporter
10383_at 629.0 P
questionable ORF
10384_at 143.5 A
ribonucleoprotein 1
10385_i_at 19045.9 P
Ribosomal protein L8B (L4B) (rp6) (YL5)
10386_s_at 15592.8 P
Ribosomal protein L8B (L4B) (rp6) (YL5)
10387_at 392.2 P
questionable ORF
10388_at 3884.0 P
Suppressor of tps1\/fdp1 and member of the MIP family of transmembrane channels\; may be involved in glycerol efflux
10389_at 689.1 P
hypothetical protein
10390_at 4459.0 P
Succinate dehydrogenase (ubiquinone) iron-sulfur protein subunit
10391_at 4135.3 P
involved in regulating membrane traffic
10392_at 4438.8 P
ubiquitin
10393_at 905.9 P
weak similarity to YJR125c and YDL161w
10394_at 44.0 P
weak similarity to human platelet-activating factor receptor
10395_at 1878.0 P
RNA splicing factor
10351_at 492.6 P
hypothetical protein
10352_at 5132.7 P
similarity to mammalian valosin
10353_at 391.2 P
hypothetical protein
10354_at 580.9 P
hypothetical protein
10355_at 3869.5 P
similarity to hypothetical protein YJL062w
10356_at -216.0 A
hypothetical protein
10357_at 2806.5 P
similarity to M.jannaschii X-Pro dipeptidase and S.pombe hypothetical protein
10358_at 10939.4 P

similarity to multidrug resistance proteins
10359_at 3427.0 P
similarity to H.influenzae and E.coli hypothetical proteins
10360_at 5391.6 P
heat shock protein 104
10361_f_at 330.4 P
strong similarity to members of the Srp1p/Tip1p family
10362_at 7644.6 P
member of 70 kDa heat shock protein family
10363_at 7467.4 P
similarity to hypothetical protein YLR064w
10364_at 4122.0 P
Hat1 Interacting Factor 1
10365_at 3215.2 P
spindle pole antigen
10366_i_at 6187.4 P
questionable ORF
10367_r_at 4748.3 P
questionable ORF
10368_s_at 3684.7 P
questionable ORF
10369_at 455.7 P
protein kinase homolog
10370_at 12298.2 P
Aspartyl-tRNA synthetase, cytosolic
10371_at 19.6 A
maybe part of SCD25
10372_at 233.9 P
homologous to cdc25
10328_at 1307.7 P
similarity to metal resistance proteins
10329_at 6281.0 P
hypothetical protein
10330_at 2360.4 P
similarity to Drosophila pumilio protein
10331_at 6456.3 P
similarity to triacylglycerol lipases
10332_at 4151.1 P
56 kDa nucleolar snRNP protein that shows homology to beta subunits of G-proteins and the splicing factor Prp4
10333_at 3545.1 P
strong similarity to hypothetical protein YLR019w
10334_at 3206.8 P
cysteine-rich cytoplasmic protein
10335_at 2331.0 P
putative ATP dependent RNA helicase
10336_at 467.2 P
hypothetical protein
10337_at 1701.0 P
mitochondrial outer membrane protein
10338_at 77.1 A
similarity to A.thaliana hyp1 protein
10339_at 1431.1 P
Third subunit of the origin recognition complex
10340_at 836.0 P
protein of unknown function

10341_at	1253.5	P	Killed in Mutagen, sensitive to diepoxybutane and\/or mitomycin C
10342_at	1510.1	P	Dynamin-related protein
10343_at	1090.3	P	hypothetical protein
10344_at	3831.5	P	similarity to hypothetical C. elegans protein
10345_at	2754.5	P	hypothetical protein
10346_at	801.7	P	similarity to allantoate transport protein
10347_at	5125.2	P	Component of RNA polymerase transcription factor TFIIH
10348_at	1543.5	P	Two-component signal transducer that with Sln1p regulates osmosensing MAP kinase cascade(suppressor of sensor kinase)
10349_at	1110.5	P	hypothetical protein
10350_at	4435.9	P	similarity to hypothetical protein YNL328c
10305_at	6505.9	P	similarity to ribosomal protein L24.e.B
10306_at	744.3	P	weak similarity to Aquifex aeolicus adenylosuccinate synthetase
10307_at	1506.0	P	weak similarity to E.coli hypothetical 20.4 kDa protein
10308_at	-41.9	A	hypothetical protein
10309_at	-79.1	A	weak similarity to nitrogen regulatory proteins
10310_at	1289.5	P	zinc-finger transcription factor of the Zn(2)-Cys(6) binuclear cluster domain type
10311_at	488.7	P	weak similarity to S.pombe hypothetical protein SPBC13G1
10312_at	765.9	P	hypothetical protein
10313_at	5637.1	P	Protein that regulates ADH2 gene expression
10314_at	2133.9	P	hypothetical protein
10315_at	1659.0	P	strong similarity to YLL010c
10316_at	2154.8	P	similarity to triacylglycerol lipase
10317_at	1354.5	P	hypothetical protein
10318_at	1394.4	P	similarity to C.elegans and M.jannaschii hypothetical proteins
10319_at	6287.1	P	similarity to S.pombe hypothetical protein SPAC30D11.11
10320_at	1864.6	P	similarity to ubiquitin--protein ligase Ubr1p
10321_at	3368.8	P	involved in derepression of SUC2 in response to glucose limitation
10322_at	839.0	P	

Sed5p is a t-SNARE (soluble NSF attachment protein receptor) required in ER to Golgi transport.
10323_at 12078.9 P
aspartate aminotransferase, cytosolic
10324_at 7090.9 P
5-aminoimidazole-4-carboxamide ribonucleotide (AICAR) transformylase\/IMP cyclohydrolase
10325_at 12937.3 P
Ribosomal protein L15A (YL10) (rp15R) (L13A)
10326_g_at 11588.8 P
Ribosomal protein L15A (YL10) (rp15R) (L13A)
10327_at -129.9 A
hypothetical protein
10283_at 153.2 P
similarity to hypothetical protein YMR124w
10284_at 1295.6 P
putative ATPase\/DNA helicase
10285_at 1007.5 P
hypothetical protein
10286_at 8810.6 P
strong similarity to SMF2 protein
10287_at 564.9 P
similarity to human mutL protein homolog
10288_at 2295.1 P
similarity to YIL089w
10289_f_at 3013.7 P
strong similarity to members of the Srp1p/Tip1p family
10290_at 11054.9 P
subunit VIb of cytochrome c oxidase
10291_at 1747.2 P
involved in transcription of ribosomal proteins and ribosomal RNA
10292_at 10147.6 P
weak similartity to hypothetical protein YIL011w
10293_at 76.2 P
questionable ORF
10294_at 1051.1 P
hypothetical protein
10295_at 8831.7 P
thioredoxin
10296_at 10329.7 P
pyruvate decarboxylase
10297_at 1956.1 P
May play a role in attachment, organization, and\/or dynamics of microtubule ends at the spindle pole body
10298_at 799.4 P
strong similarity to Rta1p and Rtm1p protein
10299_at 351.9 P
similarity to hypothetical protein YGL160w
10300_f_at 12054.1 P
Ribosomal protein S0B
10301_at 5489.1 A
Ribosomal protein S0B
10302_g_at 7796.9 P
Ribosomal protein S0B
10303_at 2501.3 P
hypothetical protein
10304_at 9505.9 P
weak similarity to human MAC30 C-terminus

10260_at	2609.7	P	similarity to human acidic 82 kDa protein
10261_at	1441.2	P	hypothetical protein
10262_at	75.2	A	hypothetical protein
10263_at	481.8	P	hypothetical protein
10264_at	3220.4	P	transcription factor, probable member of histone acetyltransferase SAGA complex
10265_at	10754.4	P	C-5 sterol desaturase
10266_at	1077.7	P	weak similarity to mouse alpha-mannosidase
10267_at	10501.4	P	serine hydroxymethyltransferase
10268_at	2436.3	P	suppressor of rna12/yme2
10269_at	9536.2	P	Phenylalanyl-tRNA synthetase, alpha subunit, cytoplasmic
10270_at	7918.8	P	Ribosomal protein L22A (L1c) (rp4) (YL31)
10271_at	539.8	P	questionable ORF
10272_at	1139.1	P	ser/thr protein kinase
10273_at	6324.7	P	weak similarity to Anopheles NADH-ubiquinone oxidoreductase, chain 4
10274_at	9698.2	P	hypothetical protein
10275_at	4523.0	P	signal peptidase subunit
10276_at	296.6	P	Involved in expression of mitochondrial COX1 by regulating translation of COX1 mRNA and by affecting transcription or stability of COX1 mRNAs
10277_at	208.8	P	hypothetical protein
10278_at	4925.1	P	mitochondrial elongation factor G-like protein
10279_at	918.9	P	strong similarity to sugar dehydrogenases
10280_at	4167.0	P	component of RNA polymerase II holoenzyme\/mediator complex, interacts with Sin4p, Gal11p, and a 50 kd polypeptide
10281_at	1252.2	P	similarity to YFL042c, YFL043c, YDR326c and YHR080c
10282_at	1855.0	P	hypothetical protein
10238_at	5968.8	P	weak similarity to human zinc finger protein
10239_at	7610.9	P	Ribosomal protein L10\; Ubiquinol-cytochrome C reductase complex subunit VI requiring protein
10240_at	1559.8	P	questionable ORF
10241_at	1856.4	P	weak similarity to Xenopus RCC1 protein

10242_at	1955.7	P
necessary for vesicular transport from the ER to the Golgi complex		
10243_at	2055.7	P
P40 inhibitor of Cdc28p-Clb5 protein kinase complex		
10244_at	402.0	P
strong similarity to Emp47p		
10245_at	-146.6	A
galactose permease		
10246_at	689.1	P
Suppressor of rad53 lethality		
10247_at	11112.1	P
integral membrane protein\; p24a protein		
10248_at	3306.9	P
weak similarity to S.pombe hypothetical protein SPAC6F6		
10249_at	1858.3	P
Actin-related protein		
10250_at	693.7	P
Smc4 protein, member of SMC family		
10251_at	2778.6	P
hypothetical protein		
10252_at	2892.6	P
Possible component of GPI:protein transamidase		
10253_at	10421.4	P
strong similarity to alanine transaminases		
10254_at	2240.4	P
Homolog of E. coli DnaJ, closely related to Ydj1p		
10255_at	78.1	A
hypothetical protein		
10256_at	912.7	P
high affinity sulfate permease		
10257_at	1051.3	P
vacuolar v-SNARE		
10258_at	728.0	P
hypothetical protein		
10259_at	3833.1	P
hypothetical protein		
10215_at	3908.8	P
Serine\/threonine protein kinase		
10216_at	682.8	P
hypothetical protein		
10217_at	521.4	P
DNA-binding transcriptional activator or CHA1		
10218_at	12919.3	P
similarity to YDR125c		
10219_at	11543.1	P
similarity to rat ovarian specific protein		
10220_at	348.1	P
questionable ORF		
10221_at	490.7	P
subunit of the anaphase promoting complex (APC)		
10222_at	1361.8	P
omosomal DNA replication initiation protein		
10223_at	2557.5	P
hypothetical protein		
10224_at	2412.1	P
tRNA splicing endonuclease subunit		

10225_at	3968.8	P	similarity to Kaposi s sarcoma-associated herpes-like virus ORF73 homolog gene
10226_at	1211.8	P	similarity to Pan troglodytes prot GOR
10227_at	452.9	P	strong similarity to YDR132c
10228_at	11760.2	P	similarity to C.boidinii peroxisomal membrane protein 20K A
10229_at	407.4	A	strong similarity to Flo1p
10230_at	-319.7	A	hypothetical protein
10231_at	4073.7	P	hypothetical protein
10232_at	8876.1	P	mitogen-activated protein kinase (MAP kinase)
10233_at	1883.9	P	similarity to C.elegans hypothetical protein and YOR054c
10234_at	1154.5	P	Component of cleavage factor II (CF II)\; 105-kDa protein associated with polyadenylation factor 1 (PF I)
10235_at	2082.4	P	Branchpoint bridging protein -- component of the splicing commitment complex
10236_at	671.6	P	SYnthetic lethal with cdc40 (Forty)
10237_at	4873.1	P	similarity to several esterases
10192_at	417.0	P	suppressor of rna1-1 mutation
10193_at	8282.9	P	GPI-anchored aspartic protease
10194_at	6376.9	P	GPI-anchored aspartic protease
10195_at	73.6	A	hypothetical protein
10196_g_at	469.9	P	hypothetical protein
10197_at	355.7	P	questionable ORF
10198_at	230.3	P	hypothetical protein
10199_at	-45.7	A	hypothetical protein
10200_at	737.0	P	weak similarity to P.aeruginosa anthranilate synthase component II
10201_at	268.7	P	subunit of the anaphase promoting complex (APC)
10202_at	1410.2	P	similarity to S.pombe hypothetical protein SPBC24E9
10203_at	4447.5	P	DOM34 Interacting Protein
10204_at	5092.7	P	Low-affinity zinc transport protein
10205_at	1695.2	P	zinc finger transcription factor
10206_at	1135.8	P	hypothetical protein

10207_at	2395.6	P	choline kinase
10208_at	4533.4	P	pyruvate decarboxylase
10209_at	626.8	P	hypothetical protein
10210_at	604.6	P	zinc finger containing homolog of mammalian TIS11, glucose repressible gene
10211_at	1615.7	P	hypothetical protein
10212_at	1694.6	P	Putative Na+\/H+ antiporter
10213_at	351.4	P	73 kDa mitochondrial integral membrane protein
10214_at	76.8	A	questionable ORF
10170_g_at	3817.0	P	questionable ORF
10171_at	1304.0	P	transcription factor, member of UAF (upstream activation factor) along with Rrn9p and Rrn10p
10172_at	290.8	P	proline oxidase
10173_at	1395.3	P	weak similarity to Pyrococcus horikoshii hypothetical protein PHBJ017
10174_at	2574.4	P	Identified as an activity necessary for actin polymerization in permeabilized cells
10175_at	401.7	P	hypothetical protein
10176_at	2123.4	P	Spermine Synthase
10177_at	2541.6	P	encodes a core snRNP protein
10178_at	489.9	A	vacuolar membrane protein
10179_at	168.9	P	hypothetical protein
10180_at	12539.2	P	specific affinity for guanine-rich quadruplex nucleic acids
10181_at	496.1	P	weak similarity to A.thaliana hypothetical protein ATU78721
10182_at	2024.0	P	similarity to YOR3165w and YNL095c
10183_at	8143.7	P	acetyl-coenzyme A synthetase
10184_at	4812.2	P	hypothetical protein
10185_s_at	7424.9	P	nitrogen catabolite-regulated cell-wall L-asparaginase II
10186_s_at	254.8	A	identical to hypothetical proteins YLR161w and YLR159w
10187_at	5278.4	P	hypothetical protein
10188_at	3294.8	P	mitochondrial processing protease subunit
10189_at	355.1	A	strong similarity to Sdh4p

10190_at 439.6 P
weak similarity to H.influenzae hypothetical protein HI0176
10191_at 1640.5 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 11878.0 P
Ribosomal protein S31 (S37) (YS24)
10148_at 1865.6 P
probably involved in intramitochondrial protein sorting
10149_at 397.4 A
questionable ORF
10150_at 2270.7 P
clathrin-associated protein complex, small subunit
10151_at 606.6 P
questionable ORF
10152_at 7550.4 P
S-adenosylmethionine (AdoMet)-dependent methyltransferase of diphthamide biosynthesis
10153_at 382.6 P
hypothetical protein
10154_at 609.9 P
Cytosolic form of NADP-dependent isocitrate dehydrogenase
10155_at 10481.0 P
major low affinity 55 kDa Centromere\/microtubule binding protein
10156_at 1137.0 P
DNA binding protein, homologous to a family of mammalian RFX1-4 proteins which have a novel highly conserved DNA binding domain
10157_at 3615.3 P
similarity to suppressor protein Psp5p
10158_at 2112.1 P
suppressor of cdc25
10159_at 13748.3 P
similarity to Tfs1p
10160_at 9018.4 P
S-adenosylmethionine synthetase
10161_g_at 4457.9 A
S-adenosylmethionine synthetase
10162_at 928.0 P
hypothetical protein
10163_at 1420.6 P
regulatory protein
10164_at 1060.2 P
similarity to YDR501w
10165_at 609.6 A
weak similarity to ribulose-bisphosphate carboxylase
10166_at 355.1 A
60S ribosomal protein L37A (L43) (YL35)
10167_at 7181.6 P
strong similarity to S.pombe hypothetical protein C18G6.07C
10168_at 1145.1 P
similarity to hypothetical protein YNL278w
10169_at 7314.9 P
ATP-binding cassette (ABC) transporter family member
10124_at 3012.8 P
similarity to P.aeruginosa rhamnosyltransferase 1 chain B
10125_at 2576.1 P
hypothetical protein

10126_at	602.9	P	Peroxisomal membrane protein that contains Src homology 3 (SH3) domain
10127_at	10753.1	P	weak similarity to fruit fly transcription factor 5 large chain
10128_at	1740.4	P	similarity to G.gallus px19 and Msf1p
10129_at	7758.6	P	hypothetical protein
10130_at	4026.7	P	N-myristoyl transferase
10131_at	8167.8	P	Protein with periodic trytophan residues that resembles members of beta-transducin superfamily because of presence of WD-40 repeats
10132_at	8093.9	P	homology to microtubule binding proteins and to X90565_5.cds
10133_at	1338.8	P	questionable ORF
10134_at	3059.8	P	hypothetical protein
10135_at	2819.7	P	Polypeptide 6 of a Yeast Non-native Actin Binding Complex, homolog of a component of the bovine NABC complex
10136_at	3241.3	P	similarity to hypothetical S. pombe protein
10137_at	830.5	P	questionable ORF
10138_g_at	851.1	P	questionable ORF
10139_i_at	12633.8	P	questionable ORF
10140_r_at	6560.1	P	questionable ORF
10141_at	6020.3	P	Protein involved in maturation of COX1 and COB mRNA
10142_at	2180.9	P	protein of unknown function
10143_at	5939.5	P	hypothetical protein
10144_at	4890.6	P	similarity to human tricohyalin and protein KIAA0171
10145_at	823.9	P	HMG-CoA Reductase Degradation
10146_at	10987.7	P	cytoplasmic protein involved in release of transport vesicles from the ER
10101_at	4239.0	P	strong similarity to purine-nucleoside phosphorylases
10102_at	1128.8	P	G(sub)2-specific B-type cyclin
10103_at	876.1	P	hypothetical protein
10104_at	1582.7	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	484.7	P	similarity to UTR2 protein
10106_at	7021.0	P	

Ferric (and cupric) reductase
10107_at 1473.1 P
strong similarity to rat cell cycle progression related D123 protein
10108_at 11929.5 P a
cyclophilin related to the mammalian CyP-40\; physically interacts with RPD3 gene product
10109_at 731.6 P
questionable ORF
10110_at 1002.2 P
hypothetical protein
10111_at 1990.7 P
hypothetical protein
10112_at 2004.1 P
Possible transmembrane Ca2+ transporter
10113_at 4127.8 P
hypothetical protein
10114_at 3605.5 P
similarity to Dip2p
10115_at 2305.3 P
has a weak RNA-dependent ATPase activity which is not specific for rRNA
10116_at 1675.3 P
hypothetical protein
10117_at 2843.3 P
strong similarity to YDR222w
10118_at 2181.6 P
hypothetical protein
10119_at 177.5 P
hypothetical protein
10120_at 2504.7 P
strong similarity to YDR213w, weak similarity to Lys14p
10121_at 13394.1 P
member of the Rho subfamily of Ras-like proteins
10122_at 286.8 P
questionable ORF
10123_at 2372.3 P
strong similarity to rat kynureninase
10079_at 157.9 A
questionable ORF
10080_at 318.3 M
Telomere elongation protein (ever shorter telomeres)
10081_at 242.8 P
DNA Topoisomerase III
10082_at 358.1 A
questionable ORF
10083_g_at -253.4 A
questionable ORF
10084_at 741.7 A
hypothetical protein
10085_at 3241.1 P
thiamine transporter
10086_at 915.8 P
similarity to YDR200c
10087_at 1159.6 P
weak similarity to H.influenzae lipoate biosynthesis protein B
10088_at 2680.5 P
phosphatidylinositol 3-kinase
10089_at 1956.5 P

similarity to hypothetical S.pombe protein SPAC2G11.09
10090_at 411.2 P
weak similarity to C.elegans R05H5.5 protein and Nup120p
10091_at 6613.0 P
strong similarity to YOR262w
10092_at 5976.0 P
methionine aminopeptidase
10093_at 1684.3 P
strong similarity to B.subtilis cytidine deaminase
10094_at 1742.3 P
similarity to human DHHC-domain-containing cysteine-rich protein
10095_at 2512.2 P
similarity to S.pombe rad8 protein and Rdh54p
10096_at 7053.6 P
Serine\/threonine protein kinase
10097_at 8838.7 P
EF-3 (translational elongation factor 3)
10098_at 2820.4 P
secretory protein
10099_at 58.2 P
similarity to peroxisomal rat membrane protein PMP22
10100_at 507.4 P
questionable ORF
10055_at 1241.3 P
weak similarity to bacterial aminoglycoside acetyltransferase regulators
10056_at 818.7 P
hypothetical protein
10057_at 258.5 P
hypothetical protein
10058_at 1816.0 P
zinc-finger transcription factor of the Zn(2)-Cys(6) binuclear cluster domain type
10059_at 4139.5 P
hypothetical protein
10060_at 1166.1 P
Glycogen synthase (UDP-gluocse--starch glucosyltransferase)
10061_at 8534.3 P
heat shock protein 60\; chaperonin protein
10062_at 2854.5 P
sphingoid long chain base (LCB) kinase
10063_i_at 621.9 P
questionable ORF
10064_s_at 1656.3 P
questionable ORF
10065_at 521.8 P
highly homologous to the human GTPase, Rab6
10066_s_at 2536.9 P
strong similarity to F49C12.11 (Z68227_K) from C. elegans
10067_at 312.6 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 14053.3 P
Ribosomal protein S28B (S33B) (YS27)
10069_f_at 6997.7 P
Ribosomal protein S28B (S33B) (YS27)
10070_at 171.1 P
hypothetical protein

10071_at 372.0 P
weak similarity to transcription factors
10072_at 7.8 A
Bypass of PAM1
10073_at 2931.0 P
Synaptobrevin (v-SNARE) homolog present on ER to Golgi vesicles
10074_at 8.0 A
questionable ORF
10075_at 2734.0 P
strong similarity to YOR173w
10076_at 569.4 P
hypothetical protein
10077_at 1141.8 P
similarity to human hypothetical ORF
10078_at 561.5 P
Protein similar to Gac1p, a putative type 1 protein phosphatase targeting subunit
10032_at 476.1 P
Member of complex that acts at ARS s to initiate replication
10033_at 1066.7 P
U1 snRNP protein of the Sm class
10034_at 5637.6 P
DEAD-Box Protein 9
10035_at 2357.5 P
subunit of Polyadenylation factor I (PF I)
10036_at 1189.0 P
weak similarity to regulatory proteins
10037_at 1213.2 A
questionable ORF
10038_i_at 1926.2 P
questionable ORF
10039_s_at 225.7 A
questionable ORF
10040_at 270.5 P
similarity to polypeptide chain release factors
10041_at 467.1 A
questionable ORF
10042_at 302.6 P
weak similarity to Smc2p
10043_at 236.5 A
Peroxisomal enoyl-CoA hydratase
10044_at 3432.5 P
hypothetical protein
10045_at 16489.7 P
Endochitinase
10046_at 561.9 P
weak similarity to S.pombe hypothetical protein SPAC22E12
10047_f_at 10379.1 P
Ribosomal protein S30A
10048_at 821.7 P
involved in checkpoint control and DNA repair
10049_at 573.8 P
GTPase
10050_at 2257.2 P
hypothetical protein
10051_at 7871.4 P
translation initiation factor eIF2b, 43 kDa subunit\; negative regulator of GCN4 expression

10052_at 5042.0 P
protein involved in membrane protein insertion into the ER
10053_at 12847.1 P
GTP-binding protein
10054_at 7744.5 P
questionable ORF
10010_at 5909.6 P
ATP synthase subunit h
10011_at 154.2 P
hypothetical protein
10012_at 1371.2 P
weak similarity to Vibrio vulnificus VvpC protein
10013_at 492.4 P
U1 snRNP protein required for pre-mRNA splicing
10014_at 2506.6 P
gamma-glutamyltransferase homolog
10015_at 10379.0 P
Exo-1,3-beta-glucanase
10016_at 8027.8 P
hypothetical protein
10017_at -100.5 A
questionable ORF
10018_at 11897.9 P
O-Acetylhomoserine-O-Acetylserine Sulfhydralase
10019_at 12070.0 P
Aconitase, mitochondrial
10020_at 4360.7 P
encodes a phosphatidylinositol-4-kinase, homologous to VPC34
10021_at 921.0 P
Ubiquitin-conjugating enzyme
10022_at -40.1 A
Chitin Deacetylase
10023_at -280.0 A
Chitin Deacetylase
10024_at 3122.5 P
similarity to human centromere protein E
10025_at 811.8 P
regulatory protein of adenylate cyclase
10026_at -186.7 A
weak similarity to S.tarentolae cryptogene protein G4
10027_at 63.3 A
hypothetical protein
10028_at 679.7 A
homologous to Spa2p, localizes to sites of polarized growth
10029_at 1177.1 P
Component of 10 nm filaments of mother-bud neck
10030_at 236.8 P
weak similarity to rat apolipoprotein A-IV
10031_at 2614.3 P
weak similarity to H.influenzae hypothetical protein HI0906
9986_at 789.7 P
questionable ORF
9987_at 157.2 P
103 kD basic protein, catalytic subunit of telomerase
9988_at 1377.1 P
Actin Interacting Protein

9989_at 815.1 P
hypothetical protein
9990_at 2080.1 P
homolog of Snf5p, member of the chromatin remodeling complex, RSC
9991_at 46.2 A
questionable ORF
9992_at 795.6 P
weak similarity to N.crassa uvs2 protein
9993_at 290.2 P
strong similarity to YGR004w
9994_at 9937.9 P
Ribosomal protein L38
9995_at 2288.2 P
hypothetical protein
9996_at 571.1 P
strong similarity to Stf2p
9997_at 5134.7 P
strong similarity to YGR010w
9998_at -0.9 A
23 kDa protein containing a putative leucine zipper\; meiosis specific recombination protein\; mRNA is induced early in sporulation
9999_at 3758.6 P
Involved in chitin synthase III activity, also required for homozygosis in the first stages of mating
10000_at 8.3 A
questionable ORF
10001_at 4307.5 P
Protein required for mating
10002_i_at 14324.1 P
Ribosomal protein S25B (S31B) (rp45) (YS23)
10003_f_at 12814.0 P
Ribosomal protein S25B (S31B) (rp45) (YS23)
10004_at 71.6 M
questionable ORF
10005_at 4160.0 P
nuclear pore complex protein with central repetitive domain similar to that of NSP1 and NUP1
10006_at 2388.5 P
Suppressor of Glycerol Defect
10007_at 5166.4 P
Proline-rich protein verprolin
10008_at -273.3 A
questionable ORF
10009_at -254.0 A
questionable ORF
9964_at 3278.0 A
60S ribosomal protein P0 (A0) (L10E)
9965_at 55.1 A
hypothetical protein
9966_at 9848.1 P
1,3-beta-D-glucan synthase
9967_at 422.7 P
strong similarity to Gas1p and C.albicans pH responsive protein
9968_s_at 5641.1 P
Ribosomal protein L26A (L33A) (YL33)
9969_at 1578.1 P
similarity to Pfk26p and other 6-phosphofructo-2-kinases
9970_at 4485.8 P

weak similarity to YGR035c
9971_at 3205.8 P
95 kDa structural and functional homolog of vertebrate karyopherin beta (importin 90)
9972_at 5605.4 P
mitochondrial dicarboxylate transport protein
9973_at 833.0 P
questionable ORF
9974_at 9931.2 P
strong similarity to YGR038w
9975_at 9846.7 P
Nit3 nitrilase
9976_at 979.8 P
hypothetical protein
9977_at 1895.4 P
budding protein
9978_at 11138.5 P
Transaldolase, enzyme in the pentose phosphate pathway
9979_at 11494.1 P
acetohydroxyacid reductoisomerase
9980_at 1193.0 P
similarity to SCM4 protein
9981_at 648.7 P
questionable ORF
9982_at 2103.8 P
Member of RSC complex.
9983_at 9275.3 P
Adenylosuccinate Lyase
9984_at 150.0 M
protein involved in vacuolar sorting
9985_at 1537.4 P
similarity to YOR3329c
9941_at 1508.0 P
Ser\/Thr protein kinase\; MEKK homolog
9942_at 399.1 P
putative Upf1p-interacting protein
9943_at 1588.3 P
hypothetical protein
9944_at 98.0 M
weak similarity to Udf2p
9945_at 12.0 A
hypothetical protein
9946_at 9548.3 P
Ribosomal protein S22B (S24B) (rp50) (YS22)
9947_i_at 18978.4 P
Ribosomal protein S22B (S24B) (rp50) (YS22)
9948_f_at 11535.8 P
Ribosomal protein S22B (S24B) (rp50) (YS22)
9949_at 2415.1 P
hypothetical protein
9950_at 890.3 P
Hsp70 protein
9951_at 3798.6 P
Arp2\/3 Complex Subunit
9952_at 2688.9 P
GDP-GTP Exchange Protein (GEP) for the Rho1p Small GTP-binding Protein\; high copy suppressor of cik1 and kar3 deletion mutants.

9953_at	12161.7	P	required for conversion of 24-carbon fatty acids to 26-carbon species
9954_at	2919.6	P	similarity to hypothetical protein YGR071c
9955_at	448.1	A	questionable ORF
9956_at	6105.3	P	Involved in pre-tRNA splicing and in uptake of branched-chain amino acids
9957_at	879.9	P	hypothetical protein
9958_at	172.5	P	fructose-1,6-bisphosphatase
9959_at	11512.6	P	membrane component of ER protein translocation apparatus
9960_at	-50.8	A	questionable ORF
9961_at	4862.1	P	weak similarity to SEC14 protein
9962_at	600.5	P	hypothetical protein
9963_at	2104.4	P	mitochondrial leucyl tRNA synthetase
9918_at	1770.4	P	Protein involved in recombination repair, homologous to S. pombe rad18
9919_at	6653.9	P	confers sensitivity to killer toxin
9920_at	189.7	P	hypothetical protein
9921_at	1875.2	P	similarity to hypothetical S. pombe protein
9922_at	4887.6	P	similarity to YBR267w
9923_f_at	8384.9	P	Ribosomal protein S29A (S36A) (YS29)
9924_at	1640.6	P	protease involved in a-factor processing
9925_at	2862.9	P	ExtraCellular Mutant
9926_at	10366.8	P	Secretory Stress Response protein 1
9927_at	264.2	P	hypothetical protein
9928_at	707.7	P	essential for assembly of a functional mitochondrial ATPase complex
9929_at	700.2	P	weak similarity to chicken RING zinc finger protein
9930_at	8791.5	P	Cytochrome-c oxidase chain VIII
9931_at	1245.5	P	Vacuolar sorting protein essential for vacuolar morphogenesis and function
9932_at	3945.8	P	homology to the CDC48 gene product
9933_at	4448.2	P	antiviral protein, putative helicase
9934_at	2389.7	P	Bdf1p contains two bromodomains, localizes to the nucleus and to chomosomes in spread meiotic nuclei

but is excluded from the nucleolus
9935_at 239.8 P
hypothetical protein
9936_at 2938.4 P
similarity to A.brasilense nifR3 protein
9937_at 1601.6 P
hypothetical protein
9938_at 1052.2 P
split zinc finger protein
9939_at 932.1 P
hypothetical protein
9940_at 1888.1 P
similarity to A.brasilense nifR3 protein
9895_i_at 7866.1 P
Ribosomal protein L31B (L34B) (YL28)
9896_f_at 9288.0 P
Ribosomal protein L31B (L34B) (YL28)
9897_f_at 18390.1 P
Ribosomal protein L31B (L34B) (YL28)
9898_at 1700.7 P
hypothetical protein
9899_at 696.0 P
hypothetical protein
9900_at 4222.7 P
strong similarity to S. pombe beta-transducin
9901_at 5178.3 P
Homologous to S. pombe asp1+
9902_at 8574.2 P
Copper Transporter
9903_at 2581.3 P
weak similarity to Candida maltosa cytochrome P450
9904_at 5093.6 P
strong similarity to YKL187c
9905_at 9219.0 P
weak similarity to YLR413w
9906_at -236.9 A
questionable ORF
9907_at 223.0 P
hypothetical protein
9908_at 580.6 P
defective in vacuolar protein sorting
9909_at 5028.5 P
Accessory factor associated with RNA polymerase II by affinity chromatography
9910_at 2893.8 P
similarity to helicases
9911_at 10743.4 P
dihydrooratase
9912_at 9060.2 P
weak similarity to human 42K membrane glycoprotein
9913_at 3877.8 P
similarity to human DOCK180 protein
9914_at 224.9 P
hypothetical protein
9915_at 176.1 P
weak similarity to Stu1p
9916_at 1381.9 P

hypothetical protein
9917_at 4678.0 P
weak similarity to 3-oxoacyl-[acyl-carrier-protein] reductase from E. coli
9873_at 633.8 P
weak similarity to 3-oxoacyl-[acyl-carrier-protein] reductase from E. coli
9874_at 3265.3 P
weak similarity to human transcription regulator Staf-5
9875_at 840.2 P
questionable ORF
9876_at 4554.3 P
has homology to the Dictyostelium and human actin-binding protein coronin
9877_at 2289.2 P
component of a nuclear-localized tRNA splicing complex
9878_at 225.7 P
weak similarity to rabbit trichohyalin
9879_f_at 10978.9 P
strong similarity to IMP dehydrogenases, Pur5p and YML056c
9880_at 4259.3 P
Calcineurin subunit A\; type 2B protein serine\/threonine phosphatase catalytic subunit A1\; cytoplasmic
9881_at 3014.5 P
questionable ORF
9882_at 1931.2 P
hypothetical protein
9883_at 2250.2 P
ExtraCellular Mutant
9884_at 1947.8 P
hypothetical protein
9885_at 6642.3 P
ornithine aminotransferase
9886_at 6088.1 P
Putative snRNP protein containing Sm-like domain\; coprecipitates with U4, U5 and U6 snRNAs
9887_at 3323.7 P
Mitochondrial 60S ribosomal protein L4
9888_at 2127.3 P
hypothetical protein
9889_i_at 9861.2 P
Ribosomal protein S1A (rp10A)
9890_s_at 7701.0 P
Ribosomal protein S1A (rp10A)
9891_at 1787.4 P
regulator of silent mating loci
9892_at 1910.0 P
ExtraCellular Mutant
9893_at 218.0 P
questionable ORF
9894_at -3.5 A
hypothetical protein
9850_at 343.2 A
weak similarity to hexokinases
9851_at 9137.0 P
36 kDa subunit (D subunit of VO sector) of the vacuolar H(+) ATPase\; required for assembly
9852_at 8843.8 P
60S ribosomal subunit protein L6B (L17B) (rp18) (YL16)
9853_at 7012.5 P
60 kDa nuclear FK506 binding protein
9854_at 4450.0 P

3-hydroxy-3-methylglutaryl-coenzyme A (HMG-CoA) reductase isozyme
9855_at 653.6 P
zinc-finger transcription factor of the Zn(2)-Cys(6) binuclear cluster domain type
9856_at 5226.8 P
Protein involved in desensitization to alpha-factor pheromone
9857_at 267.3 A
Nuclear protein
9858_at 3200.8 P
similarity to YPR117w
9859_at 1967.3 P
weak similarity to human G/T mismatch binding protein
9860_at 713.8 P
strong similarity to YPR172w
9861_at 288.1 P
Nap1p-binding protein
9862_at -112.4 A
questionable ORF
9863_at 3679.0 P
cell division control protein
9864_at 182.7 A
similarity to C.carbonum toxD protein
9865_f_at 1562.3 P
member of the seripauperin protein\/gene family (see Gene_class PAU)
9866_i_at 360.0 A
questionable ORF
9867_s_at 325.9 P
questionable ORF
9868_at 2092.5 P
hypothetical protein identified by SAGE
9869_at 5766.1 P
identified by SAGE
9870_s_at 1768.6 P
Mitochondrial ribosomal protein MRPL15 (YmL15)
9871_at 1061.5 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 1027.8 P
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 3328.9 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 2404.4 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 1729.9 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 1462.0 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 449.0 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 280.9 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 -326.5 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 23.8 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 469.2 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 3532.2 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 10405.0 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 6672.1 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 9243.9 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 5597.2 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 75.4 P
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 115.3 A
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 3286.0 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 47.0 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 8258.4 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 3434.4 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 164.9 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 3887.3 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 256.1 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 2596.0 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 943.3 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 735.0 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 8676.4 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 835.5 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 582.0 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 11.6 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 216.8 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 485.1 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 365.1 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 598.4 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 83.1 A

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 336.5 A

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 1892.4 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 179.4 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 -6.6 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 73.4 A

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 1591.0 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 -124.1 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 454.8 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	6821.7	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	4011.5	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	795.0	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	531.1	P	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	793.8	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	71.4	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	-266.8	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	1370.3	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	637.4	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	915.8	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	1123.4	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	4966.2	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	631.3	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	1112.9	A	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	-3.9	A	Centromere
9791_f_at	-7.5	A	Centromere
9792_s_at	1897.3	P	CEN12-associated
9793_at	282.9	P	snRNA
9794_at	3678.7	P	snRNA
9795_at	5666.2	P	snRNA
9796_at	1371.8	P	

snRNA
9797_i_at 318.5 P
snRNA
9798_at 7763.7 P
snRNA
9799_at 1195.6 P
snRNA
9800_s_at 2761.2 P
hypothetical protein Y .2
9801_at 478.7 P
similarity to human leukotriene b4 12-hydroxydehydrogenase
9802_at 3609.6 P
required for protein disulfide bond formation in the ER
9803_at 3660.3 P
mitochondrial membrane protein
9757_at 937.5 P
C-terminal part starting with aa 262 cause growth inhibition when overexpressed
9758_at 7660.8 P
weak similarity to Los1p
9759_at 10830.5 P
Hydroxymethylglutaryl-CoA Synthase
9760_at 8713.7 P
strong similarity to cytochrome-b5- and nitrate reductases
9761_at 9042.3 P
alpha-tubulin
9762_at 11135.3 P
inorganic phosphate transporter, transmembrane protein
9763_at -308.5 M
hypothetical protein
9764_at 4265.8 P
Putative small GTPase
9765_at 2829.9 P
mitochondrial NADH ubiquinone 6 oxidoreductase
9766_at 624.3 P
hypothetical protein
9767_at 161.4 A
similarity to YMR285c
9768_at 1775.4 P
similarity to YPL184c
9769_g_at 2700.3 P
similarity to YPL184c
9770_at 3148.4 P
questionable ORF
9771_at 1642.7 P
predicted protein is very hydrophobic, has many membrane-spanning regions, several potential glycosylation sites, potential ATP-binding site
9772_at 3183.3 P
Vanadate resistance protein
9773_at 2490.4 P
hypothetical protein
9774_at 3252.3 P
datin, an oligo(dA).oligo(dT)-binding protein
9775_at 1042.9 P
CTD kinase-I gamma subunit
9776_at 1539.9 P
strong similarity to ubiquitination protein Bul1p

9777_at 11773.8 P
DBF2 Interacting Protein
9778_at 1014.8 P
multicopy suppressor of a sin4 defect
9734_at 1046.9 P
hypothetical protein
9735_at 3080.9 P
hypothetical protein
9736_at 10616.7 P
Orotate phosphoribosyltransferase 1
9737_at 4775.6 P
signal recognition particle subunit, homologue of mammalian SRP19
9738_at 1233.6 P
Intermediate filament protein involved in organelle inheritance
9739_at 2325.8 P
Nucleoporin
9740_at 2896.7 P
p60 subunit of the yeast omatin Assembly Factor-I (CAF-I)
9741_at -510.2 A
questionable ORF
9742_at 6617.8 P
weak similarity to YMR264w
9743_at 4510.9 P
123 kD regulatory subunit of trehalose-6-phosphate synthase\/phosphatase complex\; homologous to TPS3 gene product
9744_at 549.4 P
questionable ORF
9745_at 780.3 P
zinc-finger transcription factor of the Zn(2)-Cys(6) binuclear cluster domain type
9746_at 1911.0 P
TFIID subunit
9747_at 3537.7 P
required for Golgi to vacuole trafficking, shares similarity to mammalian ras inhibitors
9748_at 1300.1 P
similarity to asparagine synthases
9749_at 388.8 P
Endonuclease (with Rad1p) that degrades single-stranded DNA for repair
9750_at 137.6 A
questionable ORF
9751_at 4450.2 P
Putative homolog of subunit 5 of bovine prefoldin, a chaperone comprised of six subunits
9752_at 2485.4 P
similarity to P.falciparum liver stage antigen LSA-1
9753_at 12382.0 P
proteasome component Y7
9754_at 1293.4 P
subunit of mitochondrial RNase P
9755_at 101.2 A
hypothetical protein
9756_at -39.7 A
questionable ORF
9711_at 1736.2 P
hypothetical protein
9712_at -65.1 A
strong similarity to YML125c, similarity to cytochrome-b5- and nitrate reductases
9713_at 7803.2 P

D-arabinono-1,4-lactone oxidase
9714_at 12532.9 P
alpha-tubulin
9715_at -227.4 A
hypothetical protein
9716_at -458.5 A
hypothetical protein
9717_at 1508.1 P
similarity to N.crassa O-succinylhomoserine (thiol)-lyase
9718_at 2951.3 P
strong similarity to ZMS1 protein
9719_at 2086.7 P
similarity to A.brasilense nifR3 protein
9720_at 1916.0 P
weak similarity to Synechocystis sp. hypothetical protein sll1188
9721_at 11433.1 P
cyclophilin-3 (cyclosporin-sensitive proline rotamase-3)
9722_at 3915.9 P
Bet5p\/18kD component of TRAPP
9723_at 1465.4 P
weak similarity to transcription factor
9724_at 10268.5 P
3-hydroxy-3-methylglutaryl-coenzyme A (HMG-CoA) reductase isozyme
9725_at 9394.8 P
Prolyl cis-trans isomerase, also called proline rotamase or peptidylprolyl cis-trans isomerase (PPIase)
9726_at 12722.0 P
Ribosomal protein L6A (L17A) (rp18) (YL16)
9727_at 6378.1 P
similarity to YOR3141c and YNL087w
9728_at 3646.8 P
hypothetical protein
9729_at 5833.1 P
putative dihydroxyacetone kinase
9730_at 4483.5 P
Binds to catalytic subunit of DNA polymerase alpha (Pol1p)
9731_at 821.9 P
similarity to C.elegans hypothetical protein
9732_at 6332.5 P
weak similarity to YAL042w
9733_at 10.3 A
hypothetical protein
9689_at 1337.6 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 1127.8 P
GTP-binding protein of the ras superfamily involved in termination of M-phase
9691_i_at 13875.1 P
Ribosomal protein S1B (rp10B)
9692_at 1430.7 P
Protein involved in mitochondrial import of fusion proteins
9693_at 1307.3 P 5
to 3 DNA helicase
9694_at 2491.1 P
43-kDa 8-oxo-guanine DNA glycosylase
9695_at 2883.9 P
similarity to C.elegans ZK370.4 protein

9696_at 8415.3 P
Suppressor of mec lethality
9697_at 127.9 A
questionable ORF
9698_at 2779.3 P
Catalytic A subunit of calcineurin, type 2B protein serine\/threonine phosphatase\; redundant with Cna1\; cytoplasmic
9699_at 11024.9 P
strong similarity to IMP dehydrogenases
9700_at 11447.1 P
strong similarity to IMP dehydrogenases
9701_at 5638.1 P
subunit of signal peptidase complex, homologous to mammalian protein SPC25
9702_at 390.1 P
Cytochrome b2 [L--lactate cytochrome-c oxidoreductase]
9703_at 3653.1 P
hypothetical protein
9704_at 8007.2 P
putative integral membrane protein
9705_at 5570.7 P
regulatory protein
9706_at 331.7 P
weak similarity to potato sucrose cleavage protein
9707_at 2137.5 P
RNA splicing and ER to Golgi transport
9708_at 7008.2 P
Glucose Signaling Factor
9709_at 795.0 P
questionable ORF
9710_at 543.6 P
strong similarity to YJR054w
9666_at 2406.9 P
RNA splicing factor associated with U1 snRNP
9667_at 270.3 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 335.7 P
Carnitine O-acetyltransferase, peroxisomal and mitochondrial
9669_at 3010.5 P
hypothetical protein
9670_at 3322.1 P
hypothetical protein
9671_at 391.1 P
hypothetical protein
9672_at 1959.8 P
weak similarity to C.elegans hypothetical protein CELW03F8
9673_at 3611.4 P
putative alpha-mannosidase
9674_at 158.1 A
questionable ORF
9675_at 1312.8 P
similarity to YDR458c
9676_at 1434.7 P
similarity to YDR458c
9677_at 3624.6 P
Interacts with Rad51p by two hybrid analysis. mRNA is induced in meiosis during recombination

9678_at	615.3	A	questionable ORF
9679_at	4163.4	P	Nuclear envelope protein with multiple putative transmembrane domains
9680_at	3948.3	P	hypothetical protein
9681_at	2020.8	P	hypothetical protein
9682_at	9355.0	P	Thiol-specific antioxidant
9683_at	4686.0	P	Homeobox-domain containing protein
9684_s_at	13083.4	P	Ribosomal protein S18B
9685_at	1298.4	P	ribosomal protein, mitochondrial
9686_s_at	6597.5	P	Ribosomal protein S17A (rp51A)
9687_at	2727.5	P	weak similarity to Nmd2p
9688_at	7746.9	P	Adenine phosphoribosyltransferase
9643_at	2509.6	P	uracil DNA glycosylase
9644_at	1484.0	P	hypothetical protein
9645_at	5171.3	P	Putative new 37kDa subunit of N-oligosaccharyltransferase complex
9646_at	2762.6	P	similarity to YDR438w
9647_at	426.2	P	Polymerase suppressor 2\; Suppressors of group II intron-splicing defect.
9648_at	2197.5	P	serine-threonine phosphatase Z
9649_at	1546.0	P	TFIID subunit
9650_at	2179.2	P	similarity to C.elegans hypothetical protein C14B1.5
9651_at	2240.5	P	hypothetical protein
9652_at	4.4	A	questionable ORF
9653_at	10866.7	P	Component of the COPII coat of certain ER-derived vesicles
9654_at	2221.9	P	hypothetical protein
9655_at	1544.4	P	transcription factor
9656_g_at	6801.3	P	transcription factor
9657_i_at	657.4	P	questionable ORF
9658_r_at	192.8	P	questionable ORF
9659_at	624.5	P	questionable ORF

9660_at 7602.4 P
Mitochondrial ribosomal protein MRPL39 (YmL39)
9661_at 11156.3 P
S-adenoslymethionine: delta 24-methyltransferase
9662_at 1797.4 P
jun-like transcription factor
9663_at 3114.5 P
hypothetical protein
9664_at 1144.5 P
similarity to hypothetical S.pombe protein
9665_at 8333.6 P
lactoylglutathione lyase (glyoxalase I)
9620_at 444.8 P
hypothetical protein
9621_at 507.1 P
hypothetical protein
9622_at 8339.8 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 2296.6 P
protein kinase which functions at the G(sub)2\/M boundary
9624_at 8730.0 P
similarity to hypothetical S.pombe and C.elegans proteins
9625_at 1314.2 P
hypothetical protein
9626_at 4172.2 P
Protein required for sorting proteins to the vacuole
9627_at 3892.9 P
Protein required for protein synthesis
9628_at 6187.4 P
strong similarity to Plb1p
9629_at 300.8 P
hypothetical protein
9630_at 9514.2 P
Phospholipase B (lypophospholipase)
9631_at 8546.3 P
weak similarity to P.aeruginosa regulatory protein mmsR
9632_at 2698.8 P
weak similarity to hypothetical protein YDR352w
9633_at 4561.2 P
high affinity hexose transporter-2
9634_at 5917.7 P
CLU1 is similar to the Dictyostelium cluA gene
9635_at 974.9 P
membrane protein required for core glycosylation
9636_at 1785.0 P
weak similarity to S.pombe hypothetical protein SPAC4F10
9637_at 8418.1 P
cytochrome P450 involved in C-22 denaturation of the ergosterol side-chain
9638_at 2006.4 P
displays homologies to several transcription factors
9639_at 133.7 P
DBF2 Interacting Protein\; SNAP 25 homolog
9640_at 193.8 A
similarity to tetratricopeptide-repeat protein PAS10

9641_at 1189.2 P
Binds Sin3p in two-hybrid assay
9642_at 1490.1 P
Multicopy suppressor of fenpropimorph resistance (fen2 mutant), shows similarity to Candida albicans corticosteroid-binding protein CBP1
9598_at 1566.3 P
metal-binding transcriptional activator
9599_at 6813.0 P
ubiquitin conjugating enzyme
9600_at 629.4 A
putative mitochondrial GTPase
9601_at 2432.1 P
Mitochondrial ribosomal protein MRPL3 (YmL3)
9602_at 770.5 A
hypothetical protein
9603_at 1154.6 P
C3HC4 zinc-binding integral peroxisomal membrane protein
9604_at 5741.2 P
High level expression reduced Ty3 Transposition
9605_at 721.5 P
42 kDa protein that pysically associates with the PP2A and SIT4 protein phosphatase catalytic subunits
9606_at 732.2 P
weak similarity to human nuclear autoantigen
9607_at 483.0 P
hypothetical protein
9608_at 1602.5 P
similarity to YKL050c and human restin
9609_at 351.9 A
questionable ORF
9610_at 1965.8 P
Cytokinesis
9611_at 4393.7 P
Actin-related protein
9612_at 226.9 A
weak similarity to YPR201w
9613_at 1283.3 P
Inner membrane protease (mitochondrial protein)
9614_at 1266.7 P
homolog of S. pombe cdc25
9615_at 3004.2 P
zinc finger protein
9616_at 8373.5 P
Homocitrate
9617_at 5595.1 P
suppressor of TFIIB mutations
9618_at 691.3 P
strong similarity to Yet1p
9619_at 877.7 P
weak similarity to Pseudomonas L-fucose dehydrogenase
9575_at 1699.2 P
Regulator of arginine-responsive genes with ARG81 and ARG82
9576_at 6303.0 P
putative transcriptional activator of alpha-specific genes
9577_at 3774.7 P
hypothetical protein
9578_at 3719.9 P

Nuclear pore complex protein that is member of GLFG repeat-containing family of nucleoporins and is highly homologous to Nup100p
9579_at 803.1 P
hypothetical protein
9580_at 8556.9 P
weak similarity to A.thaliana PRL1 protein
9581_at 263.8 P
Required for arrest in G1 in response to pheromone
9582_at 607.5 P
questionable ORF
9583_at 123.9 A
Binds Sin3p in two-hybrid assay and is part of large protein complex with Sin3p and Stb1p
9584_at 4141.9 P
vacuolar proton pumping ATPase, 110-kDa subunit\; not in vacuole membrane
9585_at 2267.8 P
Protein required for cell cycle arrest in response to loss of microtubule function
9586_at 1857.9 P
mitochondrial ADP\/ATP translocator
9587_at 113.7 A
hypothetical protein
9588_at 7969.7 P
multicopper oxidase
9589_at 1523.5 P
15kDa subunit of the tetrameric tRNA splicing endonuclease
9590_at 1047.8 P
mitochondrial import receptor, heterodimerizes with Tom70p, preferentially recognizes the mature regions of precursor proteins associated with ATP-dependent cytosolic chaperones
9591_at 504.0 P
component of the cleavage and polyadenylation factor CF I involved in pre-mRNA 3 -end processing
9592_at 2228.9 P
acetylornithine acetyltransferase
9593_at 443.7 M
Regulator of Rim1p, required for IME1 expression
9594_at 1079.7 P
basic, hydrophilic protein of 59 kDa
9595_at 716.6 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 100.5 A
Synthesis Of Var
9597_at 2131.5 P
hypothetical protein
9553_at 129.5 P
weak similarity to mouse transcription factor NF-kappaB
9554_at 479.0 P
hypothetical protein
9555_at 715.0 P
2 Cys2-His2 zinc fingers at c-terminus, glutamine and asparagine rich
9556_at 7129.9 P
hypothetical protein
9557_at 8862.9 P
HMG-1 homolog, mitochondrial
9558_at 2887.0 P
weak similarity to C-terminal part of cytochrome b5 and b2
9559_at 2707.9 P
strong similarity to hypothetical S. pombe protein

9560_at 512.7 P
weak similarity to human Mi-2 protein
9561_at 205.2 P
questionable ORF
9562_at 2505.0 P
Precocious Dissociation of Sister chromatids
9563_at 889.0 P
similarity to SNF7 protein
9564_at 1234.2 P
chromosome transmission
9565_at 9902.2 P
phosphatidylinositol transfer protein
9566_at 3136.9 P
putative helicase
9567_at 396.6 P
May regulate NAM7 function, possibly at level of mRNA turnover
9568_at -67.0 A
hypothetical protein
9569_at 11893.6 P
alcohol dehydrogenase isoenzyme III
9570_at 478.9 P
putative pseudogene
9571_at -23.3 A
putative pseudogene
9572_at 2383.4 P
similarity to YKL105c
9573_at 396.0 P
questionable ORF
9574_at 619.1 P
hypothetical protein
9530_at 4390.2 P
similarity to multidrug resistance proteins
9531_at 3253.8 P
mitochondrial membrane ATPase of the CDC48\/PAS1\/SEC18 (AAA) family
9532_at 675.6 P
strong similarity to B. subtilis conserved hypothetical protein yhfK
9533_at 1950.9 P
nuclear protein localization factor
9534_at 3787.1 P
Protein localizes to actin cortical patches. Probable binding site on actin lies on front surface of subdomain 3 and 4.
9535_at 3123.0 P
weak similarity to Pwp2p
9536_at 256.4 P
58 kd component (Cbf3c) of the multisubunit Cbf3 kinetochore protein complex, which binds to the CDE III element of centromeres
9537_at 2000.8 P
SNZ1 proximal ORF, stationary phase induced gene
9538_at 3716.0 P
encodes highly conserved 35 kDa protein that shows increased expression after entry into stationary phase
9539_at 1011.7 P
weak similarity to M.genitalium hypothetical protein homolog MG442
9540_at 1001.3 P
hypothetical protein
9541_at 7296.6 P

similarity to P.ciliare possible apospory-associated protein
9542_at 1764.0 P
Homolog of samB gene of Aspergillus nidulans (deletion of samB results in mislocalization of septa
9543_at 515.4 P
similarity to YBR002c
9544_at 6618.3 P
strong similarity to YKL121w
9545_at 2138.5 P
hypothetical protein
9546_at 538.4 P
protein kinase
9547_at 1149.8 P
Phosphoglucomutase
9548_at 613.0 P
Ku80 homolog, exhibits DNA binding activity on its own, associates with Hdf1p to form major DNA end-binding complex
9549_at -23.9 A
hypothetical protein
9550_at 8959.1 P
acetolactate synthase
9551_at 4402.8 P
myosin I
9552_at 6949.2 P
similarity to aldehyde dehydrogenase
9507_at 400.5 P
weak similarity to MSN1 protein
9508_at 1484.9 P
hypothetical protein
9509_at 4445.3 P
similarity to folylpolyglutamate synthetases and strong similarity to YKL132c
9510_at 132.5 P
similarity to B. subtilis conserved hypothetical proteins yoqW and yoaM
9511_at 1521.3 P
similarity to YKL133c
9512_at 9296.0 P
WD repeat protein (G-beta like protein) that interacts with the translational machinery
9513_at 9398.0 P
WD repeat protein (G-beta like protein) that interacts with the translational machinery
9514_at 53.5 A
component of spindle pole
9515_at 79.1 A
strong similarity to succinate dehydrogenase
9516_at 2128.1 P
similarity to YNL008c
9517_g_at 4516.6 P
similarity to YNL008c
9518_at 2131.7 P
questionable ORF
9519_at 6900.6 P
5-aminoimidazole-4-carboxamide ribonucleotide (AICAR) transformylase\/IMP cyclohydrolase
9520_at 7104.6 P
Ribosomal protein L15B (YL10) (L13B) (rp15R)
9521_at 411.8 A
hypothetical protein
9522_at 10575.9 P
resistance against Pichia farinosa killer toxin (SMK toxin) when expressed by a multi copy plasmid

9523_at 732.0 P
weak similarity to YLR031w
9524_at 3924.9 P
transcriptional activator of glycolytic genes
9525_at 763.1 P
hypothetical protein
9526_at 611.7 P
Protein involved in silencing HMR, homologous to acetyltransferases
9527_at 4024.4 P
ExtraCellular Mutant
9528_at 4509.0 P
Nuclear pore membrane glycoprotein
9529_at 497.8 P
similarity to D.melanogaster Dreg-2 protein
9484_at 8043.6 P
similarity to human retinoblastoma-binding protein
9485_at 130.2 P
similarity to hypothetical S. pombe protein
9486_at -73.0 A
mRNA is induced early in sporulation
9487_at 3040.5 P
hypothetical protein
9488_at 717.8 P
hypothetical protein
9489_at 197.4 M
questionable ORF
9490_at 483.8 P
weak similarity to YIR013c and YLR013w
9491_at 447.8 A
interstrand crosslink repair protein
9492_at 710.2 M
GTP-binding protein
9493_at 2979.0 P
Serine\/threonine protein kinase, phosphorylates the mitotic activator IME1
9494_at 3031.0 P
hypothetical protein
9495_at 174.5 P
hypothetical protein
9496_at 15919.7 P
Ribosomal protein L13B
9497_i_at 3070.6 P
Ribosomal protein S16A (rp61R)
9498_f_at 10111.1 P
Ribosomal protein S16A (rp61R)
9499_at 388.2 P
weak similarity to Mlp1p
9500_at 9152.8 P
mitochondrial cytosolically directed NADH dehydrogenase
9501_at 9806.5 P
p39 subunit of translation initiation factor eIF3
9502_at 1727.3 P
hypothetical protein
9503_at 6008.7 P
hypothetical protein
9504_at 8258.2 P
oligosaccharyl transferase glycoprotein complex, delta subunit

9505_at	4025.4	P	Inner membrane protease (mitochondrial protein)
9506_at	147.8	A	hypothetical protein
9462_at	1248.6	P	mitochondrial inner membrane protease
9463_at	2838.1	P	similarity to Asm4p
9464_at	13.6	A	questionable ORF
9465_at	233.6	A	Involved in proteolytic processing of Rim1p
9466_at	459.9	P	weak similarity to E.coli hypothetical protein f402
9467_at	572.2	P	weak similarity to S.pombe hypothetical protein SPAC23C11
9468_at	2495.9	P	hypothetical protein
9469_at	1002.7	P	weak similarity to E.coli ribosomal S8 protein
9470_at	-171.5	A	questionable ORF
9471_at	60.3	A	Protein homologous to human Sin3 complex component SAP18, possible coiled-coil protein
9472_at	1472.1	P	weak similarity to fruit fly ecdysone-inducible protein
9473_at	1211.4	P	Homologous to E coli dnaJ protein
9474_at	788.0	P	similarity to ATPases
9475_at	302.0	P	hypothetical protein
9476_at	1096.7	P	Predicted 758 amino acid polypeptide with poly-glutamine and poly-asparagine domains
9477_at	1639.5	P	involved in plasmid maintenance
9478_at	2025.2	P	similarity to members of the mitochondrial carrier protein family
9479_at	329.9	A	MutL homolog, forms a complex with Pms1p and Msh2p to repair mismatched DNA
9480_at	384.9	P	contains an N-terminal Zn2Cys6 type zinc finger domain, a C-terminal acidic domain and a putative coiled coil dimerization domain
9481_at	363.3	P	Aldehyde Dehydrogenase (NAD(P)+)
9482_g_at	2093.6	P	Aldehyde Dehydrogenase (NAD(P)+)
9483_at	648.9	P	aldehyde dehydrogenase, (NAD(P)+), likely cytosolic
9439_at	588.5	P	similarity to YKL124w
9440_at	423.8	P	similarity to MSN1 protein
9441_at	-463.8	A	questionable ORF
9442_s_at	6241.0	P	

flocculent specific protein\; contains >35 repeats of the amino acid sequence NNNDSYGS
9443_at 9394.8 P
questionable ORF
9444_at 1545.3 P
Cytoplasmic inhibitor of proteinase Pep4p
9445_at -29.5 A
protein of unknown function
9446_at 590.4 P
ExtraCellular Mutant
9447_at 1446.7 P
Protein involved in mitochondrial iron accumulation
9448_at 2017.0 P
similarity to C.elegans hypothetical protein
9449_at 290.4 P
non-specific DNA binding protein
9450_at 702.0 P
similarity to YPL228w
9451_at 838.8 P
similarity to YPL229w
9452_at 152.3 A
Putative transcriptional repressor with proline-rich zinc fingers
9453_at 3632.4 P
SSO1 and SSO2 encode syntaxin homologs\; act in late stages of secretion
9454_at 3733.3 P
hypothetical protein
9455_at 1321.5 P
hypothetical protein
9456_at 8960.9 P
constitutively expressed heat shock protein
9457_g_at 5607.9 P
constitutively expressed heat shock protein
9458_at 2871.1 P
hypothetical protein
9459_at 1545.5 P
weak similarity to bacterial ribosomal protein S17
9460_at 5575.1 P
Glycine decarboxylase complex (P-subunit), glycine synthase (P-subunit), Glycine cleavage system (P-subunit)
9461_at 802.8 P
has DNA helicase signature motifs
9416_at 3107.6 P
hypothetical protein
9417_at 198.3 P
similarity to mouse Tbc1 protein
9418_at 3531.2 P
Mitochondrial ribosomal protein MRPL24 (YmL24)
9419_at 506.4 P
questionable ORF
9420_i_at 4452.9 P
Ribosomal protein L36A (L39) (YL39)
9421_s_at 13850.6 P
Ribosomal protein L36A (L39) (YL39)
9422_at 6952.4 P
similarity to YPL250c
9423_at 891.3 P
hypothetical protein

9424_at 2803.1 P
Vti1p is a v-SNARE that interacts with two t-SNARES, Sed5p and Pep12p
9425_at 1901.3 P
spindle pole body associated protein
9426_at 2322.7 P
G(sub)1 cyclin
9427_at 4750.9 P
putative membrane protein
9428_at 611.3 P
human xeroderma pigmentosum group A DNA repair gene homolog
9429_at 15271.8 P
C-8 sterol isomerase
9430_at 10761.1 P
Mitochondrial outer membrane protein\; forms the outer membrane import channel
9431_at 659.6 P
weak similarity to D.melanogaster hypothetical protein DMC39E1
9432_at 12078.6 P
phosphofructokinase beta subunit
9433_at -195.9 A
weak similarity to hypothetical protein YNR014w
9434_at 1134.6 P
Similar to acetyl-coenzyme A carboxylase
9435_at 6225.7 P
mevalonate kinase
9436_at 1452.6 P
hypothetical protein
9437_at 1597.4 P
similarity to P.glauca late embryogenesis abundant protein and YBR177c and YPL095c
9438_at 1114.1 P
weak similarity to beta tubulins
9394_at 2626.1 P
weak similarity to myosins
9395_at 433.6 P
S. cerevisiae homologue of S. pombe cdc5+
9396_at 4645.5 P
dnaJ homolog
9397_at 6873.7 P
similarity to GAS1 protein
9398_at 6187.1 P
Serine Protein Kinase
9399_at 11463.0 P
GMP synthase
9400_at 1298.3 P
hypothetical protein
9401_at 1269.7 P
Establishes Silent omatin
9402_at 10796.9 P
48 kDa Phosphomevalonate kinase
9403_at 7717.9 P
weak similarity to photosystem II protein D2
9404_at 5687.6 P
similarity to S.pombe dihydrofolate reductase
9405_at 1695.2 P
encodes putative deubiquitinating enzyme
9406_at 949.3 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 2380.6 P
Mitochondrial ribosomal protein MRPL44 (YmL44)
9408_at 1617.6 P
Mitochondrial ribosomal protein MRPL44 (YmL44)
9409_at 11461.8 P
similarity to ketoreductases
9410_at 1031.1 P
TFIID subunit
9411_at 1643.1 P
Mitochondrial RNA polymerase specificity factor
9412_at 9561.8 P
Protein required for processing of pre-rRNA
9413_f_at 339.1 P
Ribosomal protein S10B
9414_f_at 8357.9 P
Ribosomal protein S10B
9415_at 458.0 P
peripheral vaculor membrane protein\; putative Zn-finger protein
9371_at 565.7 A
involved in cell fusion during mating, also required for the alignment of parental nuclei before nuclear fusion
9372_at 2715.9 P
strong similarity to YOR295w
9373_at 492.2 P
ribonuclease H
9374_at 6595.5 P
Protein involved in RNA processing and export from nucleus
9375_at 7657.1 P
TFIID subunit
9376_at 4813.8 P
similarity to CHS6 protein
9377_at 6460.9 P
Protein required for filamentous growth, cell polarity, and cellular elongation
9378_at 1627.4 P
Ribonuclease III
9379_at 682.3 P
U2 snRNP protein
9380_at 9313.8 P
DNA-binding protein, mtDNA stabilizing protein, mitochondrial inner membrane protein with low homology to RIM2
9381_s_at 14763.5 P
Ribosomal protein L20A (L18A)
9382_at 9755.7 P
Zinc- and cadmium-resistance protein
9383_at 156.9 A
similarity to Uth1p, Nca3p, YIL123w and Sun4p
9384_at 2429.8 P
questionable ORF
9385_at 1239.9 P
weak similarity to mouse thyrotropin-releasing hormone receptor
9386_at 7547.0 P
long-chain fatty acid--CoA ligase and synthetase 4
9387_at 5251.1 P
hypothetical protein

9388_at 804.5 P
similarity to glutamate decarboxylases
9389_at 179.8 A
strong similarity to YKR076w and YGR154c
9390_at 7024.5 P
hyperosmolarity-responsive gene
9391_at 1214.0 P
hypothetical protein
9392_at 805.7 P
strong similarity to YPL264c
9393_at 183.1 P
hypothetical protein
9349_at 1047.2 P
hypothetical protein
9350_at 10303.2 P
subunit VII of cytochrome c oxidase
9351_at 559.5 P
translational activator of cytochrome c oxidase subunit II
9352_at 1222.9 P
hypothetical protein
9353_at 2014.0 P
hypothetical protein
9354_at 8669.4 P
Translation initiation factor eIF1A
9355_at 4244.0 P
115 kD regulatory subunit of trehalose-6-phosphate synthase\/phosphatase complex
9356_at 1008.9 P
similarity to S.pombe scn1 protein
9357_at 1432.5 P
subunit of the histone deacetylase B complex
9358_at 4371.7 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 810.6 P
hypothetical protein
9360_at 8495.8 P
similarity to A.thaliana hyp1 protein
9361_at 1851.4 P
mitochondrial inorganic pyrophosphatase
9362_at 487.2 P
U4\/U6 snRNA-associated splicing factor
9363_at 2312.9 P
weak similarity to C.elegans hypothetical protein CELT23B3
9364_at 1535.0 P
Upstream activation factor subunit
9365_at 661.9 P
Orotate phosphoribosyltransferase 2
9366_at 7639.0 P
desaturase\/hydroxylase enzyme
9367_at 2170.8 P
Negative regulator of cell polarity
9368_at 805.5 P
Protease involved in ras and a-factor terminal proteolysis
9369_at 2213.3 P
Involved in the ubiquination pathway, possibly by functioning with Rsp5
9370_at 11144.6 P

ubiquitin-like protein
9326_at 1885.1 P
TFIIF interacting Component of CTD Phosphatase
9327_at 1654.1 P
similarity to phosphomannomutases
9328_at 205.7 A
strong similarity to aminotriazole resistance protein
9329_at 40.7 A
Zinc-cluster protein involved in activating gluconeogenic genes\; related to Gal4p
9330_at 2016.1 P
hypothetical protein
9331_at 923.9 P
basic, hydrophilic 67.5 kDa protein
9332_at 743.3 P
Initiator methionine tRNA 2 -O-ribosyl phosphate transferase
9333_at 884.3 P
DNA binding protein
9334_at 1149.9 P
similarity to Ccr4p
9335_at 4802.6 P
Mitochondrial ribosomal protein MRPL33 (YmL33) (E. coli L30)
9336_at 656.0 P
Protein essential for mitochondrial biogenesis
9337_at 989.5 P
strong similarity to hypothetical S.pombe and C.elegans proteins
9338_at 1790.0 P
hypothetical protein
9339_at 5870.5 P
Putative RNA-dependent helicase
9340_at 30.5 A
questionable ORF
9341_at 2519.1 P
similarity to ser/thr protein kinase
9342_at 8723.9 P
strong similarity to C.elegans hypothetical protein
9343_at 739.7 P
similarity to amidases
9344_at 288.6 P
Coiled-coil domain protein required for proper nuclear migration during mitosis (but not during conjugation)
9345_at 787.9 A
questionable ORF
9346_at 13097.1 P
similarity to YGR273c
9347_at 7990.3 P
Probable component of serine palmitoyltransferase, which catalyzes the first step in biosynthesis of long-chain sphingolipids
9348_at 11489.6 P
carboxypeptidase Y (proteinase C)
9304_at 9414.8 P
hypothetical protein
9305_at 416.5 P
weak similarity to hypothetical protein YJL062w
9306_at 1095.6 P
phosphoribosylpyrophosphate amidotransferase
9307_at 2075.8 P

mitochondrial ABC transporter protein

9308_at 2157.0 P

Integral membrane mitochondrial protein

9309_at 1477.7 P

alcohol dehydrogenase II

9310_at 1283.9 P

encodes putative deubiquitinating enzyme

9311_at 447.4 P

questionable ORF

9312_at 13130.3 P

member of the glucanase gene family

9313_at 45.8 P

Protein with similarity to Gls1p and Gls2p (GB:Z49212)

9314_at 202.6 A

questionable ORF

9315_at 9293.1 P

cell surface glycoprotein 115-120 kDa

9316_at 12483.8 P

Karyopherin

9317_at 6705.5 P

~100 kDa cytoplasmic protein

9318_at 3545.2 P

similarity to YGR283c

9319_at 1550.5 P

Regulates activity of protein phosphatase 1, Glc7p, which is involved in proper chromosome segregation

9320_at 4401.0 P

hypothetical protein

9321_at 990.3 P

similarity to YKR089c and YOR081c

9322_at 11786.0 P

alpha-type of subunit of 20S proteasome

9323_at 8901.8 P

similarity to hypothetical S. pombe protein

9324_at 6375.6 P

similarity to YOR385w and YNL165w

9325_at 955.0 P

questionable ORF

9281_at 832.6 P

questionable ORF

9282_at 34.4 A

similarity to mucins, glucan 1,4-alpha-glucosidase and exo-alpha-sialidase

9283_at 8778.3 P

strong similarity to alcohol-dehydrogenase

9284_at 1218.0 P

Low-affinity Fe(II) transport protein

9285_at 601.9 P

hypothetical protein

9286_s_at 7277.0 P

strong similarity to hypothetical proteins YPL273w and YLL062c

9287_s_at 373.7 P

strong similarity to YPL280w, YOR391c and YDR533c

9288_s_at 808.3 P

strong similarity to phosphopyruvate hydratases

9289_at 225.3 P

strong similarity to YBL108w, YCR103c and YKL223w

9290_f_at 1761.9 P

strong similarity to members of the Srp1p/Tip1p family
9291_at 11298.9 P
protein associated to the ATP synthase
9292_at 187.9 P
hypothetical protein identified by SAGE
9293_at 644.3 P
identified by SAGE
9294_at 7668.3 P
hypothetical protein
9295_g_at 4213.7 A
hypothetical protein
9296_at 217.5 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 525.9 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 517.0 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 418.5 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 41.0 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 100.3 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 12.9 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 370.5 P
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 -44.1 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 228.6 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 339.7 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 -8.8 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 276.2 A
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 695.9 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 652.7 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 546.4 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 1110.2 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 11978.4 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 1008.1 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 4390.0 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 -35.2 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 6326.3 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 70.9 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 -172.1 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 87.7 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 70.7 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 80.5 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 41.3 A
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 -43.1 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 251.7 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 330.6 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 59.2 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 798.8 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 914.2 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 1016.4 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 324.0 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 164.8 M
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 53.8 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 1848.5 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 -58.3 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 143.1 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 132.0 P
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 -78.5 A
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 749.9 P
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 663.8 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 191.9 P
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 -1.1 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 -40.4 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 396.1 A
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 14657.8 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 12976.7 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 621.0 P
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 -114.8 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 -90.6 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 -79.8 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 5683.8 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 1708.1 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 5127.9 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 -212.0 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 29.6 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 -170.3 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 422.4 P
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 140.4 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 472.6 A
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 453.3 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 110.8 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 130.0 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 -0.4 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 126.2 M
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 88.2 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 1100.2 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 213.3 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 549.6 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 8160.2 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 5957.7 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 286.8 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 204.9 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 331.2 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 60.5 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 1240.0 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 2728.9 P
snRNA
9187_i_at 192.0 P
Centromere
9188_at 241.8 P
snRNA
9189_at 10980.0 P
snRNA
9190_at 600.9 P
snRNA
9191_at 2411.8 P
snRNA
9192_at 315.2 P
snRNA
9193_at 1319.9 P
snRNA
9194_at 2384.6 P
snRNA
9195_at 8277.2 P
snRNA
9196_s_at 293.6 A
similarity to M.verrucaria cyanamide hydratase, identical to hypothetical protein YFL061w
9197_s_at 2768.0 P
SNZ2 proximal ORF, stationary phase induced gene
9198_s_at 949.9 P
Snooze: stationary phase-induced gene family
9199_at 2414.4 P
Hypothetical aryl-alcohol dehydrogenase
9200_at 2420.6 P

histone deacetylase
9201_at 1165.2 P
Member of the AAA-protein family that includes NSFp and PEX1p
9202_at 316.0 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 6551.6 P
Cell-cycle regulation protein, may be involved in the correct timing of cell separation after cytokinesis
9204_at 1447.4 P
similarity to YOL003c, YLR246w and C.elegans hypothetical protein ZK757.1
9205_at 898.2 P
FIG4 expression is induced by mating factor.
9206_at 317.2 A
hypothetical protein
9207_at 3998.4 P
strong similarity to YCR094w and YNR048w
9208_at 10128.7 P
Cell wall beta-glucan assembly
9163_at 3639.0 P
weak similarity to Vcx1p
9164_at 3639.7 P
strong similarity to S.pombe Bem46 protein
9165_at 350.1 A
questionable ORF
9166_at 7.6 A
hexose transport protein
9167_at 1035.8 P
similarity to A.thaliana PRL1/2 protein
9168_at 1480.3 P
prephenate dehydratase
9169_at 4168.1 P
essential for assembly of a functional F1-ATPase
9170_at 911.1 P
positive regulator of allophanate inducible genes
9171_at 2120.5 P
similarity to C.elegans hypothetical protein
9172_at 5864.9 P
subunit 2 of replication factor RF-A\; 29\% identical to the human p34 subunit of RF-A
9173_at 420.4 P
hypothetical protein
9174_at 3202.9 P
similarity to S.pombe hypothetical protein SPAC24H6.02c
9175_at 698.5 A
Binds Sin3p in two-hybrid assay and is present in a large protein complex with Sin3p and Stb2p
9176_at 7123.8 P
similarity to S.pombe and C.elegans hypothetical proteins
9177_at 9228.1 P
43.1 kDa Serine\/threonine\/tyrosine protein kinase
9178_at 2481.3 P
ribosomal protein of the small subunit, mitochondrial
9179_at 7053.3 P
similarity to C-term. of A.nidulans regulatory protein (qutR)
9180_at 672.4 P
similarity to Ypt1p and rab GTP-binding proteins
9181_at 1214.1 P
hypothetical protein

9182_s_at 9498.0 P
Ribosomal protein S19B (rp55B) (S16aB) (YS16B)
9183_s_at 7682.5 P
Ribosomal protein L18B (rp28B)
9184_at 11715.8 P
Ribosomal protein L18B (rp28B)
9185_at 10503.9 P
hypothetical protein
9140_at 447.1 P
exhibits homology to Trf4p and Top1p
9141_at 2153.6 P
protein kinase, homologous to Ste20p, interacts with CDC42
9142_at 3153.4 P
similarity to S.pombe hypothetical protein SPAC23D3.13c
9143_at 66.2 A
questionable ORF
9144_at 416.6 P
hypothetical protein
9145_at 1144.2 P
hypothetical protein
9146_at 823.5 P
Multicopy Suppressor of Bud Emergence
9147_at 3034.0 P
Pseudouridine synthase
9148_at 3125.3 P
N-glycosylated integral plasma membrane protein
9149_at 2226.7 P
Subunit 3 of Replication Factor C\; homologous to human RFC 36 kDa subunit
9150_at 1195.4 P
G(sub)1 cyclin that associates with PHO85
9151_at 3132.4 P
strong similarity to C.elegans hypothetical protein
9152_at 9091.8 P
non-clathrin coat protein involved in transport between ER and Golgi
9153_at 1072.7 P
Cold sensitive U2 snRNA Supressor
9154_at 366.7 P
hypothetical protein
9155_at 2639.5 P
Mitochondrial ribosomal protein MRPL10 (YmL10)
9156_at 3442.5 P
Putative integral membrane protein containing novel cysteine motif. Similarity to SLG1 (WSC1), WSC3 and WSC4
9157_at 1385.0 P
involved in processsing of tRNAs and rRNAs
9158_at 7788.4 P
strong similarity to YDR214w
9159_at 5822.0 P
sterol C-14 reductase
9160_at 979.7 P
hypothetical protein
9161_at 1616.6 P
similarity to YLR187w
9162_at 260.8 P
homoserine O-trans-acetylase
9118_at 536.2 A

questionable ORF
9119_at 1256.5 P
similarity to human band 3 anion transport protein
9120_at 1594.6 P
similarity to glycerate- and formate-dehydrogenases
9121_at 1971.9 P
topoisomerase I interacting factor 1
9122_at 929.5 P
Protein with coiled-coil domain essential for vesicular transport
9123_at 4895.7 P
contains formin homology domains\; homologous to BNR1 (BNI1 related protein)
9124_at 869.7 P
Protein highly homologous to permeases Can1p and Lyp1p for basic amino acids
9125_at 131.9 P
hypothetical protein
9126_at 9378.7 P
lysine permease
9127_at 2005.9 P
Phosphatidylinositol 4-kinase
9128_at 411.6 P
questionable ORF
9129_at 810.2 P
similarity to human protein KIAA0174
9130_at 2287.6 P
weak similarity to Sec14p
9131_at 5997.6 P
YIP1-Interacting Factor, shows similarity to NADH dehydrogenases
9132_at 2979.8 P
DNA polymerase II
9133_at 1565.9 P
Fifth largest subunit of origin recognition complex\; contains possible ATP-binding site
9134_at 598.9 P
hypothetical protein
9135_at 5502.7 P
Antioxidant protein and metal homeostasis factor, protects against oxygen toxicity
9136_at 1642.4 P
hypothetical protein
9137_at 1376.8 P
Interacts with SNF1 protein kinase
9138_at 2405.7 P
similarity to bacterial dihydropteroate synthase
9139_at 11578.8 P
strong similarity to nucleic acid-binding proteins
9095_at 322.0 P
hypothetical protein
9096_at 668.1 P
hypothetical protein
9097_at 2575.9 P
ribosomal protein of the large subunit (YmL30), mitochondrial
9098_at 2232.3 P
RNA recognition motif-containing protein that participates in sequence-specific regulation of nuclear pre-mRNA abundance
9099_at 684.3 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 188.0 P
similarity to YDR109c
9101_at 8163.0 P
49-kDa alpha subunit of RNA polymerase A
9102_at 6444.0 P
cysteinyl-tRNA synthetase
9103_at 2723.4 P
similarity to D.melanogaster SET protein
9104_at 466.2 P
hypothetical protein
9105_at 9425.0 P
translation initiation factor 3 (eIF3)
9106_at 8013.0 P
transmembrane protein
9107_at 1217.1 P
similarity to human hypothetical protein KIAA0404
9108_at 10215.1 P
Glucose-6-phosphate dehydrogenase
9109_at 2164.6 P
strong similarity to K.marxianus LET1 protein
9110_at 5075.1 P
Ca2+-dependent serine protease
9111_at 462.0 P
Yeast putative Transmembrane Protein
9112_at 2923.9 P
component of RNA polymerase II holoenzyme\/mediator complex
9113_at 509.5 P
questionable ORF
9114_at 567.7 P
weak similarity to mouse hemoglobin zeta chain
9115_at 2106.8 P
Is required to link Chs3p and Chs4p to the septins
9116_at 3543.4 P
hypothetical protein
9117_at 10187.4 P
weak similarity to Sec14p
9073_at 1312.4 P
weak similarity to mammalian transcription elongation factor elongin A
9074_at 2408.9 P
transcriptional regulator, putative glutathione transferase
9075_at 483.4 P
similarity to dnaJ-like proteins
9076_at 63.0 A
questionable ORF
9077_at -166.8 A
questionable ORF
9078_at 917.7 P
chaotic nuclear migration\; predicted mass is 67kDa
9079_at 950.1 P
hypothetical protein
9080_at 225.3 P
Aut2p interacts with Tub1p and Tub2p\; Aut2p forms a protein complex with Aut7p\; Aut2p mediates attachment of autophagosomes to microtubules
9081_at 2663.5 P
functionally related to TFIIB, affects start site selection in vivo
9082_at 3036.8 P

Component of nuclear RNase P and RNase MRP
9083_at 10342.7 P
adenylosuccinate synthetase
9084_at 5490.2 P
mannosyltransferase
9085_at 122.1 M
similarity to E.coli hypothetical protein in serS 5 region
9086_at 2848.1 P
weak similarity to E.coli bis(5 -nucleosyl)-tetraphosphatase
9087_at 1935.9 P
repressor activator protein
9088_at 586.6 P
similarity to hypothetical S. pombe protein
9089_at 312.4 A
23 kDa peroxisome associated protein, binds Pex14p
9090_at 1016.0 P
hypothetical protein
9091_at 3477.9 P
weak simlarity to C.cardunculus cypro4 protein
9092_at 1193.4 P
hypothetical protein
9093_at 52.5 M
encodes protein with RNA-binding motifs required for MRE2-dependent mRNA splicing
9094_s_at 10377.9 P
Heat shock protein of HSP70 family, homolog of SSB1
9050_at 10957.9 P
weak similarity to Colletotrichum gloeosporioides nitrogen starvation-induced glutamine rich protein
9051_at 5310.2 P
similarity to M.jannaschii hypothetical protein MJ1073
9052_at 1590.1 P
similarity to structure-specific recognition proteins
9053_at -132.2 A
questionable ORF
9054_g_at 31.5 A
questionable ORF
9055_at 257.2 P
sporulation-specific protein
9056_at -291.2 A
weak similarity to B.subtilis CDP-diacylglycerol--serine O-phosphatidyltransferase
9057_at 771.0 P
peroxisomal 2,4-dienoyl-CoA reductase
9058_at 1189.7 P
involved in regulation of carbon metabolism
9059_at 1320.9 P
strong similarity to human TGR-CL10C
9060_at 964.9 P
Activates transcription of glycolytic genes\; homologous to GCR1\; may function in complex with Gcr2p
9061_at 232.1 A
questionable ORF
9062_at 1844.4 P
Protein involved in regulation of cell size
9063_at -206.8 A
sporulation-specific protein with a leucine zipper motif, regulated by the transcription factor Ume6 and expressed early in meiosis
9064_at 959.5 P
hypothetical protein

9065_at -103.2 A
strong similarity to YDL222c and similarity to Sur7p
9066_at 1326.9 P
hypothetical protein
9067_at 5448.3 P
chitin synthase 1
9068_at 1755.1 P
similarity to Synechocystis hypothetical protein
9069_at 12769.1 P
hypothetical protein
9070_at 5454.6 P
karyopherin alpha homolog of 60 kDa
9071_at 560.5 P
involved in spindle pole body duplication and karyogamy, interacts with Cdc31p, localizes to the spindle pole body
9072_at 708.0 P
hypothetical protein
9028_at 9005.1 P a
deubiquitinating enzyme
9029_at 1089.9 P
ribosomal protein of the large subunit, mitochondrial
9030_at 1210.7 P
questionable ORF
9031_at 1644.9 P
protein kinase homolog
9032_at 1942.7 P
weak similarity to S.pombe hypothetical protein
9033_at 3569.7 P
similarity to hypothetical S. pombe protein
9034_at 540.3 P
hypothetical protein
9035_at 10304.6 P
Ribosomal protein S3 (rp13) (YS3)
9036_at 1045.4 P
hypothetical protein
9037_at 2322.3 P
weak similarity to Hkr1p
9038_at 5601.9 P
similarity to S.pombe Rnp24p
9039_at 773.3 P
hypothetical protein
9040_at 930.5 P
multicopy suppressor of bem1 mutation, may be involved in G-protein mediated signal transduction
9041_at 2143.5 P
Component of the anaphase-promoting complex
9042_at 222.8 P
questionable ORF
9043_at 251.6 P
questionable ORF
9044_at 8509.7 P
Phosphatidylserine Decarboxylase 1
9045_at 3695.4 P
similarity to C.elegans ZK688.3 protein and E.coli hpcEp
9046_at 2547.2 P
CREB like repressor, bZIP protein that binds to CRE motifs, interacts with Mig1p
9047_at 1875.5 P

hypothetical protein
9048_at 1476.6 P
similarity to YOR385w and YMR316w
9049_at 1947.4 P
hypothetical protein
9005_at 2628.8 P
translation elongation factor eEF4
9006_s_at 10992.7 P
Ribosomal protein L42A (YL27) (L41A)
9007_at 1463.3 P
Protein kinase
9008_at 10069.6 P
YGP1 encodes gp37, a glycoprotein synthesized in response to nutrient limitation which is homologous to the sporulation-specific SPS100 gene
9009_at 1165.4 P
hypothetical protein
9010_at 1190.8 P
hypothetical protein
9011_at 5634.7 P
weak similarity to S.pombe hypothetical protein SPAC10F6
9012_at 6613.3 P
similarity to YHR133c
9013_at 1942.2 P
hypothetical protein
9014_at 3441.3 P
membrane-bound casein kinase I homolog
9015_at 6235.0 P
Putative homolog of subunit 4 of bovine prefoldin, a chaperone comprised of six subunits
9016_at 1496.0 P
hypothetical protein
9017_at 3307.8 P
31-kDa subunit of RNA polymerase III (C)\; HMG1 like protein
9018_at 1420.4 P
hypothetical protein
9019_at 5116.7 P
weak similarity to S.pombe hypothetical protein
9020_at 578.1 A
cofactor B
9021_at 1779.3 P
Sm-like protein
9022_at 290.3 P
hypothetical protein
9023_at 450.8 A
mating a-factor pheromone precursor
9024_at 220.6 P
similarity to YHR131c
9025_at 232.0 A
hypothetical protein
9026_at 663.9 P
Ammonia transport protein
9027_at 6852.7 P
Adenosine deaminase\/adenine aminohydrolase
8982_i_at 789.1 P
questionable ORF
8983_s_at 1908.9 P
questionable ORF

8984_at 11265.7 P
70-kDa adenylyl cyclase-associated protein
8985_at 4300.2 P
putative mitochondrial S4 ribosomal protein
8986_at 1257.4 P
similarity to neurofilament triplet M protein
8987_at 9627.4 P
peptidylprolyl cis-trans isomerase
8988_at 8619.9 P
similarity to C.carbonum toxD gene
8989_at 1038.2 P
hypothetical protein
8990_at 1568.6 P
similarity to A.ambisexualis antheridiol steroid receptor
8991_at 4638.4 P
Mitochondrial import receptor complex protein
8992_at 8758.0 P
sn-1,2-diacylglycerol cholinephosphotransferase
8993_at 1897.8 P
weak similarity to M.pneumoniae uridine kinase udk
8994_at 271.2 A
Similar to human tumor suppressor gene known as TEP1, MMAC1 and PTEN1. Contains sequence motifs characteristic of protein tyrosine phosphatases.
8995_at 1157.1 P
similarity to C.elegans hypothetical protein
8996_at 189.2 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 4898.4 P
Protein with similarity to mammalian monocarboxylate transporters MCT1 and MCT2
8998_at 2190.3 P
similarity to hypothetical S. pombe protein
8999_at 6323.7 P
weak similarity to C.jejuni serine protease
9000_at 704.3 P
hypothetical protein
9001_at 6284.6 P
70 kDa mitochondrial specialized import receptor of the outer membrane
9002_at 313.6 A
questionable ORF
9003_at 1917.0 P
weak similarity to M.jannaschii hypothetical protein MJ1257
9004_at 957.6 P
essential suppressor of the respiratory deficiency of a pet mutant
8959_at 294.9 A
carbon-catabolite sensitive malate synthase
8960_at 1468.0 P
weak similarity to RING zinc finger protein from Gallus gallus
8961_at 1417.6 P
weak similarity to S.pombe hypothetical protein SPAC23C11
8962_at 1522.8 P
questionable ORF
8963_at 9814.4 P
subunit common to RNA polymerases I (A) and III (C)
8964_at 6781.6 P
ATP-dependent RNA helicase of DEAD box family

8965_at 9431.6 P

ATP-dependent RNA helicase of DEAD box family

8966_at 10798.3 P

cytochrome b5

8967_at 6655.1 P

weak similarity to fruit fly RNA-binding protein

8968_at 324.0 P

weak similarity to cytochrome-c oxidase

8969_at 3411.2 P

strong similarity to YOR110w

8970_at 1636.8 P

similarity to human AF-9 protein

8971_at 1436.8 P

inositol polyphosphate 5-phosphatase

8972_at 73.7 A

questionable ORF

8973_at 8596.0 P

alpha-isopropylmalate synthase (2-Isopropylmalate Synthase)

8974_at 1254.3 P

member of the leucine zipper family of transcriptional activators

8975_at 6367.9 P

DNA polymerase I alpha subunit, p180

8976_at 2569.8 P

similarity to YKL146w

8977_at 1835.6 P

hypothetical protein

8978_at 4769.9 P

similarity to YNL032w, YNL056w and YDR067c

8979_at 7453.8 P

Ras proto-oncogene homolog

8980_at 703.4 P

involved in transcriptional regulation of PHO5

8981_at 10019.5 P

Ribosomal protein S7B (rp30)

8936_at 14867.0 P

Ribosomal protein S7B (rp30)

8937_at 879.4 P

strong similarity to YOR092w

8938_at 1193.1 P

similarity to S.pombe hypothetical protein

8939_at 37.6 A

rab5-like GTPase involved in vacuolar protein sorting and endocytosis

8940_at 68.9 A

similarity to hypothetical C. elegans proteins Y48E1C.2 and Y48E1C.c

8941_at 3256.7 P

similarity to chicken h-caldesmon, Uso1p and YKL201c

8942_at 2692.0 P

GTP-binding protein of the rho subfamily of ras-like proteins

8943_at -62.9 A

questionable ORF

8944_at 2929.7 P

topoisomerase II, Top2p localizes to axial cores in meiosis

8945_at 4349.9 P

weak similarity to synaptogamines

8946_at 4278.1 P

hypothetical protein

8947_at 6735.7 P
Protein involved in propagation of M2 dsRNA satellite of L-A virus
8948_at 1413.3 P
Required for endocytosis and organization of the cytoskeleton
8949_at 1743.2 P
weak similarity to rabbit peroxisomal Ca-dependent solute carrier
8950_at 790.8 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 1443.6 P
similarity to ribosomal protein S13
8952_at 3160.8 P
hypothetical protein
8953_at 10475.5 P
tropomyosin I
8954_at 4861.1 P
hypothetical protein
8955_at 456.3 P
similarity to dnaJ protein homolog YDJ1
8956_at 2133.6 P
negative regulator of Ras cAMP pathway, shares weak homology with Spt2p
8957_at 6907.7 P
similarity to YHR088w and C.elegans hypothetical protein F44G4.1
8958_at 1700.4 P
Protein of unknown function
8914_at 1839.7 P
mitochondrial lysine-tRNA synthetase
8915_at 2089.3 P
RNase H(35), a 35 kDa ribonuclease H
8916_at 6023.5 P
Dihydrolipoamide acetyltransferase component (E2) of pyruvate dehydrogenase complex
8917_at 8283.1 P
translocase of the outer mito. membrane
8918_at 13383.6 P
Ribosomal protein L16B (L21B) (rp23) (YL15)
8919_at 1319.8 P
Fork Head homolog two
8920_i_at 12427.3 P
Ribosomal protein L9B (L8B) (rp24) (YL11)
8921_s_at 10014.0 P
Ribosomal protein L9B (L8B) (rp24) (YL11)
8922_at 12036.0 P
Protein involved in the aging process
8923_at 1858.0 P
similarity to resistance proteins
8924_at 8129.4 P
yeast dnaJ homolog (nuclear envelope protein)\; heat shock protein
8925_at 1150.8 P
weak similarity to Mycoplasma protoporphyrinogen oxidase
8926_at 4883.6 P
RNA-binding (zeta) subunit of translation initiation factor 3 (eIF-3)
8927_at 9282.8 P
90-kDa protein, located in nucleolus, that is homologous to a human proliferation-associated nucleolar protein, p120
8928_at 1314.1 P
Actin-related protein

8929_at	5089.7	P	similarity to YIL117c
8930_at	271.1	P	questionable ORF
8931_at	4043.6	P	similarity to YNL032w and YNL099c
8932_at	13786.8	P	Outer mitochondrial membrane porin (voltage-dependent anion channel, or VDAC)
8933_at	2837.2	P	vacuolar protein
8934_at	918.2	P	Tyrosine protein phosphatase involved in adaptation response to pheromone
8935_at	8947.6	P	Cytochrome-c oxidase chain Va
8891_at	1117.4	P	hypothetical protein
8892_at	721.6	P	hypothetical protein
8893_at	1828.2	P	putative zinc finger protein
8894_at	4175.4	P	Required for aspargine-linked glycosylation
8895_at	1245.5	P	similarity to probable transcription factor Ask10p and hypothetical protein YPR115w, and strong similarity to hypothetical protein YIL105c
8896_at	2917.3	P	hypothetical protein
8897_at	4797.3	P	strong similarity to human leukotriene-A4 hydrolase
8898_at	168.7	P	questionable ORF
8899_at	1451.8	P	Bypass of PAM1
8900_at	1440.3	P	weak similarity to Mlp1
8901_at	2093.6	P	weak similarity to M.genitalium alanine--tRNA ligase
8902_at	2513.3	P	90 kd subunit of TFIIIB, also called TFIIIB90 or B or B 90 component
8903_at	1320.1	P	hypothetical protein
8904_at	6207.9	P	alpha-4-beta-4 subunit of mitochondrial isocitrate dehydrogenase 1
8905_at	4074.0	P	involved in secretion of proteins that lack classical secretory signal sequences
8906_at	1311.8	P	hypothetical protein
8907_s_at	-1.2	A	nearly identical to YNL018c
8908_s_at	220.1	A	nearly identical to YNL019c
8909_at	2705.4	P	Tyrosine phosphatase
8910_at	10438.4	P	Histone H3 (HHT1 and HHT2 code for identical proteins)
8911_s_at	10162.6	P	

Histone H4 (HHF1 and HHF2 code for identical proteins)
8912_at 2401.3 P
Putative mannosyltransferase of the KRE2 family
8913_at -171.9 A
questionable ORF
8868_at 1930.8 P
putative transcription factor
8869_at 2647.5 P
similarity to S.pombe hypothetical protein
8870_at 631.4 P
C-type cyclin associated with the Ssn3p cyclin-dependent kinase
8871_at 1044.2 P
weak similarity to YBR271w and YJR129c
8872_at 1477.3 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 2086.7 P
weak similarity to C.burnetii FMU protein
8874_at 2747.3 P
histone deacetylase, shares sequence similarity with Rpd3p, Hos1p, Hos2p, and Hos3p
8875_at 241.7 P
Predicted Ser\/thr kinase
8876_i_at 879.8 P
hypothetical protein
8877_r_at 135.7 A
hypothetical protein
8878_s_at -129.9 A
hypothetical protein
8879_at 9039.1 P
poly(A)+ RNA-binding protein
8880_at 4794.4 P
Proteinase inhibitor I2B (PBI2), that inhibits protease Prb1p (yscB)
8881_at 405.6 A
translation elongation factor eEF3 homolog
8882_at 152.2 P
questionable ORF
8883_at 173.9 P
encodes a protein with high similarity to phospholipase B
8884_at 910.0 P
similarity to hypothetical A. thaliana protein T14G11.21
8885_at 8008.0 P
weak similarity to B.subtilis hypothetical protein ykrX
8886_at 246.0 P
peroxisomal NADP-dependent isocitrate dehydrogenase
8887_at 2872.7 P
similarity to YMR119w
8888_at 10314.3 P
sit4 suppressor, dnaJ homolog
8889_at 3889.8 P
Required for amino acid permease transport from the Golgi to the cell surface
8890_at 1732.3 P
Mitochondrial ribosomal protein MRP7 (YmL2) (E. coli L27)
8845_at 3173.3 P
hypothetical RNA-binding protein
8846_at 1564.9 P
Member of family of mitochondrial carrier proteins

8847_at 7140.3 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 2661.9 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 11275.3 P
citrate synthase. Nuclear encoded mitochondrial protein.
8850_at 243.1 P
Putative transmembrane protein
8851_at 1775.3 P
34-kDa subunit of RNA polymerase III (C)
8852_at 84.4 P
weak similarity to bovine interferon gamma precursor
8853_at 31.0 A
questionable ORF
8854_at 2321.4 P
hydrophilic protein\; has cysteine rich putative zinc finger esential for function
8855_at 709.7 P
Protein involved in autophagocytosis during starvation
8856_at 3166.5 P
weak similarity to human phosphatidylcholine--sterol O-acyltransferase
8857_at 1066.8 P
hypothetical protein
8858_at 1270.2 P
Protein required for accurate mitotic chromosome segregation
8859_at 671.7 P
putative RNA-dependent ATPase
8860_at 1446.0 P
Uridine kinase
8861_at 6503.4 P
similarity to Pho87p and YJL198w
8862_at 145.1 A
weak similarity to hypothetical protein YMR206w
8863_at 2652.3 P
Suppressor of Mitochondrial Mutation in the tRNAasp gene
8864_at 12842.3 P
acetyl-CoA carboxylase
8865_at 7211.1 P
23 kDa mitochondrial inner membrane protein
8866_at 8373.6 P
hypothetical protein
8867_at 3997.5 P
Acyl-CoA cholesterol acyltransferase (sterol-ester synthetase)
8823_at 610.6 P
hypothetical protein
8824_at 4023.3 P
hypothetical protein
8825_at 1111.0 P
weak similarity to protein phosphatases
8826_at 1580.6 P
73 kDa subunit of the SWI\/SNF transcription activation complex, homolog of Rsc6p subunit of the RSC chromatin remodeling complex
8827_at 1806.9 P
weak similarity to Rpc31p
8828_at 1151.4 P

questionable ORF
8829_at 2822.9 P
Guanine nucleotide exchange factor for Sar1p.
8830_at 3850.8 P
similarity to human pyridoxal kinase
8831_at 1524.9 P
Cyclophilin
8832_at 4012.8 P
similarity to P.denitrificans cobW protein
8833_at 3515.4 P
ExtraCellular Mutant
8834_at 2935.7 P A
MAP kinase kinase kinase\; activator of Pbs2p
8835_at 3604.1 P
Serine\/threonine protein phosphatase involved in glycogen accumulation
8836_at 2060.0 P
para-aminobenzoate synthase, PABA synthase
8837_at 1263.4 P
shows similarity to glucose-6-phosphate dehydrogenase non-catalytic domains\; homologous to Sol2p and Sol3p
8838_at 3839.0 P
Arp Complex Subunit
8839_at 4857.4 P
strong similarity to ribosomal protein S12
8840_at 1839.1 P
strong similarity to Mycoplasma ribosomal protein S19
8841_at 5010.3 P
putative RNA helicase
8842_at 1698.2 P
weak similarity to Anopheles mitochondrial NADH dehydrogenase subunit 2
8843_at 513.2 P
hypothetical protein
8844_at 2645.6 P
para hydroxybenzoate: polyprenyl transferase
8800_at 944.3 A
hypothetical protein
8801_at 13003.4 P
mevalonate pyrophosphate decarboxylase
8802_at 11864.8 P
anchorage subunit of a-agglutinin
8803_at 494.8 P
translational activator of cytochrome c oxidase
8804_at 6464.8 P
strong similarity to S.pombe hypothetical protein SPAC31A2.02
8805_at 809.4 P
similarity to ser/thr protein kinases
8806_at 629.0 P
strong similarity to YCR094w and YNL323w
8807_at 1673.2 P
small hydrophilic protein, enriched in microsomal membrane fraction, interacts with Sec1p
8808_at 7434.2 P
Saccharopine dehydrogenase (NADP+, L-glutamate forming) (saccharopine reductase) (EC 1.5.1.10)
8809_at 1430.3 P
weak similarity to chicken nucleolin
8810_at 4832.4 P
Putative transcription factor

8811_at	6823.8	P	strong similarity to human breast tumor associated autoantigen
8812_at	5239.3	P	strong similarity to human breast tumor associated autoantigen
8813_at	2035.9	P	similarity to C.elegans hypothetical protein CEESL47F
8814_at	5864.8	P	Putative ion transporter similar to the major facilitator superfamily of transporters
8815_at	223.3	A	transmembrane regulator of KAPA\/DAPA transport
8816_at	848.6	P	dethiobiotin synthetase
8817_at	651.6	P	7,8-diamino-pelargonic acid aminotransferase (DAPA) aminotransferase
8818_at	193.7	P	similarity to to alpha-1,3-mannosyltransferase
8819_at	450.5	P	similar to FRE2
8820_at	1068.4	P	weak similarity to hypothetical protein YDL218w
8821_at	190.6	A	weak similarity to H.influenzae L-lactate permease (lctP) homolog
8822_at	79.8	A	weak similarity to CYC1/CYP3 transcription activator
8776_at	5.5	A	similarity to R.capsulatus 1-chloroalkane halidohydrolase
8777_at	4616.7	P	strong similarity to YJL222w, YIL173w and Pep1p
8778_at	979.7	P	strong similarity to Pep1p
8779_at	6948.8	P	similarity to beta-glucan-elicitor receptor - Glycine max
8780_at	616.0	P	similarity to Bul1p
8781_at	76.0	P	similarity to central part of Bul1p
8782_at	66.0	P	strong similarity to Snq2p
8783_at	256.5	P	strong similarity to UDP-glucose 4-epimerase Gal10p
8784_s_at	371.9	A	strong similarity to E.coli D-mannonate oxidoreductase, identical to YEL070w
8785_at	2993.2	P	weak similarity to B.subtilis nitrite reductase (nirB)
8786_f_at	1639.1	P	member of the seripauperin protein\/gene family
8787_at	2250.5	P	hypothetical protein identified by SAGE
8788_at	1310.0	P	hypothetical protein
8789_s_at	7445.6	P	Aminopeptidase of cysteine protease family
8790_s_at	5427.3	P	protein of unknown function
8791_at	277.4	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 -271.0 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 1123.8 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 73.0 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 205.7 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 943.0 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 168.8 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 -120.4 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 627.9 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 160.3 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 491.1 P
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 17.7 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 2773.8 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 13671.2 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 -266.2 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 36.0 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 -16.2 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 62.7 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 5.9 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 2842.9 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 -118.8 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 541.8 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 1657.8 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 2245.5 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 2129.1 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 58.1 M
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 69.3 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 310.2 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 -10.9 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 4027.4 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 4700.9 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 6812.9 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 812.7 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 1162.3 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 7298.9 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 -21.9 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 -34.3 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 694.1 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 -44.9 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 959.3 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 296.3 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 116.0 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 -146.7 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 89.0 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 66.5 P
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 219.9 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 225.1 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 316.7 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 105.9 M
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 571.4 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 48.0 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 307.7 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 291.0 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 -38.4 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 -33.4 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 1940.2 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 1034.6 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	86.8	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	222.8	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	284.3	P	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	1610.5	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	719.8	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	-161.7	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
8712_r_at	-33.7	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	2251.4	P	snRNA
8714_at	344.8	P	snRNA
8715_at	120.3	A	hypothetical protein
8716_s_at	1432.3	P	Hypothetical aryl-alcohol dehydrogenase (AAD)
8717_at	633.0	P	similarity to Pseudomonas alkyl sulfatase
8718_at	229.8	P	similarity to P.putida phthalate transporter
8719_at	352.6	A	strong similarity to hypothetical protein YIL166c
8720_f_at	239.5	A	strong similarity to members of the Srp1p/Tip1p family
8721_at	-6.8	A	hypothetical protein
8722_at	1365.6	P	hypothetical protein
8723_at	7987.4	P	similarity to subtelomeric encoded proteins
8724_at	1151.4	P	similarity to glucan 1,4-alpha-glucosidase Sta1p and YAR066w
8725_g_at	1805.6	P	similarity to glucan 1,4-alpha-glucosidase Sta1p and YAR066w
8726_at	419.1	P	similarity to S.fumigata Asp FII
8727_at	29.8	A	strong similarity to Cps1p
8728_at	869.0	P	similar to FRE2
8683_at	7159.2	P	induced by osmotic stress\; similar to dihydroflavonol 4-reductase from plants
8684_at	223.9	P	

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questionable ORF
8685_at     1424.1      P
Decapping protein involved in mRNA degradation
8686_at     527.9       P
transcription factor, member of the histone acetyltransferase SAGA complex
8687_at     7594.1      P
Peroxisomal membrane protein
8688_at     2229.6      P
hypothetical protein
8689_at     526.2       P
CTR9 is required for normal CLN1 and CLN2 G1 cyclin expression
8690_at     1142.9      P
hypothetical protein
8691_at     9939.5      P
6,7-dimethyl-8-ribityllumazine synthase (DMRL synthase)
8692_at     7864.1      P
strong similarity to hypothetical S. pombe protein
8693_at     603.5       P
similarity to YDR435c and C.elegans hypothetical protein
8694_at     2194.5      P
Acetylornithine aminotransferase
8695_at     10057.5     P
mRNA cap binding protein eIF-4E
8696_at     1177.1      P
hypothetical protein
8697_at     1056.0      P
weak similarity to tetracycline resistance proteins
8698_at     1017.4      P
6-phosphofructo-2-kinase
8699_at     1382.1      P
Stoichiometric member of mediator complex
8700_at     63.4        A
questionable ORF
8701_at     3467.4      P
High level expression Reduces Ty3 Transposition
8702_at     1230.5      P
similarity to glycophospholipid-anchored surface glycoprotein Gas1p
8703_at     32.5        A
hypothetical protein
8704_at     3568.6      P
ALuminium Resistance 1
8660_at     7139.8      P
similarity to hypothetical S. pombe protein
8661_at     1326.6      P
strong similarity to protein kinase Mck1p
8662_at     12014.6     P
Ribosomal protein L25 (rpl6L) (YL25)
8663_at     10830.9     P
cytosolic malate dehydrogenase
8664_at     1844.2      P
hypothetical protein
8665_at     3639.8      P
weak similarity to M.jannaschii hypothetical protein
8666_at     6122.6      P
Putative polyadenylated-RNA-binding protein located in nucleus\; similar to vertebrate hnRNP A\/B
protein family
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8667_at	3704.8	P	has been localized to both the plasma membrane and the mitochondrial membrane
8668_at	13369.8	P	Ribosomal protein L18A (rp28A)
8669_at	2810.7	P	similarity to monocarboxylate transporter proteins
8670_at	135.7	P	hypothetical protein
8671_at	456.0	P	weak similarity to human sodium channel alpha chain HBA
8672_at	475.7	P	43 kDa protein, transcriptional activator
8673_at	937.9	P	homologous to Trf5p and Top1p, associates with Smc1p and Smc2p
8674_at	309.4	P	similarity to human DS-1 protein
8675_at	648.7	P	Serine\/threonine protein kinase with similarity to Ste20p and Cla4p
8676_at	1327.9	P	Multicopy Suppressor of Bud Emergence
8677_at	5806.1	P	weak similarity to human ubiquitin-like protein GDX
8678_at	2595.6	P	Involved in RAS localization and palmitoylation
8679_at	10174.5	P	Overexpression yields resistance to Zeocin
8680_at	959.5	P	Transcription factor involved in activation of phospholipid synthetic genes
8681_at	685.8	P	weak similarity to human PL6 protein
8682_at	860.2	P	questionable ORF
8638_at	920.8	P	Putative integral membrane protein containing novel cysteine motif. Similarity to SLG1 (WSC1), WSC2 and WSC4
8639_at	335.8	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	5504.7	P	myo-inositol transporter
8641_at	1396.5	P	tRNA 2 -phosphotransferase
8642_at	904.8	P	similarity to YOL002c and YDR492w
8643_at	366.7	P	Ser\/Thr protein kinase
8644_at	97.0	A	questionable ORF
8645_at	7360.6	P	similarity to hypothetical S.pombe protein
8646_at	10874.4	P	cytoplasmic tryptophanyl-tRNA synthetase
8647_at	1407.5	P	3,4-dihydroxy-5-hexaprenylbenzoate methyltransferase
8648_at	761.5	P	Helicase in MItochondria

8649_at 1448.4 P
Subunit 4 of Replication Factor C\; homologous to human RFC 40 kDa subunit
8650_at 1457.7 P
similarity to C.elegans hypothetical protein F25H8.1
8651_at 6341.5 P
strong similarity to YBR147w
8652_at 88.4 P
hypothetical protein
8653_at 1688.4 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 1525.3 P
putative transcription factor\; contains a zinc finger
8655_at 1730.8 P
protein disulfide isomerase related protein
8656_at 1086.7 P
similarity to S.pombe hypothetical protein
8657_at 6273.3 P
Alcohol dehydrogenase
8658_at 13.6 A
hypothetical protein
8659_at 239.9 P
similarity to A.thaliana hyp1 protein
8615_at 902.2 P
similarity to YOL082w
8616_at 2671.8 P
similarity to YOL083w
8617_at 1958.6 P
encodes a GTPase activating protein, highly homologous to Ira1p, homologue of neurofibromin
8618_at 1949.8 P
strong similarity to X.laevis XPMC2 protein
8619_at 228.5 A
similarity to NADH dehydrogenases
8620_at 875.6 P
hypothetical protein
8621_at 6551.9 P
strong similarity to C.elegans K12H4.3 protein
8622_at 2186.2 P
Dislikes Extra CIN8, (MDM) Mitochondrial distribution and morphology
8623_at 1442.1 P
similarity to A.gambiae ATP-binding-cassette protein
8624_at 2055.2 P
hypothetical protein
8625_at 2541.6 P
hypothetical protein
8626_at 1023.6 P
similarity to hypothetical S. pombe protein
8627_at 1320.7 P
hypothetical protein
8628_at 510.7 P
53-kDa coiled-coil protein
8629_at 4747.0 P
Homolog of SIR2
8630_at 317.0 P
Transcription factor (bHLH) involved in interorganelle communication between mitochondria,

peroxisomes, and nucleus
8631_at 2261.8 P
DRAP deaminase
8632_at 756.2 P
inositol polyphosphate 5-phosphatase
8633_at 5358.9 P 3
(2)5 -bisphosphate nucleotidase
8634_at 1163.7 P
hypothetical protein
8635_at 2117.7 P
Clathrin associated protein, medium subunit
8636_at 8044.0 P
Phosphoribosylpyrophosphate synthetase (ribose-phosphate pyrophosphokinase)
8637_at 2445.8 P
similarity to C.elegans hypothetical protein M02F4.4
8592_at 3970.3 P
Glycerol-3-phosphate dehydrogenase (NAD+)
8593_at 8238.0 P
arginosuccinate synthetase
8594_at 503.9 P
similarity to hypothetical C. elegans protein F02E9.6
8595_at 1583.4 P
phosphoglycerate mutase
8596_at 1217.0 P
similarity to B. subtilis transcriptional activator tenA
8597_at 1314.1 P
weak similarity to transcription factors
8598_at 907.1 P
hypothetical protein
8599_at 2505.4 P
DNA Damage Responsive
8600_at 6101.7 P
S-adenosylmethionine decarboxylase
8601_at 2791.3 P
Component of the RNA polymerase II holoenzyme complex, positive and negative transcriptional regulator of genes involved in mating-type specialization
8602_at 180.5 A
questionable ORF
8603_at 4282.0 P
Glutathione Synthetase
8604_at 977.3 P
similarity to YAL018c and YOL047c
8605_at 120.5 P
weak similarity to hypothetical proteins YAL018c and YOL048c
8606_at -31.4 A
questionable ORF
8607_at 2115.8 P
similarity to ser/thr protein kinase
8608_at 1153.2 P
44 kDa phosphorylated integral peroxisomal membrane protein
8609_at 1790.7 P
Endonuclease III-like glycosylase 2
8610_at 1836.6 P
similarity to CCR4 protein
8611_at 1455.7 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 11393.5 P
40S ribosomal protein S15 (S21) (rp52) (RIG protein)
8613_at 9396.3 P
60S acidic ribosomal protein P2A (L44) (A2) (YP2alpha)
8614_at 10783.2 P
alpha-type of subunit of 20S proteasome
8570_at 13.1 A
questionable ORF
8571_at 3538.5 P
weak similarity to YMR317w
8572_at 154.3 P
questionable ORF
8573_at 950.7 P
similarity to S.pombe rad18 and rpgL29 genes and other members of the SMC superfamily
8574_at 476.6 P
Mitochondrial glutamyl-tRNA synthetase
8575_at 697.7 P
hypothetical protein
8576_at 1323.8 P
weak similarity to Y.lipolytica Sls1 protein precursor
8577_at 6785.6 P
strong similarity to glycoprotein Gas1p
8578_at 2009.6 P
hypothetical protein
8579_at 1111.2 P
bZIP protein
8580_at 3277.8 P
similarity to YPR125w
8581_at 7315.8 P
hypothetical protein
8582_at 1961.5 P
Affects longevity
8583_at 123.3 A
hypothetical protein
8584_at 424.4 P
mitochondrial initiation factor 2
8585_at 3443.1 P
weak similarity to rat apoptosis protein RP-8
8586_at 3482.6 P
possible component of RCC1-Ran pathway
8587_at 3514.5 P
Tryptophan permease, high affinity
8588_at 5779.7 P
similarity to Rim9p and YFR012w
8589_at 786.5 P
tSNARE that affects a Late Golgi compartment
8590_at 212.1 P
similarity to YFR013w
8591_at 3304.5 P
Calmodulin-dependent protein kinase
8547_at -22.6 A
weak similarity to YKR015c
8548_at 3450.7 P
hypothetical protein
8549_at 973.4 P

Hmg-coa Reductase Degradation
8550_at 7126.8 P
An evolutionarily conserved member of the histone H2A F\/Z family of histone variants
8551_at 935.4 P
strong similarity to phospholipases
8552_at 2488.2 P
putative RNA 3 -terminal phosphate cyclase
8553_at 1306.7 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 1238.2 P
hypothetical protein
8555_at 1573.9 P
Appears to be a structural component of the chitin synthase 3 complex
8556_at 1792.4 P
topoisomerase I
8557_at 6079.2 P
RNA polymerase II subunit, homologous to S. pombe Rpb11p subunit
8558_at 5425.9 P
DNA binding protein involved in transcriptional regulation
8559_at 1565.0 P
similarity to C.elegans hypothetical protein, YDR126w, YNL326c and YLR246w
8560_at 5104.4 P
strong similarity to YDR492w and S.pombe hypothetical protein
8561_at 1407.5 P
negative transcriptional regulator
8562_at 4945.0 P
Ribosomal RNA Processing
8563_at 3896.7 P
Required for glucosylation in the N-linked glycosylation pathway
8564_at 2011.5 P
subtilisin-like protease III
8565_at 7747.1 P
weak similarity to hypothetical protein YDR339c
8566_at 250.4 P
ATP dependent DNA ligase
8567_at 1605.2 P
similarity to M.jannaschii hypothetical protein MJ0708
8568_at 9360.1 P
small glutamine-rich tetratricopeptide repeat containing protein
8569_at 2113.7 P
Cell wall integrity and stress response component 1
8525_at 18.8 A
Killed In Mutagen, reduced growth in diepoxybutane and\/or mitomycin C
8526_at 1970.2 P
similarity to Tir1p and Tir2p
8527_at 6075.0 P
Cold-shock induced protein of the Srp1p\/Tip1p family of serine-alanine-rich proteins
8528_at 1495.4 P
strong similarity to ATP-dependent permeases
8529_at 492.1 P
similarity to YDR391c
8530_g_at 837.4 P
similarity to YDR391c
8531_at 1451.3 P
strong similarity to YDR391c

8532_at	2541.0	P	B-type regulatory subunit of protein phosphatase 2A (PP2A)
8533_at	4650.4	P	hypothetical protein
8534_at	1841.7	P	p24 protein involved in membrane trafficking
8535_at	2247.4	P	Mitochondrial membrane protein
8536_at	598.0	P	Resistance to o-dinitrobenzene, calcium, and zinc
8537_at	460.8	P	similarity to YDR474c
8538_at	10612.0	P	10 kDa mitochondrial heat shock protein
8539_at	6394.6	P	similarity to Pyrococcus horikoshii hypothetical protein PHBQ041
8540_at	789.8	P	weak similarity to D.melanogaster probable Ca2+ transporter rdgB
8541_at	2731.9	P	hypothetical protein
8542_at	369.4	P	hypothetical protein
8543_at	584.8	P	Homolog of SIR2
8544_at	1435.4	P	Protein required for cell cycle arrest in response to loss of microtubule function
8545_at	10765.0	P	Heat shock protein also induced by canavanine and entry into stationary phase
8546_at	995.4	P	bZIP protein, can activate transcription from a promoter containing a Yap recognition site
8502_at	-0.8	A	hypothetical protein
8503_at	489.6	P	involved in invasive growth upon nitrogen starvation
8504_at	1097.1	P	Metallothionein-like protein
8505_at	300.5	P	myc-family transcription factor homolog
8506_at	889.0	P	Protein that complements a drug-hypersensitive mutation
8507_at	966.3	P	Protein involved in constitutive endocytosis of Ste3p
8508_at	1156.6	P	Required for mother cell-specific HO expression
8509_at	543.3	P	integral membrane protein\; c-terminal TMD\; located in endosome
8510_at	702.4	P	cytochrome c mitochondrial import factor
8511_at	2838.3	P	putative repressor protein\; contains nuclear targeting signal
8512_at	3659.2	P	Casein kinase II, beta subunit
8513_at	477.7	P	Mitochondrial glyoxylase-II
8514_at	371.5	P	questionable ORF

8515_at 1541.6 P
weak similarity to YDR273w
8516_at 1129.2 P
Protein involved in growth regulation
8517_at 3135.7 P
weak similarity to YDR275w
8518_at 11480.2 P
outer mitochondrial membrane protein, component of the mitochondiral protein translocation complex, associates with Isp42p
8519_at 11778.0 P
RNA helicase
8520_at 5033.4 P
homologous to MTH1\; interacts with the SNF1 protein kinase and TBP in two-hybrid and in in vitro binding studies
8521_at 1415.0 P
RNA trafficking protein\; transcription activator
8522_at 4777.5 P
similarity to YER185w, Rta1p
8523_at 254.3 P
hypothetical protein
8524_at 3721.9 P
weak similarity to myosin heavy chain proteins
8480_at 5127.2 P
hypothetical protein
8481_at 1004.6 P
similarity to protamines
8482_at 1161.0 P
similarity to Sis2p protein and C.tropicalis hal3 protein
8483_at 81.5 A
questionable ORF
8484_at 3463.5 P
weak similarity to human phosphorylation regulatory protein HP-10
8485_at 1225.9 P
G2 allele of skp1 suppressor
8486_at 1501.4 P
encodes component of the spindle midzone
8487_at 2847.3 P
weak similarity to YGL144c
8488_at 714.7 P
hypothetical protein
8489_at 6819.6 P
alpha subunit of casein kinase II
8490_at 1631.6 P
strong similarity to YKR075c
8491_at 11926.0 P
Ribosomal protein L3 (rp1) (YL1)
8492_at 2016.9 P
weak similarity to human retinoblastoma binding protein 2
8493_at 4515.5 P
Cytochrome c1
8494_at 2179.7 P
hypothetical protein
8495_at 7108.4 P
glycosyl transferase
8496_at 0.5 A
hypothetical protein

8497_at 1399.6 P
GTPase activating protein
8498_at 1014.4 P
strong similarity to Thi10p
8499_at 514.8 A
hypothetical protein
8500_at 942.4 P
hypothetical protein
8501_at 952.9 P
endoplasmic reticulum t-SNARE, coprecipitates with Sec20p, Tip1p. and Sec22p
8457_at 1380.7 P
similarity to Hbs1p, Sup2p and EF1-alpha
8458_at 294.2 P
similarity to mouse KIN17 protein
8459_at 3858.6 P
weak similarity to YMR172w
8460_at 3636.2 P
Multi-copy suppressor of SOD-linked defects
8461_at 1767.9 P
hypothetical protein
8462_at 5407.0 P
strong similarity to YKR089c
8463_at 1008.9 P
questionable ORF
8464_at 1095.8 P
weak similarity to YKR091w
8465_at 5735.8 P
hypothetical protein
8466_at 7458.5 P
34-kDa, gamma subunit of oligosaccharyl transferase glycoprotein complex
8467_at 3856.6 P
weak similarity to synaptogamines
8468_at 1614.2 P
hypothetical protein
8469_g_at 1820.3 P
hypothetical protein
8470_at 1787.4 P
weak similarity to human calcium influx channel
8471_at 4352.7 P
small GTP-binding protein\; geranylgeranylated\; geranylgeranylation required for membrane association\; also involved in endocytosis post vesicle internalization
8472_at 1590.3 P
similarity to ser/thr protein phosphatases
8473_at 940.4 P
similarity to hypothetical S.pombe protein D83992_G
8474_at 1580.7 P
ExtraCellular Mutant
8475_at 770.2 P
similarity to S.pombe hypothetical protein SPAC22F3.04
8476_at 2760.8 P
GTP-binding ADP-ribosylation factor
8477_at 6371.7 P
Ribose-5-phosphate ketol-isomerase
8478_at 13346.0 P
Ribosomal protein S7A (rp30)
8479_at 5500.5 P

Ribosomal protein S7A (rp30)
8434_at 1018.3 P
hypothetical protein
8435_at 4225.5 P
nuclear pore complex protein
8436_at 6402.3 P
type 2 membrane protein\; probable secretory protein
8437_at 359.7 P
similarity to mitochondrial carrier proteins
8438_at 5338.2 P
ras proto-oncogene homolog
8439_at 118.4 A
questionable ORF
8440_at 2688.8 P
16-kDa, epsilon subunit of oligosaccharyltransferase complex\; 40\% identical to vertebrate DAD1 protein
8441_at 1001.8 P
hypothetical protein
8442_g_at 977.7 P
hypothetical protein
8443_at 383.8 P
member of the syntaxin family of proteins\; predicted C-terminal TMD
8444_at 402.6 A
weak similarity to human G-0/G-1 switch regulatory protein 8
8445_at 5523.1 P
putative isoform of Leu4p
8446_at 3299.3 P
inositol polyphosphate 5-phosphatase
8447_at 2252.8 P
TFIIIC (transcription initiation factor) subunit, 55 kDa
8448_at 393.6 P
weak similarity to B.subtilis maf protein
8449_at 1551.6 P
similarity to C.elegans hypothetical protein
8450_at 307.4 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 278.2 P
hypothetical protein
8452_at 2799.0 P
involved in targeting and fusion of ER to golgi transport vesicles
8453_at 2401.8 P
RNA polymerase III large subunit
8454_at 7755.5 P
Probable 26S protease subunit and member of the CDC48\/PAS1\/SEC18 family of ATPases
8455_at 610.2 P
hypothetical protein
8456_at 866.3 P
similarity to a C.elegans ZK632.3 protein
8412_at 1599.8 P
Similar to mammalian aldo\/keto reductases
8413_at 39.4 M
questionable ORF
8414_at 11936.6 P
profilin (actin-binding protein)
8415_at 4128.8 P
extremely hydrophilic protein

8416_at 3249.8 P
Ubiquitin-specific protease
8417_at 590.6 P
may encode a protein involved in one or more monoxygenase or hydroxylase steps of ubiquinone biosynthesis
8418_at 1587.1 P
isoamyl acetate hydrolytic enzyme
8419_at 2246.7 P
rho type GTPase activating protein
8420_at 7538.6 P
phosphoribosylamino-imidazole-carboxylase
8421_at 1549.6 P
hypothetical protein
8422_at 973.9 P
mitochondrial integral membrane protein
8423_at 3378.6 P
weak similarity to E.coli hypothetical 27K protein
8424_at 3407.7 P
Peripheral membrane protein required for vacuolar protein sorting
8425_s_at 12184.0 P
translation elongation factor 2 (EF-2)
8426_at 63.1 A
GTPase activating protein (GAP)
8427_at -4.4 A
questionable ORF
8428_at 10579.9 P
NAD+-dependent isocitrate dehydrogenase
8429_at 1472.6 P
similarity to YLR361c
8430_at 2226.7 P
hypothetical protein
8431_at 722.8 P
questionable ORF
8432_at 2911.8 P
Transcription factor
8433_at 1802.5 P
Actin-related protein
8389_at 8018.3 P
Succinate-CoA Ligase (ADP-Forming)
8390_at 656.9 P
Thiamin pyrophosphokinase
8391_at 2165.4 P
weak similarity to human DNA-binding protein PO-GA and to bacterial H+-transporting ATP synthases
8392_at 9712.9 P
strong similarity to hypothtical S. pombe protein and to hypothetical C. elegans protein
8393_at 115.4 M
questionable ORF
8394_at 137.4 P
similarity to YHR194w
8395_at 2044.5 P
required for final stages of splicesome maturation\; promotes step 1 of splicing
8396_at 376.8 P
Involved in plasmid maintenance
8397_at 2189.7 P
ribosomal protein of the large subunit, mitochondrial
8398_at 7901.1 P

second largest subunit of RNA polymerase II
8399_at 972.7 P
hypothetical protein
8400_at 12692.0 P
multidrug resistance transporter
8401_at 713.0 P
similarity to hypothetical A. thaliana proteins F19G10.15 and T19F06.21
8402_at 1826.4 P
similarity to 5 -flanking region of the Pichia MOX gene
8403_at 493.0 P
Interacts with C-terminus of CDC12
8404_at 10359.5 P
putative proteasome subunit
8405_at 1756.0 P
Mitochondrial ribosomal protein of small subunit
8406_at 1494.0 P
homologue of human E core protein
8407_at 2197.6 P
Protein involved in mRNA transport from nucleus to cytoplasm
8408_at 379.8 P
similarity to C.elegans cosmid F35C8
8409_at 1029.4 P
transcription factor
8410_at 4113.5 P
strong similarity to S.pombe SPAC13G6.14 protein
8411_at 3206.3 P
hypothetical protein
8366_at 3615.9 P
similarity to E.histolytica surface lectin
8367_at 1474.2 P
hypothetical protein
8368_i_at 10716.0 P
Ribosomal protein S28A (S33A) (YS27)
8369_f_at 9283.5 P
Ribosomal protein S28A (S33A) (YS27)
8370_at 6045.9 P
glutaminyl-tRNA synthetase
8371_at 1016.5 P
questionable ORF
8372_at 273.7 P
questionable ORF
8373_at 1488.2 P
sphingoid long chain base (LCB) kinase
8374_at 1620.6 P
similarity to finger protein YKL222c, YOR162c and YLR266c
8375_at 216.9 P
strong similarity to YLR270w
8376_at 2502.7 P
Stoichiometric member of mediator complex
8377_at 4420.9 P
similarity to human and murine C3f protein
8378_at 3620.2 P
ferrochelatase (protoheme ferrolyase)
8379_at 320.8 P
weak similarity to rat SCP1 protein
8380_at 110.8 P

Regulatory subunit for Glc7p

8381_at	1356.7	P	similarity to BRR5 protein
8382_at	196.8	P	Peroxisomal enoyl-CoA hydratase
8383_at	1973.7	P	Actin assembly factor
8384_f_at	9865.9	P	Ribosomal protein S30B
8385_at	-72.0	A	hypothetical protein
8386_at	8994.4	P	phosphoserine transaminase
8387_at	2652.3	P	GTP binding protein, almost identical to Gsp1p
8388_at	370.8	A	hypothetical protein
8343_at	6678.1	P	Translation elongation factor Tu, mitochondrial
8344_at	1531.1	P	Protein that may play a role in polarity establishment and bud formation
8345_at	1537.2	P	weak similarity to chicken nonhistone chromosomal protein HMG-2
8346_at	90.6	A	sporulation-specific exo-1,3-beta-glucanase
8347_at	696.8	P	contains motifs that are present in a family of DNA-dependent ATPases, the SWI2\/SNF2-like proteins
8348_i_at	1228.0	P	strong similarity to Thi10p
8349_f_at	2116.8	P	strong similarity to Thi10p
8350_at	347.9	P	weak similarity to YPL112c
8351_at	1890.8	P	Transcription factor IIA, large chain
8352_at	641.4	P	possible leucine zipper
8353_at	2244.2	P	Involved in lipoic acid metabolism
8354_at	6994.7	P	hypothetical protein
8355_at	8481.8	P	Multicopy suppressor of BFA (Brefeldin A)-induced lethality\; implicated in secretion and nuclear segregation
8356_at	5.0	A	questionable ORF
8357_at	542.7	P	questionable ORF
8358_at	3449.0	P	Ribose methyltransferase for mitochondrial 21S rRNA
8359_at	6334.9	P	imidazoleglycerol-phosphate dehydratase
8360_at	1424.8	P	questionable ORF
8361_at	8244.9	P	ATP-dependent RNA helicase of DEAD box family\; suppressor of a pre-mRNA splicing mutation, prp8-1

8362_at	1403.4	P	hypothetical protein
8363_at	3012.8	P	similarity to Brettanomyces RAD4 and to S.pombe hypothetical protein
8364_at	8872.7	P	second-largest subunit of RNA polymerase III
8365_at	2363.0	P	protein tyrosine phosphatase
8320_at	8002.0	P	homology to bacterial nicotinate phosphoribosyl transferase
8321_at	9767.3	P	RNA polymerase II subunit
8322_at	766.5	A	encodes protein with GTP-binding domain related to dynamin
8323_at	5094.9	P	beta subunit of G protein coupled to mating factor receptor
8324_at	466.6	P	Involved in silencing at telomeres, HML and HMR
8325_at	-180.5	A	hypothetical protein
8326_at	1337.3	P	similarity to M.xanthus hypothetical protein
8327_at	729.6	P	Relieves uso1-1 Transport Defect
8328_at	2369.7	P	Subunit 1 of Replication Factor C\; homologous to human RFC 140 kDa subunit
8329_at	1046.4	P	questionable ORF
8330_at	3292.4	P	dipeptidyl aminopeptidase
8331_at	5889.2	P	hypothetical protein
8332_at	1432.3	P	malonyl-CoA:ACP transferase
8333_at	66.9	A	malonyl-CoA:ACP transferase
8334_at	3015.9	P	similarity to ADP/ATP carrier proteins
8335_at	1918.9	P	protein of unknown function
8336_at	12166.4	P	16-kDa RNA polymerase subunit (common to polymerases I, II and III)
8337_at	1130.5	P	questionable ORF
8338_at	7591.5	P	NifU-like protein A
8339_at	1998.2	P	similarity to microtubule-interacting protein Mhp1p
8340_at	2946.5	P	weak similarity to YNR013c
8341_at	5527.9	P	Transcriptional modulator
8342_at	11432.6	P	Transcriptional modulator
8297_at	1977.9	P	protein kinase involved in protein kinase C pathway

8298_at	3048.6	P	GrpE homolog, mitochondrial matrix protein
8299_at	4119.7	P	protein kinase
8300_f_at	9661.7	P	Ribosomal protein L33B (L37B) (rp47) (YL37)
8301_at	-13.1	A	encodes snRNA U3, SNR17B also encodes snRNA U3
8302_at	2265.4	P	dihydrofolate reductase
8303_at	-38.7	A	homology to human oxysterol binding protein
8304_at	2702.1	P	similarity to hypothetical S. pombe protein
8305_at	2080.1	P	hypothetical protein
8306_at	2837.6	P	similarity to C.elegans ZK1058.5 protein
8307_at	6568.8	P	tetrahydrofolylpolyglutamate synthase
8308_at	326.4	P	Sporulation Specific
8309_at	4897.0	P	similarity to M.jannaschii hypothetical protein MJ0588
8310_at	1898.0	P	Acetyltransferase in the SAS gene family
8311_at	3019.2	P	similarity to hypothetical C. elegans proteins
8312_at	5015.0	P	weak similarity to reductases
8313_at	11416.4	P	Suppressor of rad53 lethality
8314_g_at	11807.6	P	Suppressor of rad53 lethality
8315_i_at	7957.9	P	questionable ORF
8316_at	574.2	P	subunit of the anaphase promoting complex
8317_at	1327.4	P	CLeavage\/Polyadenylation factor IA subunit\; interacts with Pcf11p in the 2-hybrid system
8318_at	3507.2	P	similarity to thiosulfate sulfurtransferases
8319_at	870.0	P	hypothetical protein
8274_at	2521.3	P	hypothetical protein
8275_at	2760.7	P	Protein involved in protein import into ER
8276_at	-8.6	A	hypothetical protein
8277_at	1493.8	P	strong similarity to secretory protein Ssp134p
8278_at	3606.7	P	calcium-binding protein component of spindle pole bodies, localizes to half-bridges and interacts with KAR1
8279_at	698.5	P	

hypothetical protein
8280_at 6497.6 P
ATPase\; component of the 26S proteasome cap subunit
8281_at 8928.4 P
translation initiation factor eIF2b gamma subunit\; negative regulator in the general control of amino acid biosynthesis
8282_at 5813.2 P
Subunit of the regulatory particle of the proteasome
8283_at 1528.3 P
similarity to YLR243w
8284_at 75.2 A
questionable ORF
8285_at 1682.5 P
hypothetical protein
8286_at 5884.7 P
Binds to beta-tubulin and may participate in microtubule morphogenesis
8287_at 555.4 P
Pentamidine resistance protein
8288_at 7412.8 P
similarity to ser/thr protein kinases
8289_at 175.4 P
hypothetical protein
8290_at 581.5 P
Required for viability in the absence of the kinesin-related Cin8p mitotic motor.
8291_at 9154.5 P
Vacuolar H-ATPase 100 kDa subunit of membrane (V0) sector, essential for vacuolar acidification and vacuolar H-ATPase activity
8292_at 11679.0 P
strong similarity to Rattus tricarboxylate carrier
8293_at 6753.0 P
microtubule-associated protein
8294_at 4602.2 P
similarity to resistance proteins
8295_at 974.6 P
transfer RNA isopentenyl transferase
8296_at 558.0 P
similarity to A.nidulans palA protein
8252_at 9808.1 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 198.4 A
questionable ORF
8254_at 1618.0 P
uroporphyrinogen III synthase
8255_at 82.6 P
hypothetical protein
8256_at 3116.2 P
similarity to S.pombe dihydrofolate reductase
8257_at 5106.7 P
weak similarity to phosducins
8258_at 240.5 A
questionable ORF
8259_at 2766.8 P
weak similarity to phosphoglycerate mutases
8260_at 860.1 P
weak similarity to M.jannaschii hypothetical protein MJ0694

8261_at	9907.7	P	similarity to D.melanogaster heat shock protein 67B2
8262_at	7258.7	P	similarity to D.melanogaster heat shock protein 67B2
8263_at	1405.8	P	weak similarity to PITSLRE protein kinase isoforms
8264_at	1613.9	P	Disulfide isomerase related protein
8265_at	824.7	P	similarity to C.elegans hypothetical protein
8266_at	5355.2	P	transcriptional regulator
8267_at	3332.0	P	similarity to cation translocating ATPases
8268_at	730.7	P	similarity to human and mouse glomerulosclerosis protein Mpv17
8269_f_at	8584.9	P	Ribosomal protein S10A
8270_f_at	16339.6	P	Ribosomal protein S10A
8271_at	3610.2	P	similarity to human hypothetical protein
8272_at	211.3	P	weak similarity to SWI/SNF complex 60 KDa subunit from man and mouse
8273_at	1092.1	P	similarity to hypothetical S. pombe protein
8229_at	4071.5	P	similarity to Sdh4p
8230_at	44.3	A	required for meiosis
8231_at	9220.5	P	multiprotein bridging factor
8232_at	2139.1	P	BUD site selection
8233_g_at	1906.1	P	BUD site selection
8234_at	88.3	A	questionable ORF
8235_at	3408.0	P	hypothetical protein
8236_at	7038.6	P	CPA1 leader peptide
8237_at	7329.3	P	Carbamoyl phosphate synthetase, arginine specific
8238_at	1350.2	P	has strong homology to Drosophila ISWI
8239_at	1958.6	P	AIP3 binding protein
8240_at	1552.1	P	hypothetical protein
8241_at	6403.8	P	similarity to human X-linked PEST-containing transporter
8242_at	3218.7	P	homolog of chloroplast phosphate transporter
8243_at	789.8	P	weak similarity to YIL149c

8244_i_at	10788.7	P	questionable ORF
8245_r_at	925.3	P	questionable ORF
8246_s_at	9283.9	P	questionable ORF
8247_at	11251.8	P	57 kDa nucleolar protein
8248_at	8118.7	P	similarity to hypothetical S. pombe protein
8249_at	494.1	P	sporulation-specific protein
8250_at	246.1	P	hypothetical protein
8251_at	2292.4	P	hypothetical protein
8206_at	2861.0	P	Protein involved in cobalt accumulation\; dosage dependent suppressor of cobalt toxicity
8207_at	5115.3	P	long chain fatty acyl:CoA synthetase
8208_at	222.6	M	hypothetical protein
8209_at	517.8	P	homolog of mammalian splicing factor\/U2 snRNP protein
8210_at	2594.9	P	hypothetical protein
8211_at	1912.5	P	dolichyl phosphate-D-mannose:protein O-D-mannosyltransferase
8212_at	2619.9	P	similarity to hypothetical S.pombe protein SPAC1F12.05
8213_at	10663.9	P	gamma-glutamyl phosphate reductase
8214_at	819.8	P	similarity to YAL028w
8215_at	-148.4	A	questionable ORF
8216_at	4248.1	P	myosin-1
8217_at	9876.0	P	vesicle-associated membrane protein (synaptobrevin) homolog
8218_at	5408.0	P	Putative ABC transporter highly similar to Pdr5p
8219_at	1846.8	P	Multicopy suppressor of clathrin deficiency and of ts mutants of IPL1
8220_at	600.9	P	catalytic subunit of mitochondrial DNA polymerase
8221_at	544.6	P	questionable ORF
8222_at	8089.3	P	27-kDa subunit of the vacuolar ATPase\; E subunit of V1 sector
8223_at	471.4	P	questionable ORF
8224_at	924.9	P	splicing factor
8225_at	7172.1	P	Cytoplasmic alanyl-tRNA synthetase gene

8226_at 3568.8 P
Appears to function early in (1,6)-beta-D-glucan synthesis pathway
8227_at 1846.1 P
Mutants are defective in Ty1 Enhancer-mediated Activation
8228_at 781.6 P
similarity to YAL034c
8183_at -89.8 A
strong similarity to E2 ubiquitin-conjugating enzymes
8184_at 3822.4 P
DNA-dependent RNA polymerase I subunit A43
8185_at 11212.3 P
RNA polymerase I subunit 190 (alpha)
8186_at 1973.8 P
weak similarity to YAl037w
8187_at 508.3 P
hypothetical protein
8188_at 2742.0 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 91.2 A
questionable ORF
8190_at 1127.2 P
deoxycytidyl transferase
8191_at 2388.5 P
Pyruvate kinase, glucose-repressed isoform
8192_at 265.5 M
putative proline-specific permease
8193_at 65.8 A
Protein involved in chromosome segregation, required for microtubule stability
8194_at 422.8 P
weak similarity to Esp1p and mitochondrial L.illustris cytochrome oxidase I
8195_at -11.1 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 984.8 P
hypothetical protein
8197_at 819.4 P
weak similarity to adenylate cyclases
8198_at 1647.0 P
hypothetical protein
8199_at 5199.8 P
nam9-1 suppressor
8200_at 5535.4 P
strong similarity to human electron transfer flavoprotein-ubiquinone oxidoreductase
8201_at 1906.9 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 849.9 P
Component, along with Hap2p and Hap3p, of CCAAT-binding transcription factor
8203_at 3277.0 P
hypothetical protein

8204_at 1507.8 P
low-Km (high-affinity) cAMP phosphodiesterase
8205_at 8621.7 P
translation initiation factor eIF3 subunit
8161_at 8538.3 P
proteasome component YC1 (protease yscE subunit 1)
8162_at 870.6 P
Activator of peroxisome proliferation
8163_at 290.4 P
hypothetical protein
8164_at 88.3 A
strong similarity to YAL053w
8165_at 139.8 P
questionable ORF
8166_at 2372.1 P
Calponin homolog
8167_at 328.5 P
encodes a putative 3 ->5 exonuclease
8168_at 12805.5 P
40S ribosomal protein S12
8169_at 6567.3 P
protein of the TCD\/MRS6 family of GDP dissociation inhibitors (Rab escort protein)\; component of Rab geranylgeranyl transferase
8170_at 815.8 P
similarity to YAL056w
8171_at 1898.9 P
hypothetical protein
8172_at 1551.4 P
nuclesome assembly protein I
8173_at 3790.3 P
aldehyde dehydrogenase (E.C. 1.2.1.5) (sold by SIGMA under the catalogue number A5550, according to A. Blomberg)
8174_at 9288.3 P
NADP-specific glutamate dehydrogenase
8175_at -46.9 A
hypothetical protein
8176_at 751.0 P
Alcohol acetyltransferase
8177_at 8.6 A
strong similarity to aminotriazole resistance protein
8178_at 46.6 A
questionable ORF
8179_at 1337.8 P
weak similarity to Pdr3p
8180_at 332.4 P
similar to FRE2
8181_at 1822.8 P
hypothetical protein
8182_at 7488.7 P
weak similarity to L.mexicana secreted acid phosphatase 2
8138_at 8.2 A
similar to FRE2
8139_at 3153.5 P
strong similarity to hypothetical protein YMR316w
8140_at 464.7 P
photolyase

8141_at -16.8 A
strong similarity to YGL258w
8142_s_at -5.5 A
Protein with similarity to formate dehydrogenases
8143_at 1346.2 P
strong similarity to putative pseudogenes YPL277c and YPL278c
8144_g_at 1179.0 P
strong similarity to putative pseudogenes YPL277c and YPL278c
8145_s_at 2476.0 P
nearly identical to YPL279c
8146_at 107.8 P
hypothetical protein
8147_s_at 130.1 A
strong similarity to members of the Srp1p/Tip1p family
8148_at 286.0 P
hypothetical protein identified by SAGE
8149_at 1546.7 P
identified by SAGE
8150_s_at 1230.7 P
Sorting nexin I homologue
8151_s_at 2294.9 P
Thymidylate synthase
8152_f_at 597.8 P
Thymidylate synthase
8153_at 4753.5 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 -101.6 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 344.6 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 -19.7 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 376.8 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 3442.1 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 583.4 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 103.0 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 767.9 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 665.5 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 -62.5 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 2348.8 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 298.4 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 76.8 P
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 207.0 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
8119_f_at 611.7 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 1168.1 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 268.0 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 -18.4 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 425.3 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 2373.2 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 504.6 P
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 3295.2 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 96.6 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 1366.7 A
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 1661.9 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 187.7 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 -134.5 A
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 5180.9 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 51.5 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 -197.4 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 128.0 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 4668.5 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 10268.3 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 -189.9 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 4489.7 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 173.9 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 121.8 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 6435.8 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 2541.6 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 4016.5 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 70.4 M

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 594.2 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 135.1 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 175.0 P

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 308.2 P

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 -25.6 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 302.6 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 1763.7 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 18.0 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 1724.6 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 -53.6 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 1045.8 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 344.5 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 -100.3 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 3.6 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 40.2 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 -18.4 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 994.1 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 766.4 P

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 72.9 P

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 920.4 P

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 5380.9 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 14.4 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 38.3 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 68.9 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 280.2 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 190.7 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 -137.9 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 1116.1 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 482.7 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 207.7 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 -80.3 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 172.5 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 196.4 P
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 2042.7 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 -37.4 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 55.1 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 4.3 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 412.4 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 1424.4 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 137.8 P
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 186.2 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 241.2 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 1054.6 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 2143.5 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 392.1 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 70.6 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 6522.3 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 226.3 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 173.3 A
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 874.9 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 8283.7 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 2.8 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 -33.5 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 12.7 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
8052_r_at 108.4 P
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 459.2 A
snRNA
8054_at 1268.6 P
snRNA
8055_i_at -13.6 A
Centromere
8056_at 2876.8 P
snRNA

8057_i_at 227.7 P
snRNA
8058_r_at 302.9 P
snRNA
8059_at 762.4 P
snRNA
8060_at 1464.6 P
snRNA
8061_at 806.8 P
snRNA
8062_at 7386.5 P
snRNA
8016_at 104.5 P
snRNA
8017_at 5678.6 P
snRNA
8018_i_at 143.5 P
strong similarity to hypothetical protein YOR389w/putative pseudogene
8019_s_at 829.7 P
strong similarity to hypothetical protein YOR389w/putative pseudogene
8020_s_at -29.6 A
putative formate dehydrogenase/putative pseudogene
8021_at 1416.6 P
strong similarity to amino-acid transport proteins
8022_at 3299.3 P
weak similarity to M.leprae metH2 protein, and strong similarity to hypothetical protein YLL062c
8023_at 43.7 A
hypothetical protein
8024_at 9537.5 P
nuclear gene for ATP synthase epsilon subunit
8025_at 2286.7 P
ATP-binding cassette (ABC) transporter family member
8026_at 580.6 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 1118.9 P
phosphoinositide-specific phospholipase C
8028_at 586.6 P
weak similarity to C.elegans transcription factor unc-86
8029_at 6435.0 P
dimethyladenosine transferase
8030_at 8730.2 P
dicarboxylic amino acid permease
8031_at 1218.0 P
strong similarity to YMR253c
8032_at 1667.2 P
similarity to Kel2p and Kel3p
8033_at 15236.5 P
mitochondrial and cytoplasmic fumarase (fumarate hydralase)
8034_at 182.9 A
questionable ORF
8035_at 2402.1 P
hypothetical protein
8036_at 1493.5 P
medium subunit of the clathrin-associated protein complex
8037_at 931.3 P

similarity to B.subtilis transcriptional activator tenA, and strong similarity to hypothetical proteins YOL055c and YPR121w
8038_at 84.7 A
weak similarity to YIL029c
7993_at 2292.9 P
G(sub)1 cyclin
7994_at 235.7 P
Involved in mitotic cell cycle and meiosis
7995_at 1700.1 P
transcription factor, member of Ada\/Gcn5 protein complex
7996_at 180.5 A
Cik1p homolog
7997_at 6538.2 P
iron-sulfur protein homologous to human adrenodoxin
7998_at 13.3 A
questionable ORF
7999_at 9143.8 P
weak similarity to YMR195w
8000_i_at 7185.5 P
Ribosomal protein L36B (L39) (YL39)
8001_at 472.1 P
similarity to mouse Tbc1 protein
8002_at 1077.2 P
zinc-finger transcription factor of the Zn(2)-Cys(6) binuclear cluster domain type
8003_at 1585.0 P
similarity to human HAN11 protein and petunia an11 protein
8004_at 7612.2 P
weak similarity to mouse proteinase activated receptor 2
8005_at 2695.4 P
weak similarity to human mutL protein homolog
8006_at 3329.0 P
weak similarity to human UDP-galactose transporter related isozyme 1
8007_at 3348.1 P
component of signal recognition particle
8008_at 834.5 P
Homolog of the mammalian IQGAP1 and 2 genes\; probable regulator of cellular morphogenesis, inducing actin-ring formation in association with cytokinesis
8009_at 1482.6 P
involvement in microtubule function
8010_i_at 8248.8 P
heat shock protein
8011_at 5516.5 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 1500.0 P
questionable ORF
8013_at 7707.0 P
beta subunit of translation initiation factor eIF-2
8014_at 357.9 P
similarity to Prk1p, and serine/threonine protein kinase homolog from A. thaliana
8015_at 6084.0 P
strong similarity to TATA-binding protein-interacting protein 49 from rat
7970_at 8456.0 P
17-kDa subunit C of vacuolar membrane H(+)-ATPase
7971_at 644.4 P
hypothetical protein

7972_at 5579.9 P
SSO1 and SSO2 encode syntaxin homologs\; act in late stages of secretion
7973_at 9274.0 P
alpha subunit of fatty acid synthase
7974_at -3.0 A
Up in StarVation
7975_at 883.2 P
weak similarity to YMR181c
7976_at 1901.0 P
mRNA capping enzyme beta subunit (80 kDa), RNA 5 -triphosphatase
7977_at 2605.2 P
UDP-glucose:dolichyl-phosphate glucosyltransferase
7978_at 11712.0 P
similarity to translation elongation factor eEF3
7979_at 5939.1 P
hypothetical protein
7980_at 2610.4 P
Protein involved in mitochondrial iron accumulation
7981_at 373.9 P
Induced by osmotic stress
7982_at 68.6 A
similarity to C.perfringens hypothetical protein
7983_at 6177.3 P
Bypass of PAM1
7984_s_at 9451.8 P
Ribosomal protein L1A, forms part of the 60S ribosomal subunit
7985_at 1132.2 P
PHO85 cyclin
7986_at 10380.1 P
GTP binding protein
7987_at 2728.4 P
similarity to human hypothetical protein KIAA0187
7988_at 215.8 P
similarity to YGL133w
7989_at 1351.8 P
Protein required for assembly of ubiquinol cytochrome-c reductase complex (cytochrome bc1 complex)
7990_at 2166.9 P
TMP pyrophosphorylase, hydroxyethylthiazole kinase
7991_at 703.1 P
similarity to A.thaliana U2 snRNP protein A
7992_at 4463.6 P
intranuclear protein which exhibits a nucleotide-specific intron-dependent tRNA pseudouridine synthase activity
7947_at 4749.6 P
Nip7p is required for 60S ribosome subunit biogenesis
7948_at 2587.3 P
component of signal recognition particle
7949_at 391.2 P
Protein kinase
7950_at 1573.4 P
similarity to YHL039w
7951_at 3613.4 P
similarity to hypthetical proteins from A. fulgidus, M. thermoautotrophicum and M. jannaschii
7952_at 7140.8 P
weak similarity to glycerophosphoryl diester phosphodiesterases
7953_at 467.6 A

questionable ORF
7954_at 5579.5 P
casein kinase I isoform
7955_at 2827.9 P
cAMP-dependent protein kinase catalytic subunit
7956_at 852.2 P
similarity to cell size regulation protein Rcs1p
7957_at -26.0 A
hypothetical protein
7958_at 3.9 A
hypothetical protein
7959_at 6467.9 P
weak similarity to T.cruzi p284 protein
7960_i_at 6896.2 P
Ribosomal protein L7B (L6B) (rp11) (YL8)
7961_f_at 6902.6 P
Ribosomal protein L7B (L6B) (rp11) (YL8)
7962_s_at 11225.0 P
Ribosomal protein L7B (L6B) (rp11) (YL8)
7963_at 306.0 P
questionable ORF
7964_at 1435.5 P
weak similarity to S.pombe hypothetical protein SPAC8C9
7965_at 1346.4 P
delta-like subunit of the yeast AP-3 adaptin component of the membrane-associated clathrin assembly complex
7966_at 818.9 P
DNA damage checkpoint gene
7967_at 473.5 P
weak similarity to human centromere protein E
7968_at 427.3 P
hypothetical protein
7969_at 225.7 P
strong similarity to YGL082w
7924_at 1974.8 P
polyadenylated RNA-binding protein
7925_at 307.2 P
strong similarity to YGL084c
7926_at 1765.9 P
similarity to Utr1p and YEL041w
7927_at 9053.1 P
mating factor alpha
7928_at 394.5 P
weak similarity to Xenopus protein xlgv7
7929_at -26.0 A
questionable ORF
7930_at 2552.8 P
weak similarity to Pub1p
7931_at 4436.2 P
ribosomal protein L36, mitochondrial
7932_at 3906.3 P
similarity to Taf90p
7933_at 665.6 P
questionable ORF
7934_at 531.9 P
weak similarity to YKR029c

7935_at 2614.5 P
weak similarity to human l-caldesmon I
7936_at 2929.7 P
protein phosphatase Q
7937_at 3968.4 P
Small subunit of nuclear cap-binding protein complex
7938_at 5200.5 P
putative DNA binding protein which shows similarity in homeobox domain to human proto-oncogene PBX1
7939_at 2094.2 P
similarity to chinese hamster transferrin receptor protein
7940_at 1586.2 P
N-acetylglucosaminyl-phosphatidylinositol biosynthetic protein
7941_at 212.2 P
Nuclear import protein
7942_at 1479.7 P
Mitochondrial ribosomal protein MRPL40 (YmL40)
7943_at 1277.2 A
Putative farnesyl transferase required for heme A synthesis
7944_at 649.5 P
NAD(P)H dehydrogenase
7945_at 2854.8 P
similarity to C.elegans LIM homeobox protein
7946_at 4553.8 P
INvolved in nuclear mRNA export, binds both poly(A)
7902_at 68.0 A
weak similarity to E.coli bfpB protein
7903_at 706.6 P
DNA polymerase
7904_at 20.8 A
weak similarity to paramyosins
7905_at 213.1 A
weak similarity to YHR207c
7906_at 379.9 A
similarity to mismatch repair protein Mlh1p
7907_at 10117.4 P
Serine and threonine rich protein.
7908_at 1164.5 P
hypothetical protein
7909_at 635.7 P
Involved in polarity establishment and bud emergence\; interacts with the Rho1p small GTP-binding protein
7910_at 8665.9 P
cytosolic leucyl tRNA synthetase
7911_at 1243.3 P
weak similarity to YPR151c
7912_at 4320.2 P
weak similarity to human nucleolin
7913_at 744.5 P
weak similarity to S.pombe hypothetical protein SPAC2G11.15c
7914_at 1778.1 P
weak similarity to YDL010w
7915_at 981.0 P
kinesin-related protein
7916_at 9506.7 P
vacuolar proteinase A

7917_at 204.3 P
protein kinase, Mec1p and Tel1p regulate rad53p phosphorylation
7918_at 1192.6 P
Resistant to Rapamycin Deletion 2
7919_at 2293.6 P
strong similarity to A.thaliana PRL1 and PRL2 proteins
7920_at 591.2 A
similarity to ser/thr protein kinases
7921_at 2379.1 P
involved in autophagy
7922_at 823.4 P
Phosphopantetheine
7923_at 360.1 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 1079.8 P
weak similarity to myosin heavy chain proteins
7880_at 6536.4 P
Homologous to human oxysterol-binding protein\; implicated in ergosterol biosynthesis and regulation of Golgi-derived transport vesicle biogenesis
7881_at 5108.4 P
encodes snRNA U3, SNR17A also encodes snRNA U3
7882_f_at 12592.0 P
Ribosomal protein L33A (L37A) (YL37) (rp47)
7883_at 418.1 P
questionable ORF
7884_at 1505.6 P
strong similarity to protein kinase Kin4p
7885_at 427.1 P
protein kinase
7886_at 499.8 P
Transcriptional modulator
7887_at 934.7 P
weak similarity to fruit fly polycomblike nuclear protein
7888_at 1359.6 P
similarity to microtubule-interacting protein Mhp1p and to hypothetical protein YOR227w
7889_at -225.4 A
questionable ORF
7890_at 5762.9 P
NifU-like protein A
7891_at 1248.8 P
similarity to ADP/ATP carrier proteins
7892_at 760.0 P
weak similarity to transcription factors
7893_at 1020.9 P
Putative heme A biosynthetic enzyme involved in forming the formyl group at position 8 of the porphyrin ring
7894_at 9716.3 P
Ribosomal protein L5 (L1a)(YL3)
7895_at 145.1 P
hypothetical protein
7896_at 3910.4 P
TFIIF subunit (transcription initiation factor), 30 kD
7897_at 2225.3 P
TTAGGG repeat binding factor
7898_at 3451.2 P

histone H1
7899_at 1919.1 P
weak similarity to fruit fly TFIID subunit p85
7900_at 2503.7 P
weak similarity to YDR395w and cellular apoptosis susceptibility protein
7901_at 356.5 P
Nuclear import protein
7857_at 322.1 P
similarity to ribonucleases
7858_at 1651.6 P
TFIIH subunit Tfb2\; has homology to CAK and human IIH subunits
7859_at -13.9 A
Meiotic protein required for synapsis and meiotic recombination
7860_at 1115.0 P
Required for sorting and delivery of soluble hydrolases to the vacuole.
7861_at 689.6 P
putative ATP-dependent RNA helicase\; Dead box protein
7862_at 2189.0 P
Component of small subunit of the mitochondrial ribosome
7863_at 5269.6 P
Isopentenyl diphosphate:dimethylallyl diphosphate isomerase (IPP isomerase)
7864_at 588.8 P
Protein with similarity to Hda1p, Rpd3p, Hos2p, and Hos1p
7865_at 4250.3 P
has GTPase-activating protein activity toward the essential bud-site assembly GTPase Cdc42
7866_at 655.0 P
questionable ORF
7867_at 306.7 P
similarity to glycerate dehydrogenases
7868_at 3983.9 P
weak similarity to YOR193w
7869_at 5457.9 P
arginase
7870_at 4007.4 P
similarity to C.elegans hypothetical protein, weak similarity to Pho81p
7871_at 526.6 P
similarity to aminoglycoside acetyltransferase regulator from P. stuartii
7872_at 874.1 P
hypothetical protein
7873_at 561.5 P
hypothetical protein
7874_at 10301.9 P
HSP70 family member, highly homologous to Ssa1p and Sse2p
7875_at 3233.7 P
similarity to Smy2p
7876_at 1406.2 P
Aspartyl-tRNA synthetase, mitochondrial
7877_at 2233.9 P
similarity to hypothetical M. tuberculosis protein
7878_at 599.0 P
questionable ORF
7834_at 3918.6 P
hypothetical protein
7835_at 1526.6 P
similarity to YFR021w
7836_at 1308.0 P

weak similarity to Sulfolobus hypothetical protein
7837_at 8910.7 P
similarity to S.pombe hypothetical protein
7838_at 756.8 P
Tyrosyl-tRNA synthetase
7839_at 2165.9 P
hypothetical protein
7840_at 929.2 P
strong similarity to YBR177c
7841_at 6606.4 P
membrane component of ER protein translocation apparatus
7842_at 6862.5 P
similarity to M.jannaschii GTP-binding protein, GTP1/OBG-family, weak similarity to other GTP-binding proteins
7843_at 1366.9 P
sensitive to sulfite
7844_at 7579.8 P
Glutathione oxidoreductase
7845_s_at 11350.2 P
Ribosomal protein S6A (S10A) (rp9) (YS4)
7846_at 5816.9 P
serum response factor-like protein
7847_at 6126.3 P
similarity to aryl-alcohol dehydrogenases
7848_at 6144.8 P
strong similarity to YBR183w
7849_at 2697.4 P
Histone and other Protein Acetyltransferase\; Has sequence homology to known HATs and NATs
7850_at 1983.0 P
multidomain vesicle coat protein that interacts with Sec23p
7851_at 1126.1 P
BCK1-like resistance to osmotic shock
7852_at 788.3 P
54kDa subunit of the tetrameric tRNA splicing endonuclease
7853_at 2006.1 P
putative helicase
7854_i_at 5638.5 P
Ribosomal protein S9A (S13) (rp21) (YS11)
7855_f_at 7819.3 P
Ribosomal protein S9A (S13) (rp21) (YS11)
7856_at 192.7 A
hypothetical protein
7811_at 5002.7 A
Ribosomal protein L21B
7812_at 4819.3 P
F(1)F(0)-ATPase complex delta subunit, mitochondrial
7813_at 379.7 P
weak similarity to YBR197c
7814_at 1830.2 P
Required for synthesis of N-acetylglucoaminylphosphatidylinositol, the first intermediate in synthesis of glycosylphosphatidylinositol (GPI) anchors
7815_at 690.7 P
similarity to Vps4p and YER047c
7816_at -67.3 A
questionable ORF
7817_at 334.3 P

encodes putative deubiquitinating enzyme
7818_at 783.2 P
hypothetical protein
7819_at 876.5 P
weak similarity to Vps9p
7820_at 584.7 P
geranylgeranyl diphosphate synthase
7821_at 962.0 P
hypothetical protein
7822_at 6092.3 P
hypothetical protein
7823_at 2600.3 P
hypothetical protein
7824_at 1409.3 P
soluble, hydrophilic protein involved in transport of precursors for soluble vauolar hydrolases from the late endosome to the vacuole
7825_at 1774.5 P
weak similarity to S.pombe peptidyl-prolyl cis-trans isomerase
7826_at 5745.5 P
similarity to hypothetical protein YLR019w, YLL010c and S.pombe hypothetical protein SPAC2F7.02c
7827_at 242.3 P
hypothetical protein
7828_at 11874.2 P
cytosolic aldehyde dehydrogenase
7829_at 393.9 P
strong similarity to Mrs2p
7830_at 4184.0 P
similarity to glutaredoxins
7831_at 4154.8 P
multidrug resistance transporter
7832_at 4196.5 P
Multicopy suppressor of cls2-2\; also suppresses rvs161 mutations
7833_at 1419.9 P
hypothetical protein
7788_at 1102.0 P
hypothetical protein
7789_at 366.0 P
protein of unknown function
7790_at 7102.7 P
mannosylphosphate transferase
7791_at 3479.7 P
hypothetical protein
7792_at 1530.5 P
strong similarity to ADP-ribosylation factors
7793_at 3701.5 P
Protein required for complex glycosylation
7794_at 5523.7 P
MAP kinase-associated protein
7795_at 7648.8 P
Calcium and phospholipid binding protein homologous to translation elongation factor 1-gamma (EF-1gamma)
7796_at 2190.6 P
hypothetical protein
7797_at 1570.1 P
Elongin C transcription elongation factor
7798_at 1271.7 P

```
Vacuolar sorting protein
7799_at     268.5       P
questionable ORF
7800_at     5284.2      P
RNA recognition motif-containing protein
7801_at     1212.7      P                                                             a
cyclin(SSN8)-dependent serine\/threonine protein kinase
7802_at     1873.4      P
hypothetical protein
7803_at     1190.5      P
nuclear encoded mitochondrial isoleucyl-tRNA synthetase
7804_at     1146.8      P
hypothetical protein
7805_at     730.3       P
zinc finger DNA binding factor, transcriptional regulator of sulfur amino acid metabolism, highly
homologous to Met32p
7806_at     9648.8      P
GAL4 enhancer protein, has similarity to human transcription factor BTF3
7807_at     1016.5      P
plasma membrane ATPase
7808_at     741.8       P
questionable ORF
7809_at     1256.9      P
questionable ORF
7810_at     87.2        A
weak similarity to YLR426w
7766_at     5557.9      P
styryl dye vacuolar localization
7767_at     4998.0      P
negative transcriptional regulator, protein kinase homolog
7768_at     1995.1      P
similarity to C.elegans hypothetical protein
7769_at     948.6       P
putative ATP-dependent helicase
7770_at     7139.7      P
acetoacetyl CoA thiolase
7771_at     402.4       P
hypothetical protein
7772_at     1864.5      P
serine\/threonine protein kinase homologous to Ran1p
7773_at     111.2       A
questionable ORF
7774_at     423.0       P
(N)egative regulator of (C)ts1 (E)xpression
7775_at     3849.9      P
putative methylenetetrahydrofolate reductase (mthfr)
7776_at     902.4       P
UV endonuclease
7777_at     -5.6        A
ExtraCellular Mutant\; similar to SRD1
7778_at     3002.2      P
weak similarity to Smt4p
7779_at     8975.2      P
strong similarity to YFL004w, similarity to YJL012c
7780_at     1456.7      P
Important for chromosome segregation
```

7781_at 54.5 A
strong similarity to Lpd1p and other dihydrolipoamide dehydrogenases
7782_at 2178.2 P
Zinc-finger transcription factor
7783_at 2764.6 P
Homolog of SIR2
7784_at 1911.7 P
hypothetical protein
7785_at 3417.1 P
ribosomal protein S16, mitochondrial
7786_at 5396.4 P
hypothetical protein
7787_at 919.8 P
Component of the TAF(II) complex (TBP-associated protein complex)
7743_at 5748.2 P
coatomer complex zeta chain
7744_at 3867.7 P
similarity to M.jannaschii hypothetical protein
7745_at 733.1 P
kinetochore protein in the DEAH box family
7746_at 1186.0 P
hypothetical protein
7747_at 4487.7 P
predicted transmembrane protein
7748_at 640.7 P
weak similarity to Nup2p
7749_at 9140.5 P
strong similarity to YGR086c
7750_at 520.4 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 1155.1 P
appears to be functionally related to SNF7
7752_at 1178.2 P
histone acetyltransferase
7753_at 108.1 A
Mitochondrial isoform of citrate synthase
7754_at 541.0 P
similarity to B.subtilis mmgE protein
7755_at 213.5 M
similarity to sulphate transporter proteins
7756_at 5796.7 P
strong similarity to electron transfer flavoproteins alpha chain
7757_at 778.6 A
polar 32k Da cytoplasmic protein
7758_at 1542.0 P
Isocitrate lyase, may be nonfunctional
7759_at -44.9 A
hypothetical protein
7760_at 1643.2 P
similarity to transcription factor
7761_at 1827.3 P
similarity to sterol uptake protein Sut1p
7762_at 10166.2 P
RNA polymerase I subunit A135

7763_at	2196.0	P	similarity to ADP/ATP carrier proteins and Graves disease carrier protein
7764_at	694.1	M	hypothetical protein
7765_at	1600.5	P	similarity to transcription factors
7721_at	-11.0	A	hypothetical protein
7722_at	241.8	A	similarity to transcription factors
7723_at	9902.7	P	similar to human translation initiation factor 6 (eIF6)
7724_at	1466.2	P	GDP dissociation factor for Sec4p
7725_at	759.6	P	p90 subunit of yeast omatin Assembly Factor-I (CAF-I)
7726_at	1763.3	P	essential for initiation of DNA replication\; homolog of S. pombe CDC21
7727_at	3117.7	P	hypothetical protein
7728_at	718.4	P	similarity to human citrate transporter protein
7729_at	983.6	P	weak similarity to fruit fly dorsal protein and Snf5p
7730_at	7303.5	P	similarity to human hypothetical protein
7731_at	2553.4	P	Mitochondrial protein of the CDC48\/PAS1\/SEC18 family of ATPases
7732_at	1075.2	P	novel cyclin gene\; encodes subunits of TFIIK, a subcomplex of transcription factor TFIIH
7733_at	531.6	P	null mutant is viable\; increased tolerance to dehydration, freezing, and toxic levels of ethanol
7734_at	199.9	A	similarity to YNL019c and YNL033w
7735_at	9240.5	P	Ypt Interacting Protein
7736_at	10018.2	P	Ypt Interacting Protein
7737_at	4630.4	P	Gamma-adaptin, large subunit of the clathrin-associated protein (AP) complex
7738_at	142.7	A	similarity to YBL101c
7739_at	459.1	P	similarity to human zinc-finger protein BR140
7740_at	1155.2	P	yeast homolog of the Drosphila tumor suppressor, lethal giant larvae
7741_at	9141.1	P	cytoplasmic and mitochondrial histidine tRNA synthetases
7742_at	1802.5	P	Actin-related protein
7698_at	13714.6	P	glutamine synthetase
7699_at	9888.0	P	54-kDa vacuolar H(+) ATPase subunit of V1 sector
7700_at	4506.5	P	similarity to Erv1p and rat ALR protein

7701_at	43.6	A	questionable ORF
7702_g_at	1450.6	P	questionable ORF
7703_at	482.3	A	questionable ORF
7704_at	1375.5	P	similarity to C.elegans C02C2.6 protein
7705_at	5355.6	P	Translation initiation factor eIF-5
7706_at	2909.9	P	similarity to Jsn1p
7707_i_at	17765.1	P	Ribosomal protein L43A
7708_f_at	8313.5	P	Ribosomal protein L43A
7709_at	509.9	P	questionable ORF
7710_at	774.2	P	similarity to C.elegans hypothetical protein
7711_at	774.6	P	Required for chromosome segregation
7712_at	531.8	P	alpha subunit of yeast mitochondrial phenylalanyl-tRNA synthetase
7713_at	2501.0	P	similarity to M.domestica NADPH--ferrihemoprotein reductase and mammalian nitric-oxide synthases
7714_at	1435.7	A	similarity to Uso1p
7715_at	595.2	P	questionable ORF
7716_at	3959.2	P	N-acetyltransferase
7717_at	7964.6	P	11-kDa nonhistone chromosomal protein
7718_g_at	8870.2	P	11-kDa nonhistone chromosomal protein
7719_at	2060.3	P	questionable ORF
7720_at	-12.0	A	MAP kinase
7675_at	886.0	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	1579.5	P	Component of RNA polymerase transcription initiation TFIIH (factor b), 37 kDa subunit
7677_at	1419.7	P	Protein involved in snRNP biogenesis
7678_at	6521.9	P	putative mitochondrial carrier protein
7679_at	301.3	P	questionable ORF
7680_at	6333.9	P	chorismate mutase
7681_at	225.5	P	weak similarity to Synechococcus sp. DnaJ protein
7682_at	7393.4	P	

cytosine deaminase		
7683_at	8291.7	P
hypothetical protein		
7684_at	335.8	A
hypothetical protein		
7685_at	2543.0	P
site-specific DNA binding protein, repressor		
7686_at	884.8	P
ubiquitin-like protein activating enzyme		
7687_at	1897.7	P
weak similarity to F.alni nitrogen fixation protein		
7688_at	340.0	P
Protein with similarity to Hda1p, Rpd3p, Hos2p, and Hos3p		
7689_at	7498.7	P
putrescine aminopropyltransferase (spermidine synthase)		
7690_at	765.3	P
hypothetical protein		
7691_at	1516.6	P
strong similarity to YIL029c		
7692_at	3323.8	P
member of the NOT complex, a global negative regulator of transcription		
7693_at	1939.0	P
18-kDa phosphotyrosine phosphatase of unknown function		
7694_at	11384.6	P
Transketolase 1		
7695_at	2032.8	P
imparts Far- phenotype		
7696_at	2.7	A
questionable ORF		
7697_i_at	354.2	P
questionable ORF		
7653_s_at	-25.7	A
questionable ORF		
7654_at	0.4	A
hypothetical protein		
7655_at	787.7	P
weak similarity to human insulin-like growth factor 2 receptor		
7656_s_at	11223.4	P
translational elongation factor EF-1 alpha		
7657_at	1604.6	P
strong similarity to glycyl-tRNA synthetases		
7658_at	2362.6	P
S. pombe dim1+ in budding yeast		
7659_at	454.1	P
hypothetical protein		
7660_at	1469.5	P
hypothetical protein		
7661_at	512.2	P
hypothetical protein		
7662_at	6970.6	P
transcription factor TFIIB homolog		
7663_at	647.2	P
questionable ORF		
7664_at	7685.8	P
Signal recognition particle subunit (homolog of mammalian SRP54)		
7665_at	1196.0	P

questionable ORF
7666_at 4594.4 P
hypothetical protein
7667_at 1395.1 P
weak similarity to C.elegans LIM homeobox protein
7668_at 188.1 P
questionable ORF
7669_at 655.5 P
weak similarity to zinc-finger proteins
7670_at 3149.9 P
weak similarity to chicken lim-3 protein
7671_at 666.1 P
Suppressor of Ypt3
7672_at 220.2 A
hypothetical protein
7673_at 3646.2 P
hypothetical protein
7674_at 8233.2 P
hypothetical protein
7629_at 233.2 P
questionable ORF
7630_at 3247.2 P
weak similarity to C.elegans hypothetical protein CEC25A1
7631_at 1077.4 P
splicing factor
7632_i_at 18970.1 P
Ribosomal protein L11A (L16A) (rp39A) (YL22)
7633_s_at 13350.0 P
Ribosomal protein L11A (L16A) (rp39A) (YL22)
7634_at 11432.3 P
proteasome subunit
7635_at 544.9 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 2091.2 P
hypothetical protein
7637_at 950.2 P
protein kinase
7638_at 1676.3 P
Yeast 30kDa Homologue
7639_at 7793.3 P
Subunit of the regulatory particle of the proteasome
7640_at 838.1 P
weak similarity to human nicotinic acetylcholine receptor delta chain
7641_at 6517.5 P
RNA polymerase III (C) subunit
7642_at 196.0 P
kinase required for late nuclear division
7643_at 458.4 P
kinase required for late nuclear division
7644_at 1062.9 P
similarity to RNA-binding proteins
7645_at 12082.3 P
phosphatidylinositol synthase
7646_at 8530.1 P

similarity to YJR116w
7647_at 3664.6 P
similarity to probable transcription factor Ask10p, and to YNL047c and YIL105c
7648_at -44.1 M
hypothetical protein
7649_at 1060.0 P
similarity to YLR454w
7650_at 1175.9 P
similarity to M.jannaschii translation initiation factor, eIF-2B
7651_at 817.4 P
G(sub)2-specific B-type cyclin
7652_at 2519.4 P
B-type cyclin
7607_at 1112.4 P
similarity to B.subtilis transcriptional activator tenA, strong similarity to hypothetical proteins YPL258c and YOL055c
7608_at 1287.1 P
putative homolog of human insulin-degrading endoprotease
7609_at 751.2 A
questionable ORF
7610_at 4526.4 P
High affinity copper transporter into the cell, probable integral membrane protein
7611_at 6895.3 P
suppressor of mrs2-1 mutation
7612_at 738.0 P
questionable ORF
7613_at 1789.1 P
similarity to C-term. of N.tabacum auxin-induced protein
7614_at 4563.4 P
similarity to carrier protein FLX1
7615_at 3015.0 P
multicopy suppressor of clathrin deficiency
7616_at 554.8 P
questionable ORF
7617_at 2971.0 P
similarity to N-acetyltransferases
7618_f_at 17432.0 P
Ribosomal protein S23B (S28B) (rp37) (YS14)
7619_s_at 7920.5 P
Ribosomal protein S23B (S28B) (rp37) (YS14)
7620_at 2895.2 P
similarity to C.elegans hypothetical protein
7621_at 10469.1 P
Translocase of the Outer Mitochondrial membrane
7622_at 991.8 P
Protein involved in splicing intron a15beta of COX1
7623_at 1668.3 P
DNA polymerase alpha binding protein
7624_at 240.6 A
questionable ORF
7625_at 3481.5 P
weak similarity to Taf90p
7626_at 2804.3 P
NH4+ transporter, highly similar to Mep1p and Mep2p
7627_at 2285.5 P
hypothetical protein

```
7628_at     1402.5      P
similarity to human BTHS gene involved in Barth syndrome
7584_at     1202.6      P
kinesin-like nuclear fusion protein
7585_at     409.9       P
questionable ORF
7586_at     1676.9      P
hypothetical protein
7587_at     1907.3      P
similarity to YDR060w and C.elegans hypothetical protein
7588_at     10104.2     P
asparagine synthetase
7589_at     1273.9      P
questionable ORF
7590_at     2387.5      P
hypothetical protein
7591_at     3205.4      P
hypothetical protein
7592_at     8889.1      P
involved in secretion of proteins that lack classical secretory signal sequences
7593_at     144.5       A
questionable ORF
7594_at     684.1       P
weak similarity to YPL159c
7595_at     611.2       P
hypothetical protein
7596_at     791.1       P
hypothetical protein
7597_at     5588.8      P
similarity to chicken growth factor receptor-binding protein GRB2 homolog
7598_at     528.0       P
Regulates proper expression of subunits 6 (Atp6p) and 8 (Atp8p) of the Fo-F1 ATP synthase
7599_i_at   129.2       P
similarity to multidrug resistance proteins
7600_s_at   11627.5     P
similarity to multidrug resistance proteins
7601_at     659.1       P
strong similarity to YGR141w
7602_at     1114.1      P
similarity to YGR142w
7603_at     8158.8      P
potential beta-glucan synthase
7604_at     221.6       P
Glycogen phosphorylase
7605_at     1482.2      P
CDC28\/cdc2 related protein kinase
7606_at     2069.1      P
56-kDa subunit of origin recognition complex (ORC)
7561_at     10624.7     P
Translation initiation factor eIF-4B
7562_at     526.5       P
killed in mutagen, sensitive to diepoxybutane and\/or mitomycin C
7563_at     9623.2      P
GTP-binding protein of the rho subfamily of ras-like proteins
7564_at     3528.8      P
14 kDa mitochondrial ribosomal protein\; homologous to E. coli S14 protein
```

7565_at	1173.2	P	phosphoadenylylsulfate reductase
7566_at	413.6	P	negative regulator of URS2 of the HO promoter
7567_at	4718.4	P	hypothetical protein
7568_at	38.0	A	hypothetical protein
7569_at	645.1	P	hypothetical protein
7570_at	1027.2	P	strong similarity to YLR456w
7571_at	3761.1	P	defective in vacuolar protein sorting
7572_at	523.5	A	weak similarity to Nbp1p
7573_at	795.0	P	DNA polymerase epsilon, subunit B
7574_at	4340.2	P	Geranylgeranyltransferase Type II beta subunit
7575_at	332.2	P	questionable ORF
7576_at	1022.5	P	associated with the U4\/U6 snRNP
7577_at	318.8	P	hypothetical protein
7578_at	3142.0	P	Along with Uba2p forms a heterodimeric activating enzyme for Smt3p
7579_at	1714.5	P	cytoplasmic GTPase-activating protein
7580_at	5955.6	P	Sm or Sm-like snRNP protein
7581_at	10018.4	P	dolichol phosphate mannose synthase
7582_at	1625.8	P	similarity to human 4-alpha-glucanotransferase (EC 2.4.1.25)/amylo-1,6-glucosidase (EC 3.2.1.33)
7583_at	1114.3	P	Autophagy
7538_at	223.6	P	Transcription factor IIIA (TFIIIA) with putative Zn-fingers
7539_at	6930.0	P	subunit common to RNA polymerases I, II, and III
7540_at	954.9	P	similarity to calmodulin and calmodulin-related proteins
7541_at	1371.2	P	Contains 8 copies of the TPR domain
7542_at	3618.7	P	82-kDa subunit of RNA polymerase III (C)
7543_at	10185.0	P	40 kDa ubiquinol cytochrome-c reductase core protein 2
7544_at	238.7	A	similarity to plasma membrane and water channel proteins
7545_at	203.9	P	Histone and other Protein Acetyltransferase\; Has sequence homology to known HATs and NATs
7546_at	193.7	A	similarity to S.pombe isp4 protein

7547_at 50.4 A

hypothetical protein

7548_at 289.3 P

strong similarity to regulatory protein Mal63p

7549_g_at 3554.5 P

strong similarity to regulatory protein Mal63p

7550_at 11.5 A

questionable ORF

7551_at 3685.3 P

multi-copy suppressor of gal11 null\; member of drug-resistance protein family

7552_at 1543.9 P

Similar to transcriptional regulatory elements YAP1 and cad1

7553_at 302.8 P

Required for arsenate but not for arsenite resistance

7554_at 28.9 A

involved in arsenite transport

7555_s_at 2713.5 P

trans-acting positive regulator of the enolase and glyceraldehyde-3-phosphate dehydrogenase gene families

7556_at 801.4 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 11365.8 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 -22.9 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 745.5 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 273.2 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 4428.3 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 136.1 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 555.7 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 -41.5 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 948.2 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 609.2 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 349.7 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 465.2 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 7919.9 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 5668.6 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 -20.4 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 365.7 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 1419.2 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 1371.0 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 3563.7 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
7527_r_at 68.6 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 221.5 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
7529_at 614.0 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 901.6 A
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 6279.8 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 1214.5 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 9034.2 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 -574.9 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 -56.5 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 539.3 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 388.5 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 519.6 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 833.7 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 409.1 A
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 348.4 A
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 6789.1 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 33.8 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 18.8 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 442.2 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 -25.1 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 105.3 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 285.3 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 127.8 A
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 -193.0 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 211.4 M
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 1235.8 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 224.2 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 310.8 P
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 1481.1 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 750.6 P
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 344.1 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 454.4 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 1340.8 P
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 -356.0 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 114.0 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 72.0 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 -1.7 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 109.6 A
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 10260.6 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 76.0 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 643.5 A
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 1264.7 P
snRNA
7474_at 1525.1 P
snRNA
7475_at 5204.9 P
snRNA
7476_at 2576.0 P
snRNA
7477_at 682.3 P
snRNA
7478_s_at 885.9 P
similarity to subtelomeric encoded proteins
7479_at 1343.5 P
hypothetical protein
7480_at 916.6 P
yeast homolog of the Drosphila tumor suppressor, lethal giant larvae
7481_at 1844.8 P
putative protein kinase
7482_at 1902.8 P
hypothetical protein
7483_at 1082.7 P
Probable cytochrome c subunit, copper binding

7484_at 8140.3 P
suppressor of sed5 ts mutants
7485_at 3977.7 P
ExtraCellular Mutant
7486_at 272.7 A
questionable ORF
7487_at 8795.2 P
mitochondrial F1F0-ATPase alpha subunit
7488_at 3866.4 P
similarity to human and D.melanogaster kynurenine 3-monooxygenase
7443_at 45.7 P
BARREN, a gene with sequence similarity to Drosophila barren and Xenopus XCAP-H, and a functional homolog of human BRRN1
7444_at 1796.6 P
questionable ORF
7445_at 1163.7 P
similarity to C.albicans hypothetical protein
7446_at 598.5 P
questionable ORF
7447_at 1451.7 P
RNA polymerase II holoenzyme\/mediator subunit
7448_at 11080.9 P
Ribosomal protein L32
7449_at 2660.9 P
weak similarity to SCS2
7450_at 9945.4 P
methionine aminopeptidase 2
7451_at 359.4 P
Component of the small subunit of mitochondrial ribosomes
7452_at 2087.8 P
weak similarity to A.thaliana aminoacid permease AAP3
7453_at 1184.2 P
putative phosphatidylinositol kinase
7454_s_at 11704.5 P
Ribosomal protein L23A (L17aA) (YL32)
7455_at 672.3 P
involved in sugar metabolism
7456_at 2553.7 P
BEM1-binding protein
7457_at 2988.5 P
component of the anaphase-promoting complex
7458_i_at 220.9 P
questionable ORF
7459_s_at 3389.2 P
questionable ORF
7460_at 4465.4 P
putative Dol-P-Man dependent alpha(1-3) mannosyltransferase involved in the biosynthesis of the lipid-linked oligosaccharide
7461_at 2044.1 P
hypothetical protein
7462_at 322.9 P
62-kDa protein
7463_at 2758.2 P
Nucleoporin highly similar to Nup157p and to mammalian Nup155p (nup170 mutant can be complemented with NUP155)
7464_at 5383.7 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 470.9 P
questionable ORF
7421_at 9877.5 P
cytoplasmic isoleucyl-tRNA synthetase
7422_at 460.5 A
heat-inducible cytosolic member of the 70 kDa heat shock protein family
7423_at 631.1 P
splices pre mRNA of the MATa1 cistron
7424_at 137.5 A
questionable ORF
7425_s_at 11806.6 P
Ribosomal protein S8A (S14A) (rp19) (YS9)
7426_at 639.2 P
hypothetical protein
7427_at 14.7 A
questionable ORF
7428_at 6403.3 P
ribose-phosphate pyrophosphokinase 4
7429_at 1410.9 P
ubiquitin carboxyl-terminal hydrolase
7430_at 251.4 A
putative transcription factor
7431_at 324.5 P
questionable ORF
7432_at 2470.3 P
Homolog to thiol-specific antioxidant
7433_at 593.8 P
kinesin related protein
7434_at 494.7 A
questionable ORF
7435_at 1846.0 P
protoplast regeneration and killer toxin resistance gene, may be a post-translational regulator of chitin synthase III activity, interacts with Chs3p
7436_at 407.1 P
hypothetical protein
7437_at 100.3 A
weak similarity to hypothetical protein YER093c-a
7438_at 1005.6 P
weak similarity to hypothetical protein YER093c-a
7439_at 7901.6 P
isolated as a suppressor of the lethality caused by overexpression of the phosphoprotein phosphatase 1 catalytic subuniut encoded by GLC7
7440_at 2205.9 P
strong similarity to hypothetical S.pombe protein
7441_at 2789.2 P
protein phosphatase type 2C
7442_at 2797.7 P
similarity to hypothetical S.pombe protein
7398_at 2097.7 P
Homolog to myb transforming proteins
7399_at 1544.9 P
questionable ORF

7400_at	526.6	P		SAS3 for Something about silencing, gene 3. Influences silencing at HMR.
7401_at	3534.4	P		similarity to S.pombe Z66568_C protein
7402_at	3587.2	P		peripheral membrane protein required for vesicular transport between ER and Golgi
7403_at	322.5	P		hypothetical protein
7404_at	387.4	P		hypothetical protein
7405_at	5053.5	P		USO1 homolog (S. cerevisiae), cytoskeletal-related transport protein, Ca++ binding
7406_at	2792.1	P		weak similarity to hypothetical protein YOR054c
7407_at	7486.5	P		44 kDa core protein of yeast coenzyme QH2 cytochrome c reductase
7408_at	-5.5	A		hypothetical protein
7409_at	1563.6	P		ExtraCellular Mutant
7410_at	9999.6	P		uridine permease
7411_at	9361.8	P		proteasome subunit
7412_at	3702.0	P		encodes the HDEL receptor required for retention of ER proteins
7413_at	8965.5	P		CTP synthase, highly homologus to URA8 CTP synthase
7414_at	1205.4	P		Mitochondrial ribosomal protein MRPL16
7415_at	1421.6	P		clathrin Associated Protein complex Large subunit
7416_at	2800.4	P		Homolog to twitching motility protein (P. aeroginosa)
7417_at	1945.4	P	B	subunit of DNA polymerase alpha-primase complex
7418_at	1833.6	P		suppressor of cold-sensitive tub2 mutation\; shown to be a component of the mitotic spindle
7419_at	5039.4	P		GTP cyclohydrolase II
7420_at	7036.3	P		weak similarity to hnRNP complex protein homolog YBR233w
7374_at	335.3	P		hypothetical protein
7375_at	12172.7	P		mitochondrial ADP\/ATP translocator
7376_at	655.7	A		hypothetical protein
7377_at	2663.7	P		involved in mating-type regulation
7378_s_at	15023.0	P		Ribosomal protein L19B (YL14) (L23B) (rpl5L)
7379_i_at	258.4	P		snRNA-associated protein of the Sm class
7380_f_at	120.9	P		snRNA-associated protein of the Sm class

7381_at	3564.1	P	snRNA-associated protein of the Sm class
7382_at	682.2	P	Upstream activation factor subunit
7383_at	6475.7	P	Probable proliferating-cell nucleolar antigen (human p120)
7384_at	2954.3	P	Minichromosome maintenance protein, transcription factor
7385_at	8475.2	P	mitochondrial ATP-dependent protease
7386_at	1388.3	P	transcriptional activator protein of CYC1
7387_at	3671.3	P	67 kDa integral membrane protein
7388_at	273.7	P	AP endonuclease
7389_at	2645.0	P	integral subunit of RNase P and apparent subunit of RNase MRP
7390_at	5787.3	P	carboxypeptidase Y sorting receptor in late Golgi\; Type I integral membrane protein 166aa cytoplasmic tail, 1300 aa lumenal domain
7391_at	4685.0	P	cdc2+\/CDC28 related kinase with positive role in conjugation
7392_at	2321.4	P	acetyl CoA hydrolase
7393_at	1000.6	P	member of yeast Pol I core factor (CF) also composed of Rrn11p, Rrn7p and TATA-binding protein
7394_at	500.6	P	Probable met-tRNA formyltransferase, mitochondrial
7395_at	108.2	A	questionable ORF
7396_at	4094.2	P	High copy suppresor of choline-transport mutants
7397_at	370.6	P	hypothetical protein
7352_at	1998.6	P	strong similarity to DNA damage responsive Alk1p
7353_at	646.9	P	putative repressor protein homologous to yeast Tup1p and mammalian retinal transducin\; contains nuclear targeting signal
7354_at	6130.5	P	contains 3 SH3 domains, interacts with Bee1p
7355_at	3955.5	P	hypothetical protein
7356_at	1625.3	P	Pleiotropic drug resistance protein 3
7357_at	4113.1	P	weak similarity to Papaya ringspot virus polyprotein
7358_s_at	17923.7	P	Histone H2A (HTA1 and HTA2 code for nearly identical proteins)
7359_at	14311.6	P	Histone H2B (HTB1 and HTB2 code for nearly identical proteins)
7360_at	7041.1	P	ExtraCellular Mutant
7361_at	1823.7	P	Neutral trehalase, highly homologous to Nth1p

7362_at	2401.5	P	strong similarity to hypothetical protein YMR101c
7363_at	5143.7	P	hexaprenyl pyrophosphate synthetase
7364_at	3705.0	P	similarity to S.pombe hypothetical protein SPAC18B11.05
7365_at	2628.1	P	strong similarity to hypothetical protein YDR003w
7366_at	1195.0	P	hypothetical protein
7367_at	2895.3	P	Major Facilitator Transporter
7368_i_at	7632.9	P	Histone H3 (HHT1 and HHT2 code for identical proteins)
7369_s_at	9164.6	P	Histone H3 (HHT1 and HHT2 code for identical proteins)
7370_at	13776.2	P	Inorganic pyrophosphatase
7371_at	1135.4	P	hypothetical protein
7372_at	1297.6	P	hypothetical protein
7373_at	2542.2	P	Glutaredoxin homolog
7328_at	4916.0	P	Type II transmembrane protein
7329_at	8546.7	P	strong similarity to hypothetical proteins YDL012c and YDR210w
7330_at	3583.9	P	karyopherin beta 2, yeast transportin
7331_at	185.6	A	galactose-1-phosphate uridyl transferase
7332_at	212.6	P	UDP-glucose 4-epimerase
7333_at	272.5	P	galactokinase
7334_at	4442.6	P	uracil permease
7335_at	1706.8	P	hypothetical protein
7336_at	8188.2	P	chitin synthase 3
7337_at	1307.9	P	SCO1 protein homolog (S. cerevisiae)
7338_at	9534.2	P	probable purine nucleotide-binding protein
7339_at	1505.9	P	Nuclear protein that binds to T-rich strand of core consensus sequence of autonomously replicating sequence
7340_at	435.1	A	hypothetical protein
7341_at	991.9	P	Probable ser\/thr-specific protein kinase, homolog to YKR2 and YPK1 (S. cerevisiae)
7342_at	5627.3	P	CDP-diacylglycerol synthase, CTP-phosphatidic acid cytidylyltransferase, CDP-diglyceride synthetase
7343_at	1431.8	P	

involved in inositol biosynthesis

7344_i_at 1913.4 P

Ribosomal protein L4A (L2A) (rp2) (YL2)

7345_s_at 13466.0 P

Ribosomal protein L4A (L2A) (rp2) (YL2)

7346_at 418.9 P

hypothetical protein

7347_at 326.5 P

Probable regulatory Zn-finger protein,\/ homolog to YKL251\/

7348_at 5308.1 P

nuclear protein arginine methyltransferase (mono- and asymmetrically dimethylating enzyme)

7349_at 5914.7 P

pyridoxine (pyridoxiamine) phosphate oxidase

7350_at 6869.4 P

contains 9 or 10 putative membrane spanning regions\; putative Ca2+ binding protein (homology to EF-hand Ca2+ binding site)

7351_at 2311.4 P

inner mitochondrial membrane protein

7306_at 1897.3 P

chitin synthase 2

7307_at 10713.3 P

gamma subunit of mitochondrial ATP synthase

7308_at 626.5 P

integral membrane protein

7309_at 2183.8 P

Fatty acid transporter

7310_at 1921.8 P

Probable membrane-bound small GTPase

7311_at 3610.1 P

similarity to benomyl/methotrexate resistance protein

7312_at 746.8 A

similarity to chaperonin HSP60 proteins

7313_at 182.5 A

Glc7-interacting protein.

7314_at 1534.7 P

Homolog to quinone oxidoreductase (E. coli)

7315_at 820.2 P

hypothetical protein

7316_s_at 8981.4 P

Ribosomal protein S11B (S18B) (rp41B) (YS12)

7317_at 1244.2 P

RNA polymerase I enhancer binding protein

7318_at 890.9 P

Possible regulatory subunit for the PP1 family protein phosphatase Glc7p

7319_at 186.9 A

questionable ORF

7320_at 7804.5 P

Homolog to YCR004, obr1 (S. pombe), trp repressor binding protein (E. coli)

7321_at 1900.3 P

similarity to rat regucalcin

7322_at 4330.5 P

Homolog to HSP30 heat shock protein YRO1 (S. cerevisiae) 7

7323_at 2142.6 P

RNA splicing factor

7324_at 649.1 P

Homolog to glucan-1,3--glucosidase (EC 3.2.1.5\; S. cerevisiae) 2

7325_at 521.6 P
Muddled Meiosis
7326_at 2290.4 P
Ubiquitin-specific protease
7327_at 1622.9 P
Probable protein kinase
7283_at 3106.0 P
origin recognition complex subunit 2
7284_at 4623.3 P
Homolog to ftsJ protein (E. coli) ,\/ YCR054\/
7285_at 8958.7 P
similarity to rat neurodegeneration associated protein 1
7286_at 965.3 P
Probable phosphopanthethein-binding protein
7287_at 146.1 M
questionable ORF
7288_at 394.7 P
ExtraCellular Mutant
7289_at 1202.5 P
Probable Zn-finger protein
7290_at 9750.2 P
cell wall mannoprotein
7291_at 8694.7 P
probable amino acid permease for leucine, valine, and isoleucine
7292_at 3852.4 P
Probable amino acid transport protein
7293_at 2190.7 P
osmotolerance protein
7294_at 1492.7 P
hypothetical protein
7295_at 1632.3 P
heat shock protein 26
7296_at 2442.3 P
Putative helicase similar to RAD54
7297_at 2489.5 P
Homolog to aminopeptidase Y (S. cerevisiae)
7298_at 1595.2 P
hypothetical protein
7299_at 248.1 P
ExtraCellular Mutant
7300_at 3610.8 P
hypothetical protein
7301_at 10736.1 P
Homolog to sporulation specific protein SPS2 (S. cerevisiae)
7302_at 8589.9 P
Homolog to sporulation specific protein SPS2 (S. cerevisiae)
7303_at 6968.5 P
Exhibits significant sequence similarity with a subunit of the mammalian translation initiation factor 3
7304_at 4555.6 P
cytoplasmic protein involved in protein transport between ER and Golgi\; ATPase
7305_at 1911.6 P
transcription factor, member of the histone acetyltransferase SAGA complex
7260_at 11574.3 P
ubiquitin-conjugating enzyme
7261_at 6028.6 P
transcription factor of the TEA\/ATTS DNA-binding domain family, regulator of Ty1 expression

7262_at 8078.0 P
mitochondrial C1-tetrahydroflate synthase
7263_at 3199.2 P
mitochondrial ADP\/ATP translocator
7264_at 7678.4 P
Probable transmembrane protein
7265_at 2221.5 P
Subunit 5 of Replication Factor C\; homologous to human RFC 38 kDa subunit
7266_at 6043.9 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 -15.3 A
questionable ORF
7268_at 2375.0 P
11-kDa nonhistone chromosomal protein
7269_g_at 3821.1 P
11-kDa nonhistone chromosomal protein
7270_i_at 10959.1 P
questionable ORF
7271_at 172.9 A
questionable ORF
7272_at 2312.2 P
Nuclear protein involved in mitochondrial intron splicing
7273_at 9633.6 P
Acid phosphatase, constitutive
7274_at 6773.5 P
Acid phosphatase, repressible
7275_at 1309.4 P
weak similarity to pig tubulin-tyrosine ligase
7276_at 3614.2 P
hypothetical protein
7277_at 2474.9 P
hypothetical protein
7278_at 1960.4 P
Myristoylated Serine\/threonine protein kinase involved in vacuolar protein sorting
7279_at 194.3 P
putative transcriptional (co)activator for DNA damage
7280_at 246.2 P
weak similarity to T.brucei mitochondrion hypothetical protein 6
7281_at 237.1 P
questionable ORF
7282_at 7925.1 P
weak similarity to S.pombe hypothetical protein SPBC3B9.01
7238_at 333.5 P
hypothetical protein
7239_at 1591.3 P
weak similarity to human U3 snoRNP associated 55 kDa protein
7240_at 2460.1 P
mitochondrial carrier protein
7241_at 2291.9 P
involved in fructose-1,6-bisphosphatase degradation
7242_at 14828.7 P
May be a membrane protein involved in inorganic phosphate transport and regulation of Pho81p function
7243_at 569.4 P
weak similarity to N.crassa chitin synthase
7244_at 391.0 P

Probable transcription factor
7245_at 7908.1 P
Calmodulin
7246_at 2865.8 P
beta-1,4-mannosyltransferase
7247_at 9994.7 P
Homolog to serendipity protein (D. melanogaster)
7248_at 2899.8 P
Transcription regulatory protein
7249_at 385.4 A
questionable ORF
7250_at 429.9 P
Radiation repair protein, putative DNA helicase
7251_at 9841.3 P
alpha aminoadipate reductase
7252_at 535.1 P
questionable ORF
7253_g_at 633.9 P
questionable ORF
7254_at 89.7 A
transketolase, homologous to tkl1
7255_at 1893.9 P
U1 snRNP A protein
7256_at 867.6 P
Translational activator of COB mRNA
7257_at 11605.6 P
Glycyl-tRNA synthase
7258_at 2162.7 P
Mitochondrial ribosomal protein MRPL36 (YmL36)
7259_at 2356.5 P
transcription factor tau (TFIIIC) subunit 95
7215_at -165.7 A
questionable ORF
7216_at 1428.6 P
Probable phosphoprotein phosphatase (EC 3.1.3.16)
7217_at 6459.1 P
56 kD synthase subunit of trehalose-6-phosphate synthase\/phosphatase complex
7218_at 11257.4 P
H+-transporting ATPase, vacuolar (EC 3.6.1.35)
7219_at 90.2 P
required for autophagy
7220_at 904.2 P
imparts Far- phenotype
7221_at 4640.1 P
cytoplasmic protein involved in mother-specific HO expression
7222_at 1175.5 P
Calcium Caffeine Zinc sensitivity
7223_at 383.8 P
Amino acid permease
7224_at 2159.5 P
Negative regulator of swe1 kinase (which regulates cdc28)
7225_at 3.9 A
questionable ORF
7226_at 4047.6 P
subunit of the Cdc28 protein kinase
7227_at 1000.1 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 2731.7 P
hypothetical protein
7229_at 102.7 P
Unknown
7230_at 3797.7 P
Probable serine-type carboxypeptidase (EC 3.4.16.1)
7231_at 1940.1 P
GTPase activating protein
7232_at 1568.4 P
hypothetical protein
7233_at 2495.9 P
Probable pre-mRNA splicing RNA-helicase
7234_at 8785.8 P
Ominipotent suppressor protein of nonsense codons
7235_at 363.5 P
hypothetical protein
7236_at 5842.5 P
alcohol dehydrogenase isoenzyme V
7237_at 2173.6 P
Probable mitochondrial ribosomal protein S9
7193_at 1491.0 P
strong similarity to hypothetical protein YOL092w
7194_at 114.4 P
Spore-specific protein
7195_at 4918.6 P
D-arabinose dehydrogenase
7196_at 1397.9 P
Probable Zn-finger protein
7197_at 3377.7 P
weak similarity to potato sucrose cleavage protein
7198_at 128.2 P
U4\/U6.U5-associated snRNP protein\; contains a PEST proteolysis motif
7199_at 3300.5 P
Riboflavin biosynthesis protein
7200_at 8208.4 P
25-kDa RNA polymerase subunit (common to polymerases I, II and III)
7201_at 2229.1 P
Stress-inducible riboflavin biosynthetic protein homolog
7202_at 734.4 P
weak similarity to myosins
7203_at 176.1 A
hypothetical protein
7204_at 8099.0 P
hypothetical protein
7205_at 6993.6 P
similarity to human 17-beta-hydroxysteroid dehydrogenase
7206_at 5593.3 P
protein kinase catalytic subunit
7207_at 717.9 P
Homolog to suppressor of reduced viability of starvation (SUR1, S. cerevisiae)
7208_at 11156.5 P
similarity to hypothetical protein YJL171c
7209_at 6505.6 P
Protein that participates in secretory pathway

7210_at	2610.0	P	hypothetical protein
7211_at	6378.7	P	ADP-ribosylation factor-like protein 1
7212_at	1311.5	P	General positive regulator of CDC34\; Suppress some cdc34 mutations when over-expressed
7213_at	2718.4	P	Prephenate dehydrogenase (NADP+)
7214_at	1098.3	P	Pop7 protein, an integral subunit of RNase P and apparent subunit of RNase MRP
7170_at	55.3	P	weak similarity to hypothetical protein YLR324w
7171_at	1894.8	P	HSP70 family member, highly homologous to Sse1p
7172_at	2074.0	P	Suppressor of SEC63 (S.cerevisiae), novel ER translocation component
7173_at	6279.3	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	1408.3	P	Kinesin-related protein suppressing myosin defects (MYO2)
7175_at	1701.3	P	20S proteasome maturation factor
7176_at	40.1	A	questionable ORF
7177_at	3199.0	P	Probable GTP-binding protein
7178_at	2216.0	P	Alpha-Ketoisovalerate Hydroxymethyltransferase
7179_at	7143.7	P	Probable membrane receptor
7180_at	-20.1	A	questionable ORF
7181_at	1334.1	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	95.1	A	Probable resistance protein
7183_at	1711.6	P	Probable DNA-binding transcription factor, Homolog to SRF\/SL-2
7184_at	7044.2	P	strong similarity to hypothetical protein YPL087w
7185_at	254.2	P	alpha-galactosidase
7186_at	1273.5	P	respiratory chain assembly protein
7187_at	28.6	A	Putative ATPase
7188_at	9357.2	P	probable membrane protein
7189_at	1198.7	P	splicing factor
7190_i_at	12692.5	P	Ribosomal protein S9B (S13) (rp21) (YS11)
7191_f_at	10473.8	P	Ribosomal protein S9B (S13) (rp21) (YS11)

7192_at 150.2 P
questionable ORF
7147_at 5063.9 P
Ribosomal protein L21A
7148_at 1787.2 P
Probable carrier protein, mitochondrial
7149_at 403.2 P
Stoichiometric member of mediator complex
7150_at 1617.9 P
hypothetical protein
7151_at 1947.4 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 12140.0 P
Glucose-6-phosphate isomerase
7153_at 714.7 P
weak similarity to hypothetical protein YPL077c
7154_at 4468.7 P
Probable transcription-associated factor protein, probable -transducin type
7155_at 4147.8 P
Putative alpha-1,2-mannosyltransferase
7156_at 494.4 P
contains two SH3 domains
7157_at 3072.6 P
MCM3 protein homolog (S. cerevisiae)
7158_at 233.8 P
hypothetical protein
7159_at 1988.2 P
Probable serine-active lipase, peroxisomal (EX 3.1.1.-)
7160_at 4310.0 P
Putative alpha-1,2-mannosyltransferase
7161_g_at 6227.6 P
Putative alpha-1,2-mannosyltransferase
7162_at 3746.6 P
questionable ORF
7163_at 3358.1 P
probable membrane protein
7164_at 1050.7 P
Urea amidolyase (contains urea carboxylase and allophanate hydrolase)
7165_at 55.0 A
hypothetical protein
7166_at 3199.8 P
strong similarity to D.melanogaster cornichon protein
7167_at 404.1 P
regulator of microtubule stability
7168_at 2366.0 P
negative growth regulatory protein
7169_at 2013.7 P
Effector in the expression of PAPS reductase and sulfite reductase
7124_at 2874.2 P
strong similarity to hypothetical protein YGL056c
7125_at 1115.0 P
highly charged, basic protein
7126_at 723.4 P
strong similarity to hypothetical protein YGL060w
7127_at 655.2 P

autophagy
7128_at 9740.0 P
pyruvate carboxylase
7129_at 1920.9 P
similarity to human acetyl-coenzyme A transporter
7130_g_at 2300.0 P
similarity to human acetyl-coenzyme A transporter
7131_at 8691.1 P
beta subunit of pyruvate dehydrogenase (E1 beta)
7132_at 4562.0 P
Probable AMP-binding protein
7133_at 1573.1 P
hypothetical protein
7134_at 730.0 P
questionable ORF
7135_at 1420.7 P
hypothetical protein
7136_at 194.4 A
questionable ORF
7137_at 1958.9 P
Homolog to ATP-binding protein clpX (E.coli)
7138_at 806.6 P
similarity to hypothetical A.thaliana protein
7139_at 2857.7 P
Homolog to 1,4-a-glucosidase (S.cerevisiae) (EC 3.2.1.3) 3
7140_at 3714.7 P
hypothetical protein
7141_at 700.6 P
similarity to human p97 homologous protein
7142_at 273.9 A
questionable ORF
7143_at 864.9 P
Homolog to human hnRNP complex K protein
7144_at 6402.5 P
similarity to human Arp2/3 protein complex subunit p41-Arc and to human Sop2p-like protein
7145_at 1069.1 P
similarity to bumetanide-sensitive Na-K-Cl cotransport protein
7146_at 3681.4 P
RNA (guanine-7-)methyltransferase (cap methyltransferase)
7102_at 588.9 P
RNA helicase homolog
7103_at 2197.7 P
strong similarity to general chromatin factor Spt16p
7104_at 1461.9 P
Probable Zn-finger protein
7105_at 388.4 P
Probable Zn-finger protein
7106_at 4408.9 P
Probable sugar transport protein
7107_at 2412.9 P
Probable ATP\/GTP-binding protein
7108_at 5901.7 P
UDP-N-acetyl-glucosamine-1-P transferase (GPT)
7109_at 1243.3 P
Probable glutathione peroxidase (EC 1.11.1.9)
7110_at 3111.5 P

Homolog to SNF2\/SWI2 DNA-binding regulatory protein
7111_at 5337.4 P
hypothetical protein
7112_at 6922.0 P
Putative 57 kDa protein with an apparent MW of 70 kDa by SDS-PAGE
7113_at 8654.8 P
glutamine amidotransferase:cyclase
7114_at 10193.5 P
3-deoxy-D-arabino-heptulosonate 7-phosphate (DAHP) synthase isoenzyme
7115_at 116.3 P
hypothetical protein
7116_at 1417.0 P
Probable mitochondrial ribosomal protein S5
7117_at 10314.5 P
dUTP pyrophosphatase (dUTPase)
7118_at 380.2 P
transcription factor, part of Srb\/Mediator complex
7119_at 2139.3 P
probable membrane protein
7120_at 330.8 P
hypothetical protein
7121_at 1133.4 P
Riboflavin synthase alpha-chain
7122_at 969.5 P
Required for normal 5.8S rRNA processing and for tRNA processing\; associated with RNase MRP and RNase P
7123_at 696.8 P
hypothetical protein
7079_at 532.4 P
hypothetical protein
7080_at 2595.8 P
similarity to C.elegans GTPase-activating protein
7081_at 7330.9 P
similarity to hypothetical S. pombe protein
7082_at 3801.8 P
questionable ORF
7083_at 10902.0 P
Serine hydroxymethyltransferase, mitochondrial
7084_at 2175.9 P
Probable small GTP-binding protein
7085_at 7434.2 P
probable membrane protein
7086_at 2180.5 P
Probable mitochondrial protein L37
7087_at 2141.0 P
hypothetical protein
7088_at 355.3 P
Probable ATP\/GTP-binding protein
7089_at 1825.0 P
weak similarity to S.pombe uvi22 protein and hypothetical protein YNL024c
7090_at 810.6 P
Hsm3p may be a member of the yeast MutS homolog family
7091_at 2721.5 P
similarity to hypothetical protein YJL048c
7092_at 1137.2 P
Probable protein kinase (growth factor & cytokine receptor family)

7093_at	957.6	P	RAP1-interacting factor, involved in establishment of repressed chromatin
7094_at	3288.6	P	dual specificity protein phosphatase
7095_at	16.0	A	questionable ORF
7096_at	1152.6	P	C and C subunits of DNA polymerase II
7097_at	1947.6	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	1587.3	P	hypothetical protein
7099_at	1356.7	P	Probable G-protein, -transducin type
7100_at	2490.1	P	Mitochondrial ribosomal protein MRPL27 (YmL27)
7101_at	8482.1	P	Probable SEC61 protein homolog
7057_at	322.5	P	similarity to AMP deaminase
7058_at	-31.4	A	hypothetical protein
7059_at	14669.0	P	Aminopeptidase yscIII
7060_at	6796.3	P	similarity to hypothetical S. pombe protein
7061_at	1685.5	P	clathrin associated protein medium chain
7062_at	2086.4	P	transcriptional activator
7063_at	1760.6	P	metal homeostasis protein\; putative membrane protein
7064_at	10161.9	P	citrate tranporter in mitochondrial inner membrane
7065_at	1025.1	M	hypothetical protein
7066_at	2158.9	P	Probable multidrug resistance protein
7067_at	78.9	A	Probable sulfate transport protein
7068_at	1534.3	P	Putative P-type Cu(2+)-transporting ATPase
7069_at	8152.7	P	Homolog to phosphate-repressible phosphate permease
7070_at	410.6	P	Maltose fermentation regulatory protein
7071_s_at	646.0	P	maltose permease
7072_s_at	178.1	P	Maltase (EC 3.2.1.20)
7073_at	433.5	P	strong similarity to hypothetical protein YGR293c
7074_f_at	2026.1	P	YKL224 c homolog
7075_at	107.2	A	

hypothetical membrane protein
7076_at 2479.8 P
identified by SAGE
7077_at 5127.0 P
identified by SAGE
7078_at 1666.7 P
hypothetical protein
7033_at 337.5 P
questionable ORF - upstream ORF of ALG1
7034_i_at 6706.1 A
identified by SAGE
7035_s_at 12452.5 P
identified by SAGE
7036_s_at 2394.9 P
Protein involved in targeting of plasma membrane [H+]ATPase
7037_s_at 678.6 P
Probable aldehyde dehydrogenase (EC 1.2.1.-)
7038_s_at 1958.6 P
Degradation in the Endoplasmic Reticulum
7039_at -29.3 A
probable membrane protein
7040_g_at 130.5 A
probable membrane protein
7041_s_at 2509.6 P
Probable Zn-finger protein (C2H2 type)
7042_at 873.8 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 1769.3 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 130.0 P
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 5150.8 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 8959.4 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 3422.9 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 643.6 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 136.4 A
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 1929.4 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 47.7 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 561.4 P

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	-14.3	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	-581.5	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	-210.4	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	6.6	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	320.7	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	2550.0	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	7626.8	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	15.7	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	3037.3	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	450.3	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	1393.8	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	765.5	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	4242.3	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	1628.5	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	3574.7	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	9486.9	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	-131.1	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	1597.2	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	-62.2	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	66.9	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	1144.7	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	6249.6	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	4.5	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	-512.3	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	-183.0	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	563.6	A
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	2437.0	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	1.9	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	51.5	P
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	309.8	P
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	-124.3	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	429.4	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	756.2	A
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	908.7	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	-17.0	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	5613.7	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	1532.8	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 1714.3 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 361.3 P
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 313.7 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 105.2 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 1430.4 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 -24.8 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
7001_r_at 56.2 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 670.7 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 -8.0 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 136.3 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 69.0 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 -194.6 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 -274.6 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 2037.7 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
7009_g_at 1262.1 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 215.4 P
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 1033.1 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 1841.8 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 20.8 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 74.9 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 1817.1 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 489.1 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 2939.0 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 179.3 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 632.0 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 30.8 A

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 -121.0 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 -86.2 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 1968.1 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 7270.6 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 1605.2 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 419.7 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 1833.1 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 81.3 P

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 2304.8 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 67.8 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 316.3 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	129.6	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	2315.4	A	Saccharomyces cerevisiae chromosome II, complete chromosome sequence. Found forward in NC_001134 between 1 and 1000 with 100% identity.
6939_g_at	1932.5	P	Saccharomyces cerevisiae chromosome II, complete chromosome sequence. Found forward in NC_001134 between 1 and 1000 with 100% identity.
6940_s_at	333.7	P	Saccharomyces cerevisiae chromosome II, complete chromosome sequence. Found forward in NC_001134 between 1001 and 2000 with 100% identity.
6941_s_at	381.0	P	Saccharomyces cerevisiae chromosome II, complete chromosome sequence. Found forward in NC_001134 between 2001 and 3000 with 100% identity.
6942_at	231.8	A	Saccharomyces cerevisiae chromosome II, complete chromosome sequence. Found forward in NC_001134 between 3001 and 4000 with 100% identity.
6943_g_at	181.4	A	Saccharomyces cerevisiae chromosome II, complete chromosome sequence. Found forward in NC_001134 between 3001 and 4000 with 100% identity.
6944_at	150.7	A	Saccharomyces cerevisiae chromosome II, complete chromosome sequence. Found forward in NC_001134 between 4001 and 5000 with 100% identity.
6945_g_at	1554.2	P	Saccharomyces cerevisiae chromosome II, complete chromosome sequence. Found forward in NC_001134 between 4001 and 5000 with 100% identity.
6946_at	2850.6	P	Saccharomyces cerevisiae chromosome II, complete chromosome sequence. Found forward in NC_001134 between 5001 and 6000 with 100% identity.
6947_g_at	4261.4	P	Saccharomyces cerevisiae chromosome II, complete chromosome sequence. Found forward in NC_001134 between 5001 and 6000 with 100% identity.
6948_i_at	100.7	A	Saccharomyces cerevisiae chromosome II, complete chromosome sequence. Found forward in NC_001134 between 6001 and 6215 with 100% identity.
6949_f_at	443.0	P	Saccharomyces cerevisiae chromosome II, complete chromosome sequence. Found forward in NC_001134 between 6001 and 6215 with 100% identity.
6950_at	3282.4	P	snRNA
6951_at	6615.3	P	telomerase RNA component
6952_at	5283.3	P	telomerase RNA component
6953_at	98.9	A	snRNA
6954_at	195.6	A	snRNA
6955_s_at	127.8	A	putative pseudo-TY5
6956_s_at	225.4	P	Reverse transcriptase
6957_s_at	808.7	P	Bud site selection
6958_s_at	3049.9	P	

Mating type protein alpha-2
6959_s_at 4474.3 P
transcripton factor involved in the regulation of the alpha-specific genes
6960_at -115.4 A
questionable ORF
6961_g_at 7090.4 P
questionable ORF
6915_at 2715.7 P
catabolic serine (threonine) dehydratase
6916_at 2560.1 P
weak similarity to yeast translation regulator Gcd6p
6917_at 781.8 P
similarity to myosin heavy chain form b from Chicken and Xenopus
6918_at 3973.4 P
strong similarity to human Rev interacting protein Rip-1
6919_at 754.8 A
hypothetical protein
6920_at 4826.9 P
Saccharolysin (oligopeptidase yscD)
6921_at 5501.5 P
hypothetical protein
6922_at 1527.0 P
May assist Ste12p in pheromone-dependent expression of KAR3 and CIK1
6923_at 1919.1 P
Methyltransferase
6924_at 2518.8 P
Protease B Non-derepressible
6925_at 1518.5 P
involved in laminarinase resistance
6926_at 5791.9 P
diadenosine 5 ,5 -P1,P4-tetraphosphate phosphorylase I
6927_at 6488.9 P
hypothetical protein
6928_at 17.0 A
strong similarity to sporulation-specific protein Sps2p
6929_at 1168.5 P
hypothetical protein
6930_at 2704.4 P
weak similarity to human ORF
6931_at 82.5 A
questionable ORF
6932_at 2027.1 P
hypothetical protein
6933_at 12665.6 P
protein disulfide isomerase
6934_at 445.5 P
questionable ORF
6935_at 997.8 P
questionable ORF
6936_g_at 8854.0 P
questionable ORF
6937_at 9194.9 P
Glucokinase
6893_at 1132.1 P
regulatory protein
6894_at 2268.3 P

Membrane transporter
6895_at 9615.2 P
SRO9 may overlap in function with tropomyosin and may be involved in organization of actin filaments
6896_at 4304.1 P
similarity to hypothetical protein YDR514c
6897_at 7771.7 P
Glutaredoxin (thiol-transferase)
6898_at 3942.4 P
similarity to hypothetical S.pombe protein
6899_at 2943.9 P
Transcription regulator
6900_at 457.6 P
possesses a SAM (sterile alpha motif)\; interacts with G protein and Ste11p
6901_at 1653.1 P
involved in pre-rRNA processing and ribosome assembly
6902_at 12619.8 P
histidinol dehydrogenase
6903_at 491.0 P
Microtubule-binding protein
6904_at 7390.5 P
weak similarity to glutenins, high molecular weight chain
6905_at 2322.6 P
serine\/threonine-rich membrane protein
6906_at 995.9 P
Protein involved in the integration of lipid signaling pathways with cellular homeostatis
6907_at 3270.5 P
Amino acid permease
6908_at 108.0 P
questionable ORF
6909_at 7706.5 P
beta-IPM (isopropylmalate) dehydrogenase
6910_at 7770.3 P
NifS-like protein
6911_at 984.2 P
hypothetical protein
6912_at 1061.0 P
Cell cycle regulated protein required for axial bud formation\; co-assembles with Bud4p at bud sites
6913_at 1692.1 P
part of budding protein Bud3p due to frameshift in DNA sequence
6914_at 6149.8 P
Protein with RNA recognition motifs
6870_at 855.8 P
strong similarity to Saccharomyces pastorianus hypothetical protein LgYCL010c
6871_at 9719.3 P
Small regulatory subunit of Acetolactate synthase
6872_at 173.1 P
Calcofluor White Hypersensitivity
6873_at 268.7 P
questionable ORF
6874_at 2023.3 P
strong similarity to Saccharomyces pastorianus hypothetical protein LgYCL005w
6875_at 318.4 P
17-kDa phosphatidylserine synthase
6876_at 2256.9 P
strong similarity to Saccharomyces pastorianus hypothetical protein LgYCL002c
6877_at 4730.2 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 45.7 A
similarity to Dom34p
6879_at 37.1 A
hypothetical protein
6880_at 5836.8 P
conserved potential GTP-ginding protein
6881_at 2386.7 P
Mitochondrial ribosomal protein MRPL32 (YmL32)
6882_at 8216.0 P
FMN-binding protein
6883_at 8027.5 P
non-mitochondrial citrate synthase
6884_at 199.1 P
hypothetical protein
6885_at 5736.3 P
Ser\/Thr protein kinase
6886_at 7346.6 P
Reduced viability on starvation protein RVS161
6887_at 368.5 P
strong similarity to Y.lipolytica GPR1 protein and Fun34p
6888_at 3805.1 P
Active transport ATPase
6889_at 35.6 A
weak similarity to M.leprae B1496_F1_41 protein
6890_at 5762.0 A
3-phosphoglycerate kinase
6891_at 428.5 P
DNA polymerase IV
6892_at 819.8 P
hypothetical protein
6848_at 1054.5 P
hypothetical protein
6849_at 5519.6 P
similarity to hypothetical S.pombe protein
6850_at 1971.5 P
Transcription regulator
6851_at 1484.7 P
MAK32 sugar kinase
6852_at 331.4 P
Transcription regulator
6853_at 4122.1 P
MAK31 snRNP
6854_at 774.8 P
Protein induced by heat shock, ethanol treatment, and entry into stationary phase\; located in plasma membrane
6855_at 281.8 A
hypothetical protein
6856_at 2183.5 P
Membrane transporter
6857_at 557.5 P
Asn-tRNA synthetase
6858_f_at 12781.8 P
Proteolipid associated with plasma membrane H(+)-ATPase (Pma1p)
6859_at -156.7 A

hypothetical protein
6860_at 496.0 P
Membrane phospho-diesterase
6861_at 455.5 P
GTPase (RAS-related)
6862_at 2004.2 P
Amino acid permease
6863_at 7706.9 P
required for mitochondrial DNA replication
6864_at 8410.1 P
required for mitochondrial DNA replication
6865_at 1785.9 P
weak similarity to S.pombe hypothetical protein SPBC4C3.06
6866_at 11632.7 P
Ribosomal protein S14A (rp59A)
6867_at 997.8 P
Beige Protein Homologue 1
6868_at 3141.8 P
similarity to mouse nuclear receptor co-repressor N-Cor
6869_at 8882.2 P
Probable subunit of 1,3-beta-glucan synthase\; homolog of ELO1
6825_at 2278.8 P
Component of the exosome 3->5 exoribonuclease complex with Rrp4p, Rrp41p, Rrp42p and Dis3p (Rrp44p).
6826_at 3871.3 P
ribokinase
6827_at 3256.0 P
May collaborate with Pho86p and Pho84p in inorganic phosphate uptake\; protein contains 12 predicted transmembrane domains
6828_at 533.1 P
GTP\/GDP exchange factor for Rsr1 protein
6829_at 30.2 A
questionable ORF
6830_at 686.3 P
TATA binding protein-associated factor (TAF)
6831_at 2030.4 P
hypothetical protein
6832_at 2720.1 P
involved in manganese homeostasis
6833_at -147.8 A
Protease
6834_at 3785.9 P
required for respiration and maintenance of mitochondrial genome
6835_at 3511.6 P
Protein carboxyl methylase
6836_at 88.9 A
questionable ORF
6837_at 7899.9 P
Acyl-CoA cholesterol acyltransferase (sterol-ester synthetase)
6838_at 3.9 A
questionable ORF
6839_at 2616.8 P
weak similarity to ankyrins
6840_at 1869.2 P
a subunit of RSC, a fifteen-protein chromatin remodeling complex and related to the Swi\/snf Complex.
6841_at 8432.8 P

threonine synthase
6842_at 609.6 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 1633.2 P
regulatory protein
6844_at 5659.8 P
weak similarity to hypothetical protein YDL177c
6845_at 4759.2 P
regulatory protein
6846_at 9813.7 P
hypothetical protein
6847_g_at 8078.8 P
hypothetical protein
6803_at 7993.5 P
similarity to Ytp1p protein
6804_at 11.6 A
questionable ORF
6805_at 1533.4 P
G10-like protein
6806_at 3190.4 P
Transcription factor (fork head domain)
6807_at 332.7 P
Zn finger protein, putative ATPase
6808_at 4136.0 P
Intracellular transport protein
6809_at 752.5 P
similarity to hypothetical S.pombe protein
6810_g_at 758.1 P
similarity to hypothetical S.pombe protein
6811_at 5311.2 P
cyclophilin homolog
6812_at 1229.9 P
(required for) Integrity of Mitochondrial Genome 2
6813_at 5818.0 P
regulatory protein
6814_at 845.8 P
protein kinase
6815_at 7811.7 P
shows similarity to glucose-6-phosphate dehydrogenase non-catalytic domains\; homologous to Sol1p and Sol3p
6816_at 1817.0 P
ERS1 protein, ER defect supressor
6817_at 2222.8 P
hypothetical protein
6818_at 4770.9 P
Necessary for accurate chromosome transmission during cell division
6819_at 895.6 P
weak similarity to A.thaliana protein phosphatase 2C
6820_at 1401.7 P
activation mediator subcomplex of RNA polymerase I holoenzyme
6821_at 5792.3 P
weak similarity to Rbk1p
6822_at 2073.7 P
Thioredoxin type II
6823_at 6654.1 P

glucose repression regulatory protein, exhibits similarity to beta subunits of G proteins
6824_at 254.6 M
hypothetical protein
6780_at 1993.4 P
hypothetical protein
6781_at 1133.9 P
questionable ORF
6782_at 3240.6 P
nucleic acid-binding protein
6783_at 4592.8 P
Actin binding protein
6784_at 2829.0 P
predicted GPI-anchored cell wall protein
6785_at 3164.6 P
hypothetical protein
6786_at -7.2 A
Putative serine\/threonine protein kinase most similar to cyclic nucleotide-dependent protein kinase subfamily and the protein kinase C subfamily
6787_at 452.0 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 1988.9 P
nuclear protein that negatively regulates basal transcription
6789_at 2659.8 P
Cell Division Cycle mutant
6790_at 430.9 P
hypothetical protein
6791_s_at -21.4 A
Homeobox-domain containing protein which, together with alpha2, represses transcription of haploid-specific genes in diploid cells
6792_s_at -23.4 A
Homeobox-domain containing protein which, together with alpha2, represses transcription of haploid-specific genes in diploid cells
6793_at 281.1 A
permease involved in the uptake of glycerophosphoinositol (GroPIns)
6794_at 500.9 A
strong similarity to Pep1p
6795_at 1152.3 P
strong similarity to Pep1p
6796_at 7.6 A
strong similarity to Pep1p
6797_at 1110.2 P
Alcohol dehydrogenase
6798_f_at 1401.9 P
member of the seripauperin protein\/gene family (see Gene_class PAU)
6799_at 460.5 P
Alcohol dehydrogenase
6800_at 778.7 P
Transcription regulator
6801_at 69.2 A
hypothetical protein
6802_at 328.5 P
hypothetical protein
6755_i_at 36.9 A
hypothetical protein
6756_at 202.2 P

high-temperature lethal
6757_i_at -7.5 A
Homeobox-domain containing protein which, together with alpha2, represses transcription of haploid-specific genes in diploid cells
6758_at 103.4 P
hypothetical protein identified by SAGE
6759_at 6150.6 P
identified by SAGE
6760_g_at 11977.2 P
identified by SAGE
6761_at 590.4 P
similarity to starvation induced pSI-7 protein of C. fluvum
6762_s_at 531.0 P
Ser\/Thr protein kinase
6763_at 2508.5 P
homologous to mouse and human Tsg101 tumor susceptibility genes
6764_g_at 1081.9 P
homologous to mouse and human Tsg101 tumor susceptibility genes
6765_at -242.0 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 419.8 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 1252.3 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 1595.5 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 50.5 A
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 598.2 A
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 106.4 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 -235.0 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 339.2 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 757.9 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 8962.8 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 614.8 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 1786.7 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 6010.1 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

6779_r_at 48.6 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 190.9 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 9229.7 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 11676.7 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 30.9 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 78.6 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 15.4 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 -52.1 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 444.2 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 95.6 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 -24.0 A
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 -110.5 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 1331.7 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 233.5 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 52.2 P
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 1289.9 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 1908.3 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 4695.8 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 -25.7 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 -36.1 A
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 430.1 P
TY5-1
6751_at 462.8 P
snRNA
6752_i_at -50.6 A
Centromere
6753_at 4228.7 P
snRNA
6754_at 22.4 A
snRNA
6708_at 622.0 P
snRNA
6709_i_at 88.4 A
strong similarity to sugar transport proteins
6710_at 1940.5 P
Hypothetical aryl-alcohol dehydrogenase
6711_at 13.5 A
strong similarity to hypothetical protein YPR079w
6712_at 1224.7 P
hypothetical protein
6713_at 1071.0 P
Protein similar to LIM-domain proteins and to rho\/rac GTPase-activating family of proteins
6714_at 381.5 P
hypothetical protein
6715_at 556.4 P
similarity to E.coli hypothetical protein and to chlorohydrolases
6716_at 3916.2 P
hypothetical protein
6717_at 9651.7 P
p-nitrophenyl phosphatase
6718_at 2499.3 P
Two-component phosphorelay intermediate
6719_at 1051.8 P
protein of unknown function
6720_at 480.7 P
hypothetical protein
6721_at 9613.7 P
3.6-kDa protein, probably membrane-located
6722_at 942.9 P
hypothetical protein
6723_at 2614.0 P
phosphotyrosine-specific protein phosphatase
6724_at 273.7 P
similarity to A.klebsiana glutamate dehydrogenase
6725_at 4659.6 P
Homothallic switching endonuclease
6726_at 3882.3 P
ADP-ribosylation factor GTPase-activating protein (ARF GAP)
6727_at 2609.6 P
similarity to Cdc11p, Cdc3p and human CDC10 protein

6728_at	2344.0	P	Possible RNA binding protein. Homolog of Whi3.
6729_at	1290.2	P	weak similarity to mucin
6730_at	362.5	P	strong similarity to hypothetical protein YNL194c and similarity to YML052w
6686_at	-214.8	A	questionable ORF
6687_at	873.8	P	binds to single-stranded TG1-3 telomere G-tails
6688_at	4242.3	P	strong similarity to S.equisimilis hypothetical protein
6689_at	4750.6	P	strong similarity to S.equisimilis hypothetical protein
6690_at	257.8	P	weak similarity to hypothetical protein YNR061c
6691_at	2656.7	P	Mitochondrial inner membrane protein involved in import of proteins of the ADP\/ATP carrier (AAC) family
6692_at	279.8	P	similarity to Jun activation domain binding protein homologue of A. thaliana
6693_at	1747.8	P	NAD-dependent glutamate dehydrogenase
6694_at	-65.8	A	strong similarity to putative protein kinase NPR1
6695_at	2185.8	P	has an RNA recognition domain in the N-terminal region
6696_at	10961.6	P	Integral membrane component of the endoplasmic reticulum
6697_at	189.5	A	similarity to hypothetical protein YNL176c
6698_at	97.8	A	GABA-specific transport protein
6699_at	809.9	P	similarity to hypothetical S. pombe protein
6700_at	12405.6	P	HMG-like nuclear protein
6701_at	747.2	P	Nuclear-export-signal (NES)-containing protein
6702_at	515.5	P	weak similarity to transporter proteins
6703_at	444.2	P	phorphobilinogen deaminase (uroporphyrinogen synthase), the third step in heme biosynthesis
6704_at	191.6	P	similarity to hypothetical protein YDR233c
6705_at	620.5	P	similarity to Skt5p
6706_at	773.8	P	Mitochondrial ribosomal protein MRPL11 (YmL11)
6707_at	3897.3	P	strong similarity to human D1075-like protein
6663_at	633.2	A	6-O-methylguanine-DNA methylase
6664_at	201.7	A	similarity to sugar transporter proteins
6665_at	6763.9	P	high copy suppressor of abf2 lacking the HMG1-like mitochondrial HM protein\; putative mitochondrial

carrier protein
6666_at 1506.2 P
Anti-silencing protein that causes depression of silent loci when overexpressed
6667_at 232.6 P
hypothetical protein
6668_at 10664.5 P
involved in protein transport from endoplasmic reticulum to Golgi
6669_at 288.2 P
glucose transporter
6670_at 1988.9 P
similarity to N.crassa hypothetical 32 kDa protein
6671_at 3219.0 A
ADP-ribosylation factor
6672_s_at 8381.6 P
Ribosomal protein L35A
6673_at 3264.8 P
ubiquitin fusion degradation protein
6674_at 419.8 P
hypothetical protein
6675_at 781.4 P
hypothetical protein
6676_at 3597.3 P
serine-threonine protein phosphatase 2A
6677_at 275.5 P
questionable ORF
6678_at 266.5 A
hypothetical protein
6679_at 10625.6 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 5275.9 P
Ribosomal protein L41A (YL41) (L47A)
6681_at 324.6 P
weak similarity to S.pombe hypothetical protein SPAC23H3
6682_at 12415.7 P
homocitrate synthase, highly homologous to YDL131W
6683_g_at 13581.5 P
homocitrate synthase, highly homologous to YDL131W
6684_at 1016.6 P
ATPase inhibitor
6685_at 1886.7 P
hypothetical protein
6641_at 1223.7 P
PHO85 cyclin
6642_at 4539.6 P
D-Lactate Dehydrogenase (Cytochrome)
6643_at 570.8 P
similarity to hypothetical protein YCR059c
6644_at 141.0 P
hypothetical protein
6645_at 918.1 P
strong similarity to hypothetical protein YIL079c and weak similarity to cellular nucleic acid binding proteins
6646_at 8439.3 P
mitochondrial enzyme D-lactate ferricytochrome c oxidoreductase

6647_at	3042.8	P	hypothetical protein
6648_at	766.9	P	questionable ORF
6649_at	7570.1	P	Glutamate synthase (NADPH)
6650_at	519.7	P	zinc-finger transcription factor of the Zn(2)-Cys(6) binuclear cluster domain type
6651_at	309.4	P	protein of unknown function
6652_at	3451.0	P	Long-chain alcohol dehydrogenase (glutathione-dependent formaldehyde dehydrogenase)
6653_at	2229.4	P	Asparagine-rich protein
6654_at	3788.2	P	weak similarity to Pyrococcus horikoshii hypothetical protein PHBJ019
6655_at	3908.0	P	nuclear protein that negatively regulates basal transcription
6656_at	1748.7	P	DNA ligase
6657_at	-97.7	A	questionable ORF
6658_at	-167.3	A	hypothetical protein
6659_at	1241.4	P	strong similarity to hypothetical protein YLR206w and to human KIAA0171 protein
6660_at	3799.5	P	Putative RNA helicase of DEAD box family, required for Rap1p localization to telomeres
6661_at	1054.8	P	MEK homolog
6662_at	1519.9	P	questionable ORF
6618_at	7969.3	P	hypothetical protein
6619_at	188.1	A	weak similarity to Pas7p
6620_at	2292.5	P	G(sub)2-specific B-type cyclin
6621_at	385.0	A	MutS homolog involved in chromosome exchange
6622_at	5849.4	P	Something About Silencing 10
6623_at	282.8	M	questionable ORF
6624_at	53.7	A	questionable ORF
6625_at	2423.4	P	RNA polymerase III (C) subunit, homologus to human BN51 protein
6626_at	225.3	P	hypothetical protein
6627_at	2018.8	P	similarity to human mRNA clone RES4-25
6628_at	7003.8	P	Subunit of the regulatory particle of the proteasome
6629_at	392.5	P	weak similarity to Orc3p

6630_at 11291.3 P
alpha subunit of the coatamer complex\; gamma-alpha-COP
6631_at 3972.5 P
hypothetical protein
6632_at 7065.6 P
Cytoplasmic chaperonin subunit required for actin cytoskeleton assembly or function
6633_at 1312.5 P
Cardiolipin synthase
6634_at 1742.1 P
Biotin:apoprotein ligase
6635_at 9929.5 P
RNA polymerase II large subunit
6636_at 393.5 P
hypothetical protein
6637_at 618.4 P
suppressor of snf3 mutant
6638_at 13203.7 P
ADP-ribosylation factor 2
6639_at 6664.9 P
Rho GDP dissociation inhibitor with activity toward Rho1p
6640_at 684.9 P
serine-threonine protein phosphatase 2A
6595_at 2014.0 P
hypothetical protein
6596_at 2762.5 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 12994.2 P
homocitrate synthase, highly homologous to YDL182W
6598_at 5633.6 P
ATPase stabilizing factor
6599_at 11139.7 P
Ribosomal protein P1B (L44) (YP1beta) (Ax)
6600_at 4515.4 P
Ribosomal protein P1B (L44) (YP1beta) (Ax)
6601_at 1173.4 P
hypothetical protein
6602_at 7511.1 P
vacuolar H+\/Ca2+ exchanger
6603_at 1568.9 P
G1 cyclin
6604_at 10867.0 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 10266.9 P
Yeast member of the Histidine Triad protein family (HIT)
6606_at 463.2 A
Yeast member of the Histidine Triad protein family (HIT)
6607_at 4043.7 P
similarity to aldose reductases
6608_at 2080.6 P
similarity to hypothetical protein YJL151c
6609_at 5891.6 P
Ubiquitin-specific protease
6610_at 1757.6 P
hypothetical protein

6611_at 2794.5 P
Mitochondrial protein that regulates mitochondrial iron accumulation iron accumulation
6612_at 1359.3 P
similarity to bovine Graves disease carrier protein
6613_at 116.6 A
questionable ORF
6614_at 3844.1 P
similarity to hypothetical S. pombe protein
6615_at 3796.4 P
Protein with homology to mammalian Nup107p
6616_at 667.1 P
hypothetical protein
6617_at -267.8 A
weak similarity to Rhizobium nodulation protein nodG
6573_at 457.0 P
similarity to hypothetical protein YDR425w
6574_at 2606.0 P
similarity to C-terminus of human TRP-185 protein
6575_at 3846.8 P
Component of the exosome 3->5 exoribonuclease complex with Rrp4p, Rrp41p, Rrp43p and Dis3p (Rrp44p).
6576_at 1846.7 P
hypothetical protein
6577_at 626.7 P
strong similarity to thiamine-repressed protein Thi4p
6578_at 1229.6 P
serine-threonine kinase, subunit of transcription factor TFIIK, a subcomplex of TFIIH
6579_at 252.9 P
cox1 pre-mRNA splicing factor
6580_at 146.6 A
Homeobox-domain containing protein which is a positive regulator of PHO5 and other genes
6581_at 279.5 P
protein of unknown function
6582_at 123.8 P
similarity to H.influenzae sialoglycoprotease (gcp)
6583_at 2870.2 P
UDP-N-acetylglucosamine pyrophosphorylase
6584_at 980.2 P
largest and catalytic subunit of DNA polymerase III (delta)
6585_at 885.8 P
protein kinase
6586_at 6772.4 P
similarity to E.coli arsenical pump-driving ATPase
6587_at 3842.4 P
weak similarity to myosin heavy chain proteins
6588_at 1215.7 P
hypothetical protein
6589_at 7998.2 P
Subunit of the regulatory particle of the proteasome
6590_at 381.7 P
questionable ORF
6591_at 9477.8 P
dolichyl phosphate-D-mannose:protein O-D-mannosyltransferase
6592_at 42.4 P
questionable ORF
6593_at 2014.2 P

dolichyl phosphate-D-mannose:protein O-D-mannosyltransferase
6594_at 3673.4 P
Signal recognition particle subunit
6550_at 418.3 P
weak similarity to mouse FAF1 protein
6551_at 3341.2 P
beta subunit of farnesyltransferase
6552_at 2215.1 P
hypothetical protein
6553_at 1982.3 P
Suppressor of thermosensitive mutations in the DNA polymerase delta gene
6554_at 862.1 P
Living Under Cap-binding complex expression
6555_at 11714.6 P
similarity to hypothetical Synechocystis protein
6556_at -256.2 A
strong similarity to NADH dehydrogenase (ubiquinone)
6557_at 9614.4 P
suppressor of the cold-sensitive snRNP biogenesis mutant brr1-1
6558_i_at 12337.8 P
Ribosomal protein S16B (rp61R)
6559_f_at 11105.2 P
Ribosomal protein S16B (rp61R)
6560_at 16190.6 P
Ribosomal protein L13A
6561_at 6858.7 P
Acidic ribosomal protein P1A (YP1alpha) (A1)
6562_at 1784.3 P
positive regulatory factor with thiamin pyrophosphate-binding motif for thiamin metabolism
6563_at 651.6 P
MDS1 related protein kinase
6564_at 102.1 P
MDS1 related protein kinase
6565_at 4880.1 P
malate dehydrogenase
6566_at 1298.9 P
Required for the vacuolar morphogenesis in yeast
6567_at 1530.5 P
hypothetical protein
6568_f_at 16846.1 P
Ribosomal protein L31A (L34A) (YL28)
6569_at 7065.3 P
Ribosomal protein L31A (L34A) (YL28)
6570_at 2178.1 P
weak similarity to spindle pole body protein NUF1
6571_at 1425.8 P
weak similarity to Cyprinus carpio calcium channel protein
6572_at 5753.7 P
weak similarity to hypothetical protein YMR040w
6527_at 2007.5 P
questionable ORF
6528_at 5515.9 P
Bromodomain protein, homolog of Bdf1
6529_at 775.3 P
translational activator of cytochrome b
6530_at 239.0 A

questionable ORF
6531_at 7582.2 P
Subunit VIIa of cytochrome c oxidase
6532_at 9387.0 P
Mitochondrial form of NADP-specific isocitrate dehydrogenase
6533_at 1001.0 P
40 kDa farnesylated protein associated with peroxisomes
6534_at 5844.1 P
ubiquitin-conjugating enzyme
6535_at 3298.0 P
weak similarity to human estrogen-responsive finger protein
6536_at 193.6 P
questionable ORF
6537_f_at 10954.5 P
Ribosomal protein S29B (S36B) (YS29)
6538_at 8174.6 P
similarity to C.elegans hypothetical protein
6539_at 762.4 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 1553.5 P
Integrin analogue gene
6541_at 890.1 P
hypothetical protein
6542_at 1337.1 P
transcription factor
6543_at 14175.7 P
mannose-1-phosphate guanyltransferase, GDP-mannose pyrophosphorylase
6544_at 2507.9 P
hypothetical protein
6545_at 4004.1 P
hypothetical protein
6546_at 6848.9 P
putative 1-acyl-sn-gylcerol-3-phosphate acyl transferase
6547_at 3766.6 P
Protein homologous to human La (SS-B) autoantigen
6548_at 840.5 P
questionable ORF
6549_at 442.1 P
KRE9 homolog
6504_at 2124.2 P
SIT4 suppress mutations in DBF2
6505_at 9099.1 P
hypothetical protein
6506_at 3663.8 P
homologous to Yml37p, component of the 37 S subunit of mitochondrial ribosomes
6507_at 1071.0 P
FAD synthetase
6508_at 1048.3 P
Necessary for the stability and\/or processing of some large mitochondrial transcripts
6509_at 869.9 P
snRNA-associated protein
6510_at 1088.7 P
regulator of silent mating loci
6511_at 812.7 P

			questionable ORF
6512_at	3757.6	P	N-terminal acetyltransferase
6513_at	5115.2	P	questionable ORF
6514_at	2815.8	P	similarity to mucin proteins
6515_at	3510.9	P	strong similarity to glucan 1,4-alpha-glucosidase
6516_at	2528.7	P	strong similarity to RIB2 protein
6517_at	1735.1	P	G-protein coupled receptor
6518_at	85.5	A	questionable ORF
6519_at	1953.0	P	similarity to H.influenzae hypothetical protein HI0174
6520_at	400.1	A	questionable ORF
6521_at	3050.6	P	DEAD box protein 10
6522_at	796.1	P	RNA splicing factor
6523_at	7469.1	P	actin-related protein
6524_at	607.5	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	485.4	P	hypothetical protein
6526_at	115.9	A	questionable ORF
6482_at	1476.2	P	ser/thr protein kinase of the DEAD/DEAH box family
6483_at	1272.2	P	strong similarity to acid phosphatase
6484_at	30.8	A	questionable ORF
6485_at	4449.4	P	glycerol-3-phosphate dehydrogenase
6486_at	500.5	P	Similar to GPM1 (phosphoglycerate mutase)
6487_at	4454.2	P	involved in ubiquitin degradation pathway
6488_at	3294.0	P	similarity to Osh1p
6489_at	937.5	P	p24 protein involved in membrane trafficking
6490_at	1363.0	P	serine\/threonine protein kinase
6491_at	128.4	A	questionable ORF
6492_at	8055.3	P	similarity to rat synaptic glycoprotein SC2

6493_at 10844.3 P
nucleolar protein, homologous to mammalian fibrillarin
6494_at 2516.4 P
Protein involved in hexose metabolism
6495_at 7036.1 P
strong similarity to hypothetical protein YBR016w and YDR210w
6496_at 265.4 P
questionable ORF
6497_at 1229.9 P
similarity to hypothetical protein YBR014c and glutaredoxins
6498_at 764.8 P
questionable ORF
6499_at 2577.7 P
subunit of the anaphase promoting complex (APC)
6500_at 4717.2 P
Probable 26S protease subunit and member of CDC48\/PAS1\/SEC18 family of ATPases
6501_at 442.1 P
serine-threonine protein phosphatase
6502_at 500.8 P
Stoichiometric member of mediator complex
6503_at 6817.9 P
ATP synthase delta subunit
6459_at 1004.1 P
Mitotic omosome Determinant\; similar to S. pombe RAD21\; may function in chromosome morphogenesis from S phase through mitosis
6460_at 1321.9 P
HMG1-box containing protein
6461_at 713.9 P
similarity to hypothetical protein YFR048w, YDR282c and S.pombe hypothetical protein SPAC12G12.14
6462_at 2473.7 P
neutral trehalase (alpha,alpha-trehalase)
6463_at 11266.4 P
Yeast Ran Binder #1\; suppressor of FUS1\; homolog of mouse HTF9a and human RanBP1
6464_at 925.8 P
strong similarity to hypothetical protein YBR005w
6465_at 1817.1 P
RecA homolog (similar to DMC1, RAD51, and RAD55), interacts with Rad 55p by two-hybrid analysis
6466_at 2130.8 P
required for sorting of Mod5p
6467_at 1591.1 P
gene dosage suppressors of the conditional growth defect of several temperature-sensitive A kinase mutants
6468_at 2398.3 P
n-(5 -phosphoribosyl)-anthranilate isomerase
6469_at 50.8 A
questionable ORF
6470_at 420.7 P
galactokinase
6471_at 63.4 A
hypothetical protein
6472_at 11870.0 P
ABC transporter
6473_i_at 19136.7 P
Ribosomal protein L4B (L2B) (rp2) (YL2)
6474_at 1070.6 P
similarity to human hypothetical KIAA0186 protein

6475_at	257.0	P	weak similarity to chicken neurofilament triplet M protein
6476_at	103.0	A	hypothetical protein
6477_at	2011.4	P	hypothetical protein
6478_at	3001.3	P	Shows homology to basic leucine zipper family of transcription factors
6479_at	189.1	P	strong similarity to hypothetical protein YBR042c
6480_at	3806.5	P	glycine cleavage T protein (T subunit of glycine decarboxylase complex
6481_at	143.2	P	weak similarity to uridine kinases and phosphoribulokinases
6436_at	1315.5	P	DEAD-box protein, putative RNA helicase
6437_at	877.7	P	cik1 suppressor
6438_at	10589.4	P	seryl-tRNA synthetase
6439_at	-45.0	M	hypothetical protein
6440_at	1716.3	P	strong similarity to DNA-binding protein Reb1p
6441_at	2055.1	P	Loss Upsets Vacuole
6442_at	1273.7	P	regulatory subunit for protein phosphatase Glc7p
6443_at	449.1	P	hypothetical protein
6444_at	372.1	P	Protein involved in the same pathway as Rad26p, has beta-transducin (WD-40) repeats
6445_at	1426.7	P	hypothetical protein
6446_at	10225.9	P	strong similarity to S.pombe obr1
6447_at	9616.6	P	strong similarity to putative heat shock protein YRO2
6448_at	1254.2	P	Transcriptional activator of lysine pathway genes with 2-aminoadipate semialdehyde as co-inducer\; saccharopine reductase synthesis
6449_at	2475.1	P	identified by SAGE expression analysis
6450_at	10542.4	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	2945.5	P	similarity to enoyl CoA hydratase
6452_at	14546.2	P	lysyl-tRNA synthetase
6453_at	3143.4	P	P-type ATPase involved in Na+ efflux
6454_g_at	5980.5	P	P-type ATPase involved in Na+ efflux
6455_s_at	4800.3	P	

plasma membrane protein\; putative Na+ pump\; P-type ATPase
6456_at 2002.7 P
weak similarity to bacterial ribosomal S10 proteins
6457_at 111.8 P
hypothetical protein
6458_at 1549.9 P
Suppressor of SNf
6413_at 5472.5 P
Coproporphyrinogen III oxidase
6414_at 6537.8 P
strong similarity to S.acidocaldarius transcription elongation factor tfs
6415_at 6498.9 P
Valine transporter
6416_at 6110.6 P
uroporphyrinogen decarboxylase
6417_at -36.6 A
questionable ORF
6418_at 612.8 P
similarity to C.elegans K06H7.3 protein
6419_at 8207.5 P
triosephosphate isomerase
6420_at 3365.7 P
similarity to hypothetical A. thaliana protein BAC F7G19
6421_at 60.5 P
cyclin-like kinase required for late nuclear division
6422_at -173.5 A
questionable ORF
6423_at 1574.7 P
ubiquitin-conjugating enzyme, E2
6424_at 6817.8 P
strong similarity to SPS2 protein
6425_at 3173.1 P
hypothetical protein
6426_at 438.7 P
weak similarity to L.lactis mleR protein
6427_at 741.7 P
TriGlyceride Lipase
6428_at 1388.2 P
ubiquitin-conjugating enzyme
6429_at 2630.7 P
similarity to mouse putative CCAAT binding factor CBF1 and CBF2
6430_at 2183.4 P
similarity to E.coli modF and photorepair protein phrA
6431_at 9946.6 P
Probable component of serine palmitoyltransferase, which catalyzes the first step in biosynthesis of long-chain sphingolipids
6432_at 3510.8 P
weak similarity to glia maturation factor beta
6433_at 10545.2 P
Ribosomal protein S13 (S27a) (YS15)
6434_at 415.6 P
hypothetical protein
6435_at 406.7 P
similarity to hypothetical protein YER139c
6391_at 1058.3 P
similarity to YNL099c

6392_at	2235.1	P	involved in genome stability
6393_at	817.2	P	ubiquitin isopeptidase
6394_at	479.7	P	hypothetical protein
6395_at	7106.9	P	similarity to O.aries arylalkylamine N-acetyltransferase
6396_at	4871.4	P	inositolphosphotransferase 1
6397_at	2038.5	P	component of SWI\/SNF global transcription activator complex
6398_at	4641.7	P	Trehalose-6-phosphate phosphatase
6399_at	1190.8	P	protein phosphatase type 2A
6400_at	277.6	P	RecA homolog (related to DMC1, RAD51, RAD57), interacts with Rad51p and Rad57p by two-hybrid analysis
6401_at	9634.3	P	putative cell surface glycoprotein
6402_at	1122.7	P	Preferential Use of Neither donor locus during mating type switching.
6403_at	2550.8	P	cytochrome c oxidase-specific assembly factor
6404_at	392.2	P	vacuolar protein sorting
6405_at	2181.0	P	Asparagine and serine-rich protein
6406_at	730.0	P	Involved in telemere length regulation, may be functional in telemere metabolism during late S phase
6407_at	5249.6	P	similarity to hypothetical S.pombe protein
6408_at	4512.4	P	similarity to hypothetical C.elegans protein
6409_at	1517.1	P	coordinates regulation of alpha-factor receptor signalling and induction of morphogenesis during conjugation
6410_at	8291.9	P	endoplasmic reticulum protein that is part of the Sec61 trimeric complex and the Ssh1 trimeric complex
6411_at	2071.0	P	involved in processing rRNA precursor species to mature rRNAs
6412_at	691.4	P	involved in 3 splice site choices and 2nd step of splicing
6368_at	2025.1	P	weak similarity to Streptococcus transposase
6369_at	2709.0	P	weak similarity to YRO2 protein
6370_at	9874.6	P	strong similarity to human RNase L inhibitor and M.jannaschii ABC transporter protein
6371_at	8010.1	P	ubiquitin-conjugating enzyme
6372_at	3076.7	P	similarity to P.falciparum ATPase 2
6373_g_at	8034.2	P	similarity to P.falciparum ATPase 2

6374_at 1777.9 P
questionable ORF
6375_at 428.1 P
hypothetical protein
6376_at 824.6 P
putative zinc finger protein
6377_at 2881.7 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 3838.3 P
similarity to Legionella glutaredoxin-like protein
6379_at 8204.3 P
Homolog of mammalian 14-3-3 proteins
6380_at 5698.7 P
similarity to Dictyostelium development-specific membrane protein
6381_at 5574.7 P
weak similarity to proliferation-associated protein
6382_at 134.2 A
hypothetical protein
6383_at 1612.6 P
Protein of the pheromone pathway
6384_at 600.3 P
hypothetical protein
6385_at 2396.4 P
similarity to mouse hypothetical protein
6386_at 692.1 P
Actin-related protein
6387_at 1123.1 P
strong similarity to Emp70 protein
6388_at 551.6 P
Probably has role late in meiosis following DNA replication
6389_at 674.9 P
similarity to Mpa43p
6390_at 497.0 P
DNA replication fork blocking protein
6346_at 1131.8 P
strong similarity to alanine transaminase
6347_at 33.2 A
questionable ORF
6348_at 202.2 P
42-kDa nuclear protein
6349_at 156.3 A
questionable ORF
6350_at 3422.3 P
similarity to bacterial ribosomal L34 proteins
6351_at 1739.6 P
similarity to bacterial ribosomal L1 proteins
6352_at 2222.6 P
similarity to mouse ligatin, a trafficking receptor for phosphoglycoproteins
6353_at 386.4 P
subunit of the anaphase promoting complex (APC)
6354_at 3967.5 P
similarity to B.subtilis tetracyclin resistance
6355_at 3739.1 P
N2,N2-dimethylguanosine-specific tRNA methyltransferase
6356_at 1721.0 P

weak similarity to YNC2beta protein
6357_at 1400.8 P
Serine\/threonine protein kinase
6358_at 747.6 P
helix-loop-helix protein
6359_at 101.6 A
hypothetical protein
6360_at -26.2 A
ExtraCellular Mutant
6361_at 1327.5 P
similarity to hypothetical protein YLR246w and YOL003c
6362_at 10426.0 P
pentafunctional arom polypeptide (contains: 3-dehydroquinate synthase, 3-dehydroquinate dehydratase (3-dehydroquinase), shikimate 5-dehydrogenase, shikimate kinase, and epsp synthase)
6363_at 2551.6 P
weak similarity to Sec27p, YMR131c and human retinoblastoma-binding protein
6364_at 6654.0 P
fibrim homolog (actin-filament bundling protein)
6365_at 620.1 P
weak similarity to sea urchin myosin heavy chain
6366_at 380.5 P
similarity to hypothetical protein YJL149w
6367_at 454.1 P
strong similarity to hypothetical protein YLR108c
6323_at 10214.7 P
questionable ORF
6324_g_at 13930.9 P
questionable ORF
6325_at 3187.1 P
Metal resistance protein with similarity to human cystic fibrosis protein CFTR and multidrug resistance proteins
6326_at 190.4 P
questionable ORF
6327_at 2383.2 P
Reduced growth phenotype
6328_at 544.4 P
Hyperrecombination protein that suppresses intrachromosomal excision recombination
6329_at 6755.8 P
ubiquitin-like protein
6330_at 5858.6 P
ubiquitin-like protein
6331_at 3626.4 P
weak similarity H.influenzae protoporphyrinogen oxidase (hemK) homolog
6332_at 1712.7 P
hypothetical protein
6333_at 442.0 P
Member of beta-transducin-related (WD-40) protein family
6334_at 2718.3 P
mating-type regulation protein
6335_at 6962.3 P
aspartyl protease related to Yap3p
6336_at 1184.2 P
TFIID subunit
6337_at 1875.6 P
transcriptional activator
6338_at 501.5 P

Ethanolamine Kinase

6339_at 6508.5 P

dihydrolipoyl transsuccinylase component of alpha-ketoglutarate dehydrogenase complex in mitochondria

6340_at 80.3 A

questionable ORF

6341_at 2299.9 P

Protein with variable number of tandem repeats of a 64 amino-acid polypeptide, potential Ca2+-binding site, and pleckstrin homology domain

6342_at 1181.1 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 2224.8 P

weak similarity to C.elegans hypothetical protein CET26E3

6344_at 2754.8 P

hypothetical protein

6345_at 6449.4 P

questionable ORF

6300_g_at 10046.0 P

questionable ORF

6301_at 9637.6 P

cyclophilin peptidyl-prolyl cis-trans isomerase

6302_at 10189.9 P

RNA polymerase I subunit A14

6303_at 2250.6 P

questionable ORF

6304_at 8304.4 P

aspartic beta semi-aldehyde dehydrogenase

6305_at 1926.0 P

Leucine permease transcriptional regulator

6306_at 606.7 P

Ssy1p controls expression of several transporter genes, including BAP2, TAT1, PTR2 and YDR046c

6307_at 1933.7 P

protein phosphatase Two C-Interacting protein

6308_at 559.8 P

Nap1p-binding protein

6309_at 945.6 P

weak similarity to S.pombe hypothetical protein

6310_at 864.1 P

Hydrophilic protein involved at the late stage of secretion

6311_at 2358.6 P

weak similarity to hypothetical C.elegans protein

6312_at 2748.9 P

107 kDa component of the Exocyst complex\; required for exocytosis.

6313_at 3260.1 P

TFIID subunit

6314_at 6138.1 P

Cell cycle protein necessary for passage through START

6315_at 767.2 P

Binds Sin3p in two-hybrid assay

6316_at 9049.4 P

Guanine nucleotide exchange protein for ARF

6317_at 4053.4 P

Similar to HSP26\; expression is regulated by stress conditions

6318_at 6225.6 P

putative translation factor

6319_at 641.2 P

Regulator of arginine-responsive genes with ARG80 and ARG81
6320_at 7056.3 P
Non-histone protein
6321_at 1696.0 P
similarity to S.pombe hypothetical protein SPAC2F7.15
6322_at 538.7 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 8711.2 P
ubiquitin-conjugating enzyme
6279_at 6404.2 P
succinate dehydrogenase membrane anchor subunit
6280_at 118.6 A
hypothetical protein
6281_at 237.3 A
hypothetical protein
6282_at 1758.3 P
Sister chromatid cohesion protein
6283_at 798.2 P
Involved in silencing at telomeres, HML and HMR
6284_at 2938.6 P
Protein that affects bud emergence, intrachromosomal recombination, and nuclear division
6285_at 939.7 P
weak similarity to thioredoxin
6286_at 2166.0 P
Aip Three Complex\; interacts with AIP3, localized to the nucleus
6287_at 265.3 P
strong similarity to Msf1p
6288_at 550.6 P
hypothetical protein
6289_at 162.9 P
questionable ORF
6290_at 7804.1 P
Cytoplasmic chaperonin of the Cct ring complex (previously called TCP1 or TRiC), distantly related to Tcp1p and to Hsp60
6291_at 1217.1 P
Hydrophilic suppressor of ypt1 involved in vesicle trafficking between ER and Golgi
6292_at 7126.0 P
strong similarity to TATA-binding protein-interacting protein 49 - rat
6293_at 561.1 P
Homolog of SIR2
6294_at 938.2 P
nucleoporin
6295_at 418.1 A
questionable ORF
6296_at 6286.4 P
Mitochondrial RNA helicase of the DEAD box family
6297_at 1451.9 P
RNA-binding protein involved in cleavage step of mRNA 3 -end formation, prior to polyadenylation
6298_at 1740.5 P
similarity to C.elegans hypothetical protein T05G5.5
6299_at 723.4 P
cytochrome b translational activator
6255_at 1112.0 P
hypothetical protein

6256_at 196.3 A
questionable ORF
6257_at 399.9 P
similarity to hypothetical protein YLR238w
6258_at 1689.6 P
component of spindle pole
6259_at 1092.8 P
hypothetical protein
6260_at 9.2 A
questionable ORF
6261_at 3474.7 P
Involved in ubiquinone biosynthesis
6262_at 1004.1 P
similarity to A.eutrophus cation efflux system membrane protein czcD, rat zinc transport protein ZnT-1 and Cot1p
6263_at 1950.7 P
EST1-like bcy1 Suppressor
6264_at 1815.6 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 2710.4 P
Phosphatidylinositol 4-phosphate kinase
6266_at 1058.5 P
questionable ORF
6267_at 10070.7 P
strong similarity to hypothetical protein YBR016w
6268_at 5266.2 P
Translation initiation factor eIF-2B epsilon subunit
6269_at 8536.9 P
chaperonin subunit alpha
6270_at 461.2 P
regulatory protein involved in control of sterol uptake
6271_at 7803.5 P
similarity to hypothetical protein YNL281w
6272_at 290.7 A
hypothetical protein
6273_at 513.4 P
positive transcriptional regulator of ADH2 and peroxisomal protein genes
6274_at 699.8 P
cell cycle arrest protein
6275_at 170.2 P
Septin-related protein expressed during sporulation
6276_at 320.4 P
hypothetical protein
6277_at 330.9 P
questionable ORF
6232_at 851.6 P
weak similarity to the beta subunit of an ER luminal alpha-glucosidase from mouse
6233_at 2532.6 P
strong similarity to hypothetical protein YLR225c
6234_at 68.5 A
similarity to Ifh1p
6235_at 11093.7 P
Histone H2B (HTB1 and HTB2 code for nearly identical proteins)
6236_i_at 18931.3 P

Histone H2A (HTA1 and HTA2 code for nearly identical proteins)
6237_at 10142.2 P
cytosolic adenylate kinase
6238_at 354.0 P
regulator of silent mating loci
6239_at 655.3 P
Component of pre-mRNA cleavage and polyadenylation factor I, interacts with Rna14p and Rna15p
6240_at 776.5 P
hypothetical protein
6241_at 141.8 P
questionable ORF
6242_at 1816.8 P
hypothetical protein
6243_at 5728.8 P
5-aminolevulinate synthase
6244_at 11078.1 P
similarity to hypothetical protein YDL204w
6245_at 10059.2 P
homoaconitase
6246_at 1270.2 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 1167.1 P
similarity to hypothetical A. thaliana protein
6248_at 639.9 P
Mitochondrial ribosomal protein MRPL7 (YmL7)
6249_at 9359.0 P
encodes a subunit of yeast coatomer
6250_at 2011.6 P
hypothetical protein
6251_at 587.9 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 15.2 A
questionable ORF
6253_at 1024.6 P
putative amidase
6254_at 723.3 P
Required for the first step of splicing in vitro
6209_at 458.2 P
69-kDa protein containing tetratricopeptide repeat (TPR)
6210_at 4931.1 P
galactosyltransferase
6211_at 3937.6 P
involved in targeting and fusion of ER to golgi transport vesicles
6212_at 739.5 P
strong similarity to Sks1p
6213_at 2641.6 P
strong similarity to E.coli thermoresistant gluconokinase
6214_at 1625.9 P
weak similarity to cytochrome b
6215_at 187.6 P
hypothetical protein
6216_at 2124.1 P
coiled-coil protein multicopy suppressor of loss of PP2A
6217_at 979.0 P

Negative effect on expression of several genes transcribed by RNA polymerase II\; BTF3 homolog
6218_at 323.8 P
zinc finger DNA binding factor, transcriptional regulator of sulfur amino acid metabolism, highly homologous to Met31p
6219_at 157.5 P
Protein necessary for stability of ARS-CEN plasmids\; suggested to be required for kinetochore function
6220_at 1236.9 P
weak similarity to hypothetical S.pombe hypothetical protein SPBC29A3
6221_at 158.2 A
catalase A
6222_at 1219.8 P
Transcription regulator
6223_at 1323.1 P
Mitochondrial heat shock protein 78 kDa
6224_at 323.8 P
bZIP protein
6225_at 1363.9 P
hypothetical protein
6226_at 2321.0 P
Exo-1,3-b-glucanase
6227_at 2883.8 P
hypothetical protein
6228_at 543.3 P
DNA-damage inducible gene
6229_at 2670.6 P
Ankyrin repeat-containing protein
6230_at 710.6 P
C3HC4 zinc-binding integral peroxisomal membrane protein
6231_at 2191.6 P
similarity to hypothetical C.elegans protein
6187_at 1953.3 P
weak similarity to human TAFII100 and other WD-40 repeat containing proteins
6188_at 1155.8 P
mitochondrial tryptophanyl-tRNA synthetase
6189_at 90.5 A
questionable ORF
6190_at 4380.8 P
Copper-transporting P-type ATPase with similarity to human Menkes and Wilsons genes
6191_at 167.6 A
questionable ORF
6192_at 1730.0 P
Cytoplasmic glyoxylase-II
6193_at 223.2 P
weak similarity to YOR042w
6194_at 459.1 A
hypothetical protein
6195_at 1950.5 P
weak similarity to YOR042w
6196_at 11404.9 P
strong similarity to Hordeum vulgare blt101 protein
6197_at 403.3 P
Protein is 61\% identical to Msn3p
6198_at 109.7 P
hypothetical protein
6199_at 975.4 P
hypothetical protein

6200_at	4144.5	P	Putative 3 ->5 exoribonuclease\; component of exosome complex of 3 ->5 exonucleases
6201_at	3119.0	P	hypothetical protein
6202_at	1082.8	P	similarity to hypothetical protein YDL001w, YFR048w and S.pombe hypothetical protein SPAC12G12.14
6203_at	1428.0	P	eukaryotic initiation factor 2 alpha (eIF2-alpha) kinase
6204_at	3371.6	P	Diacylglycerol Pyrophosphate Phosphatase
6205_at	224.8	A	Synaptonemal complex protein, component of the central element
6206_at	1020.8	P	hypothetical protein
6207_at	1455.0	P	similarity to inositolmonophosphatases
6208_at	353.8	P	hypothetical protein
6163_at	395.3	P	hypothetical protein
6164_at	62.4	A	questionable ORF
6165_at	1647.5	P	similarity to B.subtilis helicases
6166_at	2788.0	P	signal recognition particle receptor - alpha subunit
6167_at	3950.1	P	putative protein phosphatase
6168_at	8122.0	P	dihydrosphingosine phosphate lyase (also known as sphingosine phosphate lyase)
6169_at	438.8	P	weak similarity to Uso1p, YPR179c and fruit fly tropomyosin
6170_at	2948.3	P	hypothetical protein
6171_at	6977.7	P	Syringomycin response protein 2
6172_at	4942.3	P	ATP synthase subunit 5\; oligomycin sensitivity-conferring protein
6173_at	1842.8	P	involved in protein transport step at the Brefeldin A blocks
6174_at	4280.9	P	gamma-glutamyl kinase
6175_at	2857.2	P	Component of pre-mRNA cleavage factor II (CFII)\; 150-kDa protein associated with polyadenylation factor 1 (PF I)
6176_at	3275.4	P	weak similarity to human GPI-anchor biosynthesis protein
6177_at	679.7	P	similarity to transcriptional regulator proteins
6178_at	9144.2	P	Cyclophilin D, Peptidyl-prolyl cis-trans isomerase D
6179_at	2641.0	P	Yeast member of the Histidine Triad protein family (HIT)
6180_i_at	196.1	P	Yeast member of the Histidine Triad protein family (HIT)
6181_r_at	31.4	A	

Yeast member of the Histidine Triad protein family (HIT)
6182_f_at 285.2 P
Yeast member of the Histidine Triad protein family (HIT)
6183_at 2144.1 P
weak similarity to S.pombe hypothetical protein SPAC6F6
6184_at 3084.6 P
similarity to Pmt1p, Pmt2p, Pmt3p and Pmt5p
6185_at 2164.0 P
RNA polymerase II holoenzyme component
6186_at 7512.8 P
GTPase-interacting component 2
6140_at 4418.3 P
Suppresor of mar1-1 (sir2) mutation
6141_at 1174.3 P
Component of transcription initiation factor IIb, 75 kDa subunit
6142_i_at 241.1 P
high copy suppressor of G beta subunit temperature sensitive mutation
6143_f_at 996.1 P
high copy suppressor of G beta subunit temperature sensitive mutation
6144_at 923.1 P
Phosphatidylinositol(3)-phosphate binding
6145_at 149.7 P
weak similarity to hypothetical S.pombe protein
6146_at 398.3 P
hypothetical protein
6147_at 1395.0 P
hypothetical protein
6148_at 350.3 P
hypothetical protein
6149_at 789.2 P
Involved in minichromosome maintenance
6150_at 2481.7 P
hypothetical protein
6151_at 319.4 P
similarity to hypothetical S. pombe protein and weak similarity to bovine auxilin
6152_at 9766.3 P
Asparaginase I, intracellular isozyme
6153_at 831.1 P
Mitochondrial ribosomal protein MRPL35 (YmL35)
6154_at 10035.9 P
subunit e of mitochondrial F1F0-ATPase
6155_at 165.7 M
cytosolic and peripheral membrane protein with three zinc fingers\; cysteine rich regions of amino acids are essential for function
6156_at 3374.6 P
weak similarity to beta transducin from S. pombe and other WD-40 repeat containing proteins
6157_at 649.8 P
weak similarity to S.pombe hypothetical protein SPAC1B9
6158_at 699.7 P
strong similarity to YHR080c, similarity to YFL042c and YLR072w
6159_at 421.1 P
questionable ORF
6160_at 6889.8 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.

ScuICdc4 complexes transfer ubiquitin to phosphorylated Sic1p, and substrate recognition is thought to involve the Cdc4p and Skp1p subunits. Following the ScuICdc4-mediated monoubiquitination of Sic1p, a polyubiquitin chain is added, andubiquitinated Sic1p is then degraded by the 26S proteosome.
6161_at 976.4 P
48-kDa peroxisomal integral membrane protein
6162_at 1230.0 P
similarity to hypothetical S. pombe protein
6117_at 3649.3 P
Protein involved in the attachment of glycosylphosphatidylinositol (GPI) anchors to proteins
6118_at 432.6 P
similarity to E.coli hypothetical protein and weak similarity to RNA helicase MSS116 / YDR194c
6119_at 1478.1 P
similarity to hypothetical S. pombe protein
6120_at 1144.8 P
similarity to nuclear Sth1p, Snf2p and related proteins
6121_at 4247.1 P
Multicopy suppressor of snf1 mutation
6122_at 1777.1 P
weak similarity to B.subtilis hypothetical protein X
6123_at 2290.2 P
Mitochondrial ribosomal protein MRPS28 (E. coli S15)
6124_at 1628.6 P
similarity to Erc1p
6125_at 6596.5 P
weak similarity to hypothetical protein YOR004w
6126_at 57.8 A
questionable ORF
6127_at 13015.3 P
strong similarity to arginine-tRNA ligase
6128_f_at 7819.4 P
Hexose transporter
6129_f_at 6369.9 P
Hexose transporter
6130_at 141.7 A
hypothetical protein
6131_at 13627.6 P
High-affinity glucose transporter
6132_at 2333.5 P
similarity to hypothetical S.pombe protein
6133_at 2525.3 P
37 kDa mitochondrial ribosomal protein
6134_at 1512.9 P
similarity to hypothetical protein YHR097c
6135_at 3895.0 P
GPI-anchored aspartic protease
6136_at 969.4 P
protein of unknown function
6137_at 2654.2 P
required for bud growth
6138_at 1049.8 P
weak similarity to hypothetical proteins YOL092w, YBR147w and YMR010w
6139_at 7886.7 P
Thioredoxin reductase
6095_at 3009.2 P
anthranilate phosphoribosyl transferase
6096_at -94.1 A

questionable ORF
6097_at 503.7 P
component of the spindle pole body that interacts with Spc42p, calmodulin, and a 35 kDa protein
6098_at 1614.3 P
hypothetical protein
6099_at 1093.1 P
strong similarity to hypothetical protein YHR108w and weak similarity to signal transducing adaptor from mouse and man
6100_at 1224.1 P
hypothetical protein
6101_at -280.7 A
questionable ORF
6102_at 2017.2 P
hypothetical protein
6103_at 968.7 P
91 kDa tau91 subunit of transcription factor IIIC (TFIIIC)
6104_at 1462.9 P
Establishes Silent omatin
6105_at 4746.8 P
Homolog of DSS1\; similar to hypothetical protein from S. pombe
6106_at 2041.3 P
Member of the beta transducin family
6107_at 1503.3 P
weak similarity to Streptococcus M protein
6108_at 162.5 A
similarity to YOL106w and YER181c
6109_at 1772.2 P
hypothetical protein
6110_at 5618.6 P
homologous to the aldo-keto reductase protein family
6111_at 369.5 A
DNA repair protein
6112_at 1764.7 P
hypothetical protein
6113_at 89.7 P
similarity to chitinases
6114_at 2778.8 P
similarity to hypothetical S. pombe protein
6115_at 3845.9 P
strong similarity to human BDR-1 protein and other calcium binding proteins
6116_at 210.3 A
similarity to hypothetical A. thaliana protein BAC F21M12
6072_at 1124.4 P
Mitochondrial protein of the CDC48\/PAS1\/SEC18 ATPase family, required for expression of functional Rieske iron-sulfur protein
6073_at 1368.1 P
adrenodoxin oxidoreductase homolog
6074_at 4327.7 P
ATP synthase subunit f
6075_at 3802.8 P
Sm-like protein
6076_at 327.5 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 6676.4 P
similarity to Pdc6p, Thi3p and to pyruvate decarboxylases

6078_at 9422.0 P
Nuclear RNA-binding RNA annealing protein
6079_at 7910.1 P
Nuclear RNA-binding RNA annealing protein
6080_at 6594.1 P
Ribosomal protein P2B (YP2beta) (L45)
6081_at 66.1 P
weak similarity to S.pombe paramyosin
6082_at 4923.3 P
strong similarity to Y.lipolytica GPR1 gene
6083_at 314.0 A
MMS and UV Sensitive\; Mus81p and Rad54p are found together in a complex from whole-cell extracts
6084_at 615.5 P
similarity to Itr1p and Itr2p and E.coli araE
6085_at 9601.1 P
involved in endocytosis
6086_at 1215.4 P
GTPase activating protein (GAP) for RHO1
6087_at 977.0 P
Protein with homology to mammalian ubiquitin activating (E1) enzyme
6088_at 1367.2 P
strong similarity to hypothetical protein YOR013w
6089_at 846.9 P
transcription factor, member of the histone acetyltransferase SAGA complex
6090_at 314.1 P
mRNA (identified by a library screen) that causes growth arrest when overexpressed
6091_at 4036.8 P
probable 26S protease subunit and member of the CDC48\/PAS1\/SEC18 family of ATPases
6092_at 3957.2 P
Sxm1p
6093_at 318.8 P
hypothetical protein
6094_at 2054.6 P
repressor of class II transcription
6049_at 5896.6 P
similarity to human KIAA0007 gene
6050_at 5560.2 P
Hypoxanthine Phosphoribosyltransferase
6051_at 6179.8 P
similarity to C. fasciculata inosine-uridine preferring nucleoside hydrolase (EC 3.2.2.1)
6052_at -70.9 A
Cytochrome P450 56, Dit2p catalyzes oxidation of N-formyl tyrosine to N,N-bisformyl dityrosine in vitro
6053_at 12.0 P
questionable ORF
6054_at 218.2 P
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 5681.9 P
dissociable subunit of RNA polymerase II
6056_at 755.4 P
263-amino acid mitochondrial ribosomal large subunit protein\; similar to L23 family of ribosomal proteins
6057_at 1255.4 P
probable multidrug resistance transporter
6058_at 2090.1 P
weak similarity to Myo1p
6059_at 7180.5 P

glycinamide ribotide transformylase
6060_at 500.6 P
similarity to Nfi1p
6061_at 5456.7 P
farnesyl cysteine-carboxyl methyltransferase
6062_at 2644.5 P
weak similarity to Der1p
6063_at 383.0 P
weak similarity to NADH dehydrogenase
6064_at 1237.8 P
questionable ORF
6065_at 1047.6 P
Protein required for retention of luminal ER proteins
6066_at 1731.1 P
strong similarity to bacterial leucyl aminopeptidase
6067_at 1156.7 P
SYnthetic lethal with cdcForty
6068_at 127.0 A
questionable ORF
6069_i_at 16070.0 P
Ribosomal protein L12B (L15B) (YL23)
6070_s_at 11854.8 P
Ribosomal protein L12B (L15B) (YL23)
6071_at 279.7 P
similar to E. coli DinB and S. cerevisiae REV1
6026_at 2337.2 P
Type 1 membrane protein with EF hand motif
6027_at 402.8 P
hypothetical protein
6028_at 1441.3 P
SNF1 protein kinase substrate
6029_at 2958.5 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 7084.5 P
putative light chain of dynein
6031_at 370.5 P
similarity to hypothetical protein YDL113c
6032_at 187.4 P
questionable ORF
6033_at 5386.6 P
Subunit of the regulatory particle of the proteasome
6034_at 2459.4 P
hypothetical protein
6035_at 8917.4 P
Translation initiation factor 3 p33 subunit
6036_at 1708.4 P
similarity to C.perfringens hypothetical hypA protein
6037_at 64.3 A
questionable ORF
6038_at 7611.0 P
nuclear shuttling protein with an RNA recognition motif
6039_g_at 14535.6 P
nuclear shuttling protein with an RNA recognition motif
6040_i_at 18911.3 P
questionable ORF

6041_at 2527.1 P
similarity to S.pombe hypothetical protein
6042_at 1843.4 P
similarity to YOL141w and hypothetical C.elegans protein
6043_at 796.3 P
serine-threonine phosphatase Z
6044_at 236.9 P
hypothetical protein
6045_at 716.1 P
strong similarity to hypothetical protein YML018c
6046_at 296.3 P
Loss of rDNA silencing
6047_at 878.9 P
Pachytene CHeckpoint
6048_at 2752.8 P
Adenine phosphoribosyltransferase
6003_at -36.7 A
questionable ORF
6004_at 2102.1 P
RNA polymerase II holoenzyme component
6005_at 697.4 P
similarity to hypothetical protein YGL144c and YDL109c
6006_at 73.5 A
questionable ORF
6007_at 36.5 A
ExtraCellular Mutant
6008_at 1306.4 P
transcription factor, member of ADA and SAGA, two transcriptional adaptor\/HAT (histone acetyltransferase)complexes
6009_at 1433.0 P
hypothetical protein
6010_at 939.9 P
strong similarity to Yox1p
6011_at 4671.6 P
similarity to human sphingomyelin phosphodiesterase
6012_at 1110.9 P
strong similarity to thiol-specific antioxidant proteins
6013_at 11233.4 P
guanylate kinase
6014_at 13.8 A
questionable ORF
6015_at 2052.9 P
Na+\/H+ exchanger
6016_at 5406.2 P
hect-domain-containing protein, required for G2\/M transition\; similar to RSP5\; contains motifs typical of protein kinases
6017_at 403.1 P
similarity to hypothetical protein YML034w and YML033w
6018_at 1107.6 P
weak similarity to YNL326c
6019_at 713.1 P
TFIIH subunit Tfb3 , contains ring finger motif\; similar to mammalian CAK subunit
6020_r_at 751.9 P
a-factor mating pheromone precursor
6021_f_at 251.1 P
a-factor mating pheromone precursor

6022_at 2423.6 P
Mitochondrial ribosomal protein MRPL28 (YmL28)
6023_at 1759.9 P
Nuclear-localized protein containing zinc finger motifs
6024_at 938.2 P
negative regulator of prp genes
6025_at 4739.6 P
Protein arginine methyltransferase
5980_at 1758.5 P
similarity to ser/thr protein kinase
5981_at 188.9 A
questionable ORF
5982_at 1176.1 P
tSNARE that affects a Late Golgi compartment
5983_at 724.7 P
hypothetical protein
5984_at 249.1 P
similarity to chromosome segregation protein Cse1p
5985_at 15268.3 P
Ribosomal protein L27B
5986_at 2303.3 P
similarity to P.falciparum 41-2 protein antigen
5987_at 841.9 P
essential splicing factor
5988_at 1044.2 P
similarity to C-terminal region of YOR019w
5989_at 54.6 A
hypothetical protein
5990_at 7323.4 P
hypothetical protein
5991_at 2621.1 P
protein serine\/threonine kinase
5992_at 1569.7 P
RNAse MRP protein component
5993_at 663.3 P
weak similarity to YHR150w
5994_at 466.0 A
MAP kinase-associated protein
5995_at 2518.4 P
repressible alkaline phosphatase
5996_at 397.4 P
hypothetical protein
5997_at 7442.2 P
alpha-1,2-mannosyltransferase
5998_at 542.8 P
May interact with actin as a component or controller of the assembly or stability of the actin cytoskeleton
5999_at 2283.8 P
similarity to trichohyalin
6000_at 2120.7 P
weak similarity to Snf7p
6001_at 8453.9 P
3,4-dihydroxy-2-butanone 4-phosphate synthase
6002_at 1565.7 P
Protein required in the absence of Cin8p
5958_at 338.8 P
hypothetical protein

5959_at	957.9	P	Ser\/Thr protein kinase
5960_at	137.9	A	questionable ORF
5961_at	7949.8	P	strong similarity to hypothetical protein YOL002c
5962_at	872.1	P	hypothetical protein
5963_at	1823.4	P	hypothetical protein
5964_at	139.0	P	Vacuolar sorting protein
5965_at	5019.8	P	similarity to hypothetical human and C.elegans proteins
5966_at	10900.0	P	myo-inositol transporter
5967_at	1980.3	P	membrane glycoprotein, sorted by HDEL retrieval system
5968_at	798.7	P	weak similarity to hypothetical C.elegans protein, M.genitalium peptide chain release factor 1 and YJL149w
5969_at	13100.9	P	60S ribosomal protein L37B (L43) (YL35)
5970_at	147.3	P	similarity to hypothetical protein YLR183c
5971_at	8033.3	P	S-adenosylmethionine synthetase
5972_at	1297.6	P	Lipid phosphate phosphatase
5973_at	4397.8	P	similarity to hypothetical T.brucei protein
5974_at	2129.1	P	high copy suppressor of ts mutations in DNA polymerase alpha
5975_at	2634.0	P	similarity to FET3, YFL041w and F.floriforme diphenol oxidase
5976_at	2943.9	P	putative serine\/threonine kinase
5977_at	8553.6	P	high-affinity glutamine permease
5978_at	377.9	P	questionable ORF
5979_at	5319.1	P	may be involved in function and\/or structure of the eukaryotic kinetochore
5935_at	3132.8	P	weak similarity to C. elegans protein F25H9.7 and to the human complement 3 precursor
5936_at	2797.8	P	questionable ORF
5937_at	7666.6	P	Glutaredoxin (thioltransferase) (glutathione reductase)
5938_at	2044.4	P	strong similarity to hypothetical protein YCL036w
5939_at	741.3	P	regulates the copper-dependent mineralization of copper sulfide complexes on the cell surface in cells cultured in medium containing copper salts
5940_at	3258.9	P	strong similarity to glucokinase

5941_at 1668.5 P
weak similarity to hypothetical S.pombe protein
5942_at 1622.9 P
Protein disulfide isomerase homolog
5943_at 5917.8 P
FKBP (FK506 binding protein) 13\; peptidylprolyl cis-trans isomerase activity
5944_at 825.7 P
weak similarity to transcription factors of the zinc finger class
5945_at -109.0 A
questionable ORF
5946_at -193.5 A
Middle\/late gene of meiosis
5947_at 153.7 P
serine\/threonine kinase homologous to Ste20p\; expressed in middle\/late meiosis
5948_at 783.0 P
similarity to hypothetical human protein and YIL044c
5949_at 5.4 A
hypothetical protein
5950_at 480.8 P
questionable ORF
5951_at 2001.6 P
weak similarity to Plasmodium yoelii rhoptry protein
5952_at 625.0 P
similarity to Lre1p
5953_at 8184.7 P
ubiquinol-cytochrome c oxidoreductase subunit 7 (14 kDa)
5954_at 1262.3 P
5 ,5 -P-1,P-4-tetraphosphate phosphorylase II
5955_at 3069.6 P
similarity to hypothetical A. thaliana and C. elegans proteins
5956_at 94.3 A
weak similarity Plasmodium repeat organellar protein
5957_at 8321.6 P
strong similarity to hypothetical proteins YPL280w, YOR391c and YMR322c
5913_at 678.5 P
similarity to YOR383c,Sta1p and pig mucin
5914_at 770.7 A
hypothetical protein
5915_at -34.3 A
sugar transporter-like protein
5916_at 214.5 A
questionable ORF
5917_at 4905.7 P
Phenylacrylic acid decarboxylase
5918_at 4935.3 P
similarity to E.coli hypothetical 55.3 kDa protein in rfah-rfe intergenic region
5919_at 178.1 P
hypothetical protein
5920_at 913.1 P
similarity to dihydroflavonol-4-reductases
5921_at 10019.2 P
hypothetical protein identified by SAGE
5922_s_at 4493.5 P
homing endonuclease with protein splicing activity
5923_at 2282.0 P
identified by SAGE

5924_at 343.2 P
identified by SAGE
5925_at 5158.5 A
identified by SAGE
5926_g_at 0.0 A
identified by SAGE
5927_at 2929.7 P
Involved in pre-tRNA splicing and in uptake of branched-chain amino acids
5928_at 305.1 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 1689.0 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 684.4 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 2445.2 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 2509.4 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 -184.1 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 1306.5 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 5279.5 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 23.7 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 215.6 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 -57.4 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 -24.3 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 100.7 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 -15.4 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 17.1 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 717.9 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 345.7 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 234.4 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 649.1 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 19.7 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 -113.2 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 4697.7 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 -92.6 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 -17.6 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 5481.2 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 213.0 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 1904.4 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 -39.4 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 6651.8 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 60.0 A
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 6246.5 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 814.5 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 742.4 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 357.5 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 87.3 P
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 364.0 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 575.5 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 456.7 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 278.4 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 15.6 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 -10.1 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 990.0 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 376.1 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 911.3 P
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 -565.6 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 6222.5 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 878.1 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 3230.3 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 2565.7 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 1447.5 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 210.0 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 1039.4 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 79.2 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 -90.7 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 2683.9 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 454.8 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 703.1 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 120.1 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 -20.0 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 16.2 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 371.8 P
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 687.6 P
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 84.6 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 30.6 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 1782.5 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 162.8 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 109.2 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 343.2 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 308.5 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 1137.7 A
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 -124.1 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 214.3 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 42.1 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 -16.7 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 -1032.7 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 172.6 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 210.2 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 649.2 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 240.5 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 418.8 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 29.8 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 3162.6 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 895.9 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 -36.5 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 28.3 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 19.8 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 190.8 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 -47.8 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 424.0 A

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 -503.3 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 3770.3 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 441.0 P

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 89.7 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 649.6 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 82.4 M

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 75.5 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 436.7 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 170.9 P

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 -149.8 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 -134.2 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 2421.4 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 2144.5 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 2705.7 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 1955.3 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 653.4 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 5924.4 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 71.7 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 356.7 P

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 61.5 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 486.2 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 1523.5 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 3399.4 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 -226.8 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 83.5 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 75.8 P

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 2756.6 P

snRNA

5805_i_at 7.5 A

Centromere

5806_i_at	740.7	P
snRNA
5807_at	9115.9	P
snRNA
5808_i_at	27.9	A
questionable ORF
5809_i_at	570.6	P
similarity to subtelomeric encoded proteins
5810_s_at	2743.5	P
similarity to subtelomeric encoded proteins
5811_at	206.9	A
similarity to YJR108w
5812_at	112.1	P
hypothetical protein
5813_at	5891.2	P
strong similarity to Aip2p
5814_at	353.6	P
hypothetical protein
5815_at	-23.6	A
weak similarity to YKL083w
5816_at	4614.3	P
Histone and other Protein Acetyltransferase\; Has sequence homology to known HATs and NATs
5769_at	1988.9	P
probably multidrug resistance protein
5770_at	451.6	P
similarity to YBL089w
5771_at	5331.9	P
arginine permease
5772_at	684.0	P
Non-membrane-embedded, PEST sequence-containing protein
5773_at	795.4	P
Kinesin-related protein involved in establishment and maintenance of mitotic spindle
5774_at	7915.4	P
vacuolar protease B
5775_at	3783.9	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	757.3	P
hypothetical protein
5777_at	10017.6	P
Phosphoacetylglucosamine Mutase
5778_at	230.2	P
hypothetical protein
5779_at	4721.0	P
subunit of a cytoplasmic histone acetyltransferase
5780_at	3221.0	P
DNA polymerase V that has motifs typical of DNA polymerase family
5781_i_at	11710.2	P
Ribosomal protein L12A (L15A) (YL23)
5782_at	1700.4	P
glucose-repressible protein
5783_at	3231.4	P
ATPase family gene
5784_at	5692.1	P
Vacuolar H-ATPase D subunit of the V1 catalytic sector
5785_at	2971.1	P

Mitochondrial ribosomal protein L2 of the large subunit
5786_f_at 677.1 A
member of the seripauperin protein\/gene family (see Gene_class PAU)
5787_at 125.1 P
hypothetical protein
5788_at 9353.2 P
strong similarity to Osm1p
5789_at 8613.5 P
Threonine Aldolase
5790_at 136.7 A
weak similarity to cytochrome c oxidase III of T.brucei kinetoplast
5791_at 3239.2 P
hypothetical protein
5747_at 4907.1 P
weak similarity to Mad1p
5748_at 8777.6 P
Guanosine diphosphatase of Golgi membrane
5749_at 244.3 A
strong similarity to Utr1p
5750_at 12133.0 P
weak similarity to Bacillus 1,3-1,4-beta-glucanase
5751_at 580.5 P
iso-2-cytochrome c
5752_at 3625.9 P
similarity to K.oxytoca enolase-phosphatase E-1
5753_at 8075.3 P
ubiquitin-like protein
5754_at 5511.2 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 -108.1 A
protein of unknown function
5756_at 8926.0 P
Translation initiation factor eIF-5A
5757_at 3897.7 P
weak similarity to Sauroleishmania mitochondrial hypothetical ORF-5 protein
5758_at 4578.7 P
Member of complex that acts at ARS s to initiate replication
5759_at 9117.1 P
P-type ATPase
5760_at 457.7 A
ExtraCellular Mutant
5761_at 1417.5 P
similarity to hypothetical protein YNR027w
5762_at 306.0 P
hypothetical protein
5763_at 11173.0 P
Vacuolar ATP synthase 17-kDa proteolipid C subunit of VO sector\; dicyclohexylcarbodiimide binding subunit
5764_at 14822.9 P
strong similarity to high mobility group-like protein Nhp2p
5765_at 733.8 P
hypothetical protein
5766_at 10888.0 P
Rieske iron-sulfur protein of the mitochondrial cytochrome bc1 complex
5767_at 348.0 P

hypothetical protein
5768_at 1469.0 P
ARF GTP\/GDP exchange factor
5724_at 342.9 P
orotidine-5 -phosphate decarboxylase
5725_at 1149.0 P
similarity to O.formigenes oxalyl-CoA decarboxylase
5726_at 169.6 P
Protein involved in DNA repair
5727_at 2033.2 P
weak similarity to Rad50p
5728_i_at 14527.9 P
Proteolipid associated with plasma membrane H(+)-ATPase (Pma1p)
5729_f_at 11577.1 P
Proteolipid associated with plasma membrane H(+)-ATPase (Pma1p)
5730_at 5775.9 P
hypothetical protein
5731_at 722.5 P
similarity to human nucleotide pyrophosphatase
5732_at 2557.4 P
weak similarity to Spa2p
5733_at 283.9 P
hypothetical protein
5734_at 2849.6 P
An armadillo repeat-containing protein localized on the vacuolar membrane
5735_at 886.0 P
1,4-glucan-6-(1,4-glucano)-transferase
5736_at -94.8 A
hypothetical protein
5737_at 9915.5 P
transcriptional activator of amino acid biosynthetic genes
5738_at -31.6 A
hypothetical protein
5739_at 3876.1 P
similarity to S.pombe pac2 protein
5740_at 2760.1 P
similarity to peroxisomal membrane and mitochondrial carrier proteins
5741_at 607.1 P
hypothetical protein
5742_at 716.6 P
Shows sequence similarity to GOG5, a gene involved in vanadate resistance
5743_at 3455.4 P
Putative homolog of subunit 2 of bovine prefoldin, a chaperone comprised of six subunits
5744_at 11556.1 P
oligosaccharyl transferase glycoprotein complex, beta subunit
5745_at 12281.6 P
hypothetical protein
5746_at 5282.7 P
Alpha-1,3-mannosyltransferase
5701_at 2637.0 P
weak similarity to chicken microfibril-associated protein
5702_at 10235.3 P
mannose-6-phosphate isomerase
5703_at 9271.0 P
similarity to hypothetical E.coli and C.elegans proteins
5704_at 1328.3 P

similarity to Gda1p

5705_at 7116.8 P

similarity to P.polycephalum myosin-related protein mlpA

5706_at 813.9 P

Required for viability in the absence of the kinesin-related mitotic motor Cin8p\; required for normal microtubule stability

5707_at 9031.4 P

putattive ORF identified by SAGE

5708_at 3599.1 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 9876.9 P

May coordinate the Ran-dependent (GSP1\/GSP2) association and disassociation reactions of nuclear import\; human homologue complements yeast mutants

5710_at 3380.0 P

similarity to L.pneumophila dlpA protein

5711_at 3901.2 P

Cold-shock induced protein of the Srp1p\/Tip1p family of serine-alanine-rich proteins

5712_at 8414.6 P

22.6 kDa proteasome subunit

5713_at 1609.4 P

helicase-like protein

5714_at 2079.3 P

protoporphyrinogen oxidase

5715_at 224.0 P

Acyl-CoA synthetase (fatty acid activator 2)

5716_at 614.5 P

BInding to Microtubules

5717_at 5930.2 P

ATP-dependent metalloprotease

5718_at 1743.3 P

component of spindle pole

5719_at 5106.7 P

putative neutral sphingomyelinase

5720_at 9124.1 P

homologous to Sbh1p

5721_at 3728.0 P

nucleotide binding regulatory protein

5722_at 3239.6 P

component of the regulatory module of the 26S proteasome, homologous to human p58 subunit

5723_at 519.2 P

subunit of RNA polymerase II holoenzyme\/mediator complex

5678_at 9626.9 P

delta 1-pyrroline-5-carboxylate reductase

5679_at 607.4 P

similarity to carnitine O-acetyltransferase Yat1p

5680_at 10880.1 P

gamma subunit of translational initiation factor eIF-2

5681_at 7112.9 P

phosphatidylserine synthase

5682_at 2474.0 P

glucose repression protein

5683_at 633.9 P

similarity to Mig1p

5684_at 3233.1 P

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

5685_at 4449.3 P
similarity to mouse nucleolin
5686_at 4426.9 P
ras-like GTPase, highly homologous to YPT32
5687_at 1036.1 P
Putative participant in 3 mRNA processing
5688_at 1256.6 P
weak similarity to Nmd2p, Kex1p and hamster nucleolin
5689_at 1180.8 P
hypothetical protein
5690_at 3768.1 P
hypothetical protein
5691_at 11713.6 P
strong similarity to members of the ABC transporter family
5692_at 748.1 P
strong similarity to hypothetical protein YGL224c
5693_at 177.6 P
hypothetical protein
5694_at 457.8 P
Homologous to VRG4
5695_at 784.5 P
positive nitrogen regulatory protein
5696_at 1076.8 P
weak similarity to DNA repair protein Rad2p and Dsh1p
5697_at 2085.2 P
responsible for the reduction of methionine sulfoxide
5698_at 9072.5 P
putative S-adenosyl-L-homocysteine hydrolase
5699_at 9462.1 P
hypothetical protein
5700_at 432.8 P
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 -24.9 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 1221.2 P
weak similarity to transcription factor Sko1p
5657_at 752.4 P
hypothetical protein
5658_at 980.1 P
member of the AAA ATPase family of proteins
5659_at 5469.8 P
Homologous to E. coli DnaJ\; contains leucine zipper-like motif
5660_at 1810.1 P
putative ORF identified by SAGE
5661_at 4848.8 P
strong similarity to hypothetical S.pombe protein YER049W

5662_at 2183.7 P
hypothetical protein
5663_at 244.1 P
similarity to C.elegans hypothetical protein
5664_at 6663.2 P
Aspartate kinase (L-aspartate 4-P-transferase) (EC 2.7.2.4)
5665_at 2792.8 P
strong similarity to mitochondrial phosphate carrier protein
5666_at 127.6 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 11534.2 P
ATP phosphoribosyltransferase
5668_at 7800.9 P
purine-cytosine permease
5669_g_at 8455.3 P
purine-cytosine permease
5670_i_at 10118.8 P
Ribosomal protein L34A
5671_s_at 8183.5 P
Ribosomal protein L34A
5672_at 10835.4 P
Inhibitor of cell Growth\; heat shock inducible
5673_at 1896.3 P
cytochrome c oxidase assembly factor
5674_at 945.4 P
PHO85 cyclin
5675_at 2466.1 P
purine-cytosine permease
5676_at 222.4 A
purine-cytosine permease
5677_at 1717.7 P
Protein homologous to beta-keto-acyl synthase
5633_at 5570.7 P
DL-glycerol-3-phosphatase
5634_at 5617.2 P
Suppressor of the Transcriptional (T) defect of Hpr1 (H) by Overexpression (O)
5635_at 5223.0 P
similarity to hypothetical protein YIL056w
5636_at 612.8 P
isocitrate lyase
5637_at 442.5 P
strong similarity to cell division control protein Cdc4p
5638_g_at 2581.2 P
strong similarity to cell division control protein Cdc4p
5639_at 694.6 P
hypothetical protein
5640_at 677.2 P
strong similarity to hypothetical protein YIL057c
5641_at 1081.2 P
putative zinc finger protein
5642_at 6434.3 P
N-acetyl-gamma-glutamyl-phosphate reductase and acetylglutamate kinase
5643_at 8894.2 P
ribonucleotide reductase

5644_at 961.9 P
hypothetical protein
5645_at 14497.4 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 6225.8 P
aldehyde dehydrogenase (NAD+)
5647_s_at 13265.4 P
40S ribosomal protein S24A
5648_at 876.7 P
Protein tyrosine phosphatase
5649_at 1055.3 P
similarity to killer toxin Khr1p
5650_at 375.3 P
hypothetical protein
5651_at 1080.8 P
similarity to E.coli X-Pro aminopeptidase II
5652_at 3510.3 P
hypothetical protein
5653_at 2662.3 P
hypothetical protein
5654_at 630.3 P
strong similarity to phosphoglycerate dehydrogenases
5610_at 1183.2 P
similarity to M.sexta steroid regulated MNG10 protein
5611_at 8564.2 P
hypothetical protein
5612_at 938.1 P
questionable ORF
5613_at 81.9 A
weak similarity to myosins
5614_at 9198.5 P
threonine deaminase
5615_at 1046.3 P
similarity to E.coli prolyl-tRNA synthetase
5616_at 6245.9 P
homologous to Sbh2p
5617_at 3067.3 P
Derepression Of Telomeric silencing
5618_at 6628.1 P
Protein phosphatase type 2C
5619_at 8304.1 P
anthranilate synthase Component I
5620_at 10450.7 P
vitamin B12-(cobalamin)-independent isozyme of methionine synthase (also called N5-methyltetrahydrofolate homocysteine methyltransferase or 5-methyltetrahydropteroyl triglutamate homocysteine methyltransferase)
5621_at 2478.3 P
hypothetical protein
5622_at 1052.7 P
weak similarity to S.epidermidis PepB protein
5623_at 1187.7 P
similarity to hypothetical protein YBL059w
5624_at 1468.7 P
similarity to hypothetical protein YBL059w
5625_at 8067.3 P

20S proteasome subunit (beta3)
5626_at 4974.5 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 227.4 P
sporulation-specific homolog of csd4
5628_at 6.3 A
weak similarity to ribosomal S3 proteins
5629_at 362.0 P
ubiquitin carboxyl-terminal hydrolase
5630_at 2667.8 P
ribose-phosphate pyrophosphokinase 2
5631_at 2169.8 P
ubiquitin-conjugating enzyme
5632_at 1197.7 P
Protein involved in targeting of plasma membrane [H+]ATPase
5588_at 1338.2 P
member of 70 kDa heat shock protein family
5589_at 520.5 P
hypothetical protein
5590_at 5360.7 P
Nucleoporin similar to Nup157p and to mammalian Nup155p
5591_at 277.9 P
hypothetical protein
5592_at 3473.9 P
homologous to S. pombe RAE1 gene\; 2-hybrid analysis demonstrates an interaction with Srp1p and Rip1p\; copurifies with Nup116p
5593_at 747.7 P
putative transcriptional activator of FLO1
5594_at 210.1 P
putative transcriptional activator of FLO1
5595_at 7483.2 P
Karyopherin beta 4
5596_at 389.1 P
transcription factor
5597_at 1697.8 P
U6 snRNA associated protein
5598_at 1815.5 P
similarity to Emp70p
5599_at 2966.6 P
Protein which binds Bem1p and contains a proline-rich sequence, an SH3 domain, and a pleckstrin homology domain
5600_at 2606.4 P
sporulation-specific protein
5601_at 149.4 P
zinc-finger protein
5602_at 1532.9 P
Transmembrane osmosensor
5603_at 1319.2 P
weak similarity to E.herbicola tyrosine permease
5604_at -28.8 A
questionable ORF
5605_at 11493.7 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 339.9 P
hypothetical protein
5607_at 2997.1 P
Zinc-finger-containing protein with similarity to Gcs1p and Sps18p
5608_at 589.7 P
plasma membrane-bound casein kinase I homolog
5609_at 1253.0 P
weak similarity to Dictyostelium WD40 repeat protein 2
5565_at 5542.0 P
Rsp5p encodes a hect (homologous to E6-AP C terminus) and encodes a ubiquitin-protein ligase (E3 enzyme)
5566_at 8912.9 P
weak similarity to E.coli colicin N
5567_at 1404.0 P
Lethal with conditional pap1 allele
5568_at 925.0 P
hypothetical protein
5569_at 709.8 P
DNA polymerase alpha suppressing protein kinase
5570_at 2673.6 P
similarity to Msn2p and weak similarity to Msn4p
5571_at 6681.6 P
Ribosomal protein S26B
5572_at 2476.9 P
Paralog of MDS3
5573_at 1227.0 P
protein phosphatase type I
5574_at 6801.4 P
protein phosphatase type I
5575_at 1472.7 P
weak similarity to S.pombe SPBC13G1 and C.elegans F26F2.d hypothetical proteins
5576_at -86.2 A
hypothetical protein
5577_at 7569.4 P
GDP dissociation inhibitor
5578_at 791.0 P
weak similarity to Mycoplasma hominis P120 protein
5579_at 361.5 P
similarity to hypothetical protein YDR066c
5580_at 803.0 P
hypothetical protein
5581_at 11516.9 P
cytochrome oxidase assembly factor
5582_at 772.7 P
3-methyladenine DNA glycosylase
5583_at 2392.9 P
DNA Damage Inducible
5584_at 1871.8 P
Putative Ubiquitin-specific protease
5585_at 4289.2 P
Iron permease
5586_at 6375.3 P
Sm-like protein
5587_at 1330.8 P
weak similarity to mouse NAD(P)H dehydrogenase (quinone)
5542_at 8732.4 P

TATA-binding protein (tfIId)
5543_at 623.8 P
Protein with coiled-coil domain
5544_at 1161.9 P
strong similarity to putative cell surface glycoprotein Sed1p
5545_at 1663.8 P
Ubiquitin-specific protease
5546_at 7332.7 P
weak similarity to E.coli hypothetical protein f470
5547_at 126.3 A
translational activator of cytochrome c oxidase subunit III
5548_at 7217.6 P
Required for correct assembly of the cytochrome c oxidase and the ATP synthase complex
5549_at 4768.0 P
Rho-type GTPase activating protein (GAP)
5550_at 6840.7 P
similarity to hypothetical C. elegans protein C27H6.5
5551_at 589.2 P
hypothetical protein
5552_at 1288.8 P
weak similarity to Afr1p
5553_at 3146.9 P
Transcriptional regulator which functions in modulating the activity of the general transcription machinery in vivo
5554_at 1037.6 P
non-specific DNA binding protein (sin1)
5555_at 404.8 P
Nucleotide excision repair protein
5556_at 3311.2 P
weak similarity to E.coli cation transport protein
5557_at 1719.8 P
transcriptional regulator
5558_at 9846.9 P
Poly(A) binding protein, cytoplasmic and nuclear
5559_at 5368.3 P
similarity to ATPase P.falciparum ATPase 2
5560_at 842.8 P
Serine\/threonine protein kinase
5561_at 884.4 P
tRNA nucleotidyltransferase (tRNA CCA-pyrophosphorylase)
5562_at 1213.6 P
Repressor of PHR1 transcription\; binds to PHR1 URS
5563_at 670.6 P
Adenylate kinase (mitochondrial GTP:AMP phosphotransferase)
5564_at 1506.5 P
DNA repair helicase component of transcription factor b
5520_at 1595.1 P
putative ATP-dependent RNA helicase
5521_at 385.5 P
checkpoint protein
5522_at 1737.8 P
similarity to Legionella glutaredoxin-like protein
5523_at 631.6 P
similarity to hypothetical protein YHR209w
5524_at 3190.3 P
DNA Helicase I

5525_at	12571.5	P	Ribosomal protein L23B (L17aB) (YL32)
5526_at	9343.8	P	alpha subunit of pyruvate dehydrogenase (E1 alpha)
5527_at	53.2	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	110.4	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
5529_at	889.5	P	Meiosis-specific protein required for spore formation
5530_at	93.3	A	questionable ORF
5531_at	987.2	P	hypothetical protein
5532_at	4093.0	P	similarity to human 5,10-methenyltetrahydrofolate synthetase
5533_at	538.9	A	similarity to multidrug resistance proteins Pdr3p and Pdr1p
5534_at	377.7	P	strong similarity to Rtm1p
5535_at	2565.7	P	weak similarity to hypothetical protein YMR316w
5536_at	427.8	P	similarity to killer toxin KHS precursor
5537_at	404.0	P	hypothetical protein
5538_at	3596.9	P	Translocase in inner membrane of mitochondria involved in mitochondrial protein import
5539_at	207.4	A	hypothetical protein
5540_at	-232.4	A	hypothetical protein identified by SAGE
5541_at	839.3	P	questionable ORF
5497_at	263.8	P	questionable ORF
5498_at	119.2	A	questionable ORF
5499_at	189.7	A	questionable ORF
5500_at	209.0	P	questionable ORF
5501_at	65.2	A	questionable ORF
5502_at	412.0	P	questionable ORF
5503_at	115.5	A	questionable ORF
5504_at	145.1	A	questionable ORF
5505_at	-59.2	A	hypothetical protein

5506_s_at 849.8 P
ubiquitin-conjugating enzyme\; ubiquitin-protein ligase
5507_at 364.6 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 -643.5 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 720.6 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 277.8 A
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 986.2 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 1002.5 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 31.8 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 5651.5 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 748.8 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 9469.4 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 10274.6 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 329.1 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 241.5 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 789.8 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 60.3 A
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 1123.5 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 7468.5 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 7493.2 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 1246.8 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 847.9 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 92.4 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
5481_at 500.1 P
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 2146.2 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 4773.0 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 -17.1 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 -1485.5 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 381.9 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 496.6 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 13.0 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 291.9 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 -17.0 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 7.2 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 -5.5 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 115.2 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 219.4 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 236.3 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 543.2 P
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 40.5 P
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 116.2 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 -86.8 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 -35.8 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 407.1 P
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 686.4 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 724.3 P
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 -41.5 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 1091.0 A
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 -9.3 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 31.8 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 1011.0 M
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 -29.0 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 126.6 A
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 1801.9 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
5464_i_at 5788.8 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 6513.2 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 30.9 A
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 11091.1 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 152.5 A
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 155.1 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 941.3 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 847.4 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 26.8 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 -55.7 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 -1.9 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 183.4 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 -57.1 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 752.7 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 1998.4 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 325.6 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 -231.5 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 455.8 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 2494.6 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 214.2 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 4189.5 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 2071.4 P
snRNA
5412_at 90.6 A

snRNA		
5413_at	1291.0	P
RNase P RNA		
5414_i_at	-54.2	A
Centromere		
5415_r_at	4.2	A
Centromere		
5416_at	769.0	P
snRNA R14		
5417_at	5322.0	P
snRNA U4		
5418_at	129.2	P
snRNA		
5419_at	547.8	P
small cytoplasmic RNA		
5420_s_at	279.7	A
weak similarity to hypothetical E.coli protein		
5421_i_at	-83.4	A
similarity to mouse period clock protein		
5422_s_at	1608.1	A
similarity to mouse period clock protein		
5423_s_at	1407.7	P
strong similarity to aryl-alcohol dehydrogenases		
5424_at	26.9	A
Hypothetical aryl-alcohol dehydrogenase (AAD)		
5425_at	199.7	P
Amino acid permease		
5426_at	933.2	P
similarity to channel proteins		
5427_at	371.0	A
dihydroxyacetone kinase		
5428_at	23.5	A
strong similarity to Mal63p, YPR196w and Mal13p		
5429_at	200.8	A
putative pseudogene		
5430_at	235.1	A
ALuminium Resistance 2		
5431_at	913.4	P
weak similarity to Npl6p		
5432_at	2295.3	P
47 kDa type I transmembrane protein localized to the Golgi		
5433_at	2177.6	P
similarity to S.pombe hypothetical protein SPAC2F7.18c		
5434_at	1097.1	P
weak similarity to middle part of C.elegans myosin heavy chain A		
5435_at	11416.9	P
phosphomannomutase		
5389_at	3577.1	P
weak similarity to human dystrophin		
5390_at	2607.7	P
multicopper oxidase, type 1 integral membrane protein		
5391_at	-48.4	A
similarity to yeast glucose transport proteins		
5392_at	7865.3	P
Actin		
5393_at	12259.8	P

Ras-like GTP-binding protein\; most similar to mammalian Rab1A protein
5394_at 10483.3 P
beta-tubulin
5395_at 2483.8 P
mitochondrial RNA polymerase II
5396_at 7319.1 P
Ribosomal protein L22B (L1c) (rp4) (YL31)
5397_at 239.0 P
similarity to hypothetical S. pombe protein and to C.elegans F35D11 protein
5398_at 825.8 P
Trehalose-associated protein kinase related to S. pombe cek1+
5399_at 147.3 A
questionable ORF
5400_at 439.5 P
similarity to several transaminases
5401_at 1878.2 P
Cyclin-dependent kinase-activating kinase
5402_at 1343.8 P
ABC ATPase
5403_at 1107.9 P
weak similarity to P.falciparum Pfmdr2 protein
5404_at 291.1 P
alpha-factor pheromone receptor\; seven-transmembrane domain protein
5405_at 2073.5 P
Negatively regulates COPII vesicle formation
5406_at 565.1 P
Probable chromatin protein because of homology to Drosophila Enahncer of Polycomb
5407_at 1425.2 P
similarity to repeat structures in a Plasmodium falciparum protein (MESA) that binds human erythrocyte protein 4.1.
5408_at 8769.5 P
Phenylalanyl-tRNA synthetase, beta subunit, cytoplasmic
5409_at 393.4 P
transcriptional activator with GATA-1-type Zn finger DNA-binding motif
5410_f_at 1148.3 P
member of the seripauperin protein\/gene family (see Gene_class PAU)
5411_at 35.1 P
hypothetical protein
5367_at 12767.4 P
dihydrolipoamide dehydrogenase precursor (mature protein is the E3 component of alpha-ketoacid dehydrogenase complexes)
5368_at 2182.1 P
snRNP G protein (the homologue of the human Sm-G)
5369_at 2797.7 P
similarity to hypothetical S. pombe protein and to hypothetical C.elegans B0024.12 protein
5370_at 2517.0 P
DnaJ homolog involved in mitochondrial biogenesis and protein folding
5371_at 295.5 A
weak similarity to YDR504c
5372_at 1587.0 P
12 kDa heat shock protein
5373_at 911.5 P
weak similarity to Dictyostelium protein kinase
5374_at -9.5 A
questionable ORF
5375_at 109.6 A

hypothetical protein
5376_at 138.1 A
High-affinity hexose transporter
5377_at 542.4 P
Involved in ammonia regulation of GAP1 activity
5378_at 8318.5 P
questionable ORF
5379_at 1008.9 P
beta subunit of large (heterotrimeric) G-proteins (beta-transducin)
5380_at 2087.2 P
omosome segregation protein
5381_at 6623.2 P
weak similarity to Mms19p
5382_at 3136.3 P
hypothetical protein
5383_at 6725.3 P
Ras-like small GTP-binding protein
5384_at 7541.8 P
strong similarity to hypothetical protein YPL019c
5385_at 343.7 P
meiosis specific protein, E.coli MutS protein, localizes to discrete sites on meiotic chromosomes
5386_at 2696.7 P
ATP-dependent RNA helicase
5387_at 1660.7 P
Depressed growth-rate protein
5388_at 5040.9 P
weak similarity to rabbit triadin Spp41p
5344_at 2222.7 P
96 kDa nucleoporin-interacting component
5345_at 2578.9 P
hypothetical protein
5346_at 5173.4 P
Similar to S. pombe PAD1 gene product
5347_at 1289.5 P
similarity to hypothetical A. thaliana proteins
5348_at 4834.0 P
similarity to X-Pro dipeptidases
5349_at 769.2 P
weak similarity to YER176w
5350_at 206.3 P
weak similarity to human centromere protein E
5351_at 7926.1 P
Member of ATP-binding cassette (ABC) family of proteins
5352_at 8054.4 P
encodes putative deubiquitinating enzyme
5353_at 1526.8 P
ochre suppressor tyr-tRNA
5354_at 434.3 P
similarity to hypothetical protein YOL019w
5355_at 831.7 P
similarity to YOL017w
5356_at 392.6 P
Calmodulin-dependent protein kinase
5357_at 312.0 P
Glycogen synthase (UDP-gluocse--starch glucosyltransferase)
5358_at 1860.7 P

similarity to mammalian neurofilament proteins and to Dictyostelium protein kinase
5359_at 552.1 P
hypothetical protein
5360_at 6930.6 P
similarity to human glutaminyl-peptide cyclotransferase
5361_at 3492.5 P
type II PI(4)P5-kinase (PIP4,5 kinase) similar to human PIP5K-II
5362_at 2256.5 P
hypothetical protein
5363_at 1795.2 P
similarity to hypothetical protein YPL100w
5364_at 297.3 P
similarity to Rod1p
5365_at 77.6 A
poly(A) binding protein\; related to PES4 protein homolog YHR015w
5366_s_at 3384.0 P
similarity to Acanthamoeba myosin heavy chain IC and weak similarity to other myosin class I heavy chains
5322_at 872.0 P
Histidinolphosphatase
5323_at 285.1 P
hypothetical protein
5324_at 345.6 P
hypothetical protein
5325_at 1310.8 P
soluble tyrosine-specific protein phosphatase
5326_at 512.2 P
Regulator of expression of the PTR2, GAP1, and BAP2 genes\; involved in the the control of peptide transport
5327_at 1552.9 P
subunit of assimilatory sulfite reductase
5328_at 1785.3 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 4341.2 A
Ribosomal protein L2A (L5A) (rp8) (YL6)
5330_at 274.4 P
weak similarity to S.pombe polyadenylate-binding protein, YPR112c and Sbp1p
5331_at 9658.4 P
Ribosomal protein L29 (YL43)
5332_at 9913.8 P
ubiquinol-cytochrome c oxidoreductase subunit 6 (17 kDa)
5333_at 1231.4 P
myc-type helix-loop-helix transcription factor
5334_at 274.3 P
hypothetical protein
5335_at 1343.0 P
cell division control protein
5336_at 2837.7 P
Rsc8 is the eighth largest subunit of RSC, a fifteen-protein chromatin remodeling complex and related to the Swi\/snf Complex.
5337_at 769.0 P
strong similarity to mouse lymphocyte specific helicase
5338_at 1497.8 P
similarity to hypothetical protein YGL228w
5339_at 1128.6 P

155 kDa SIT4 protein phosphatase-associated protein

5340_at	753.1	P	weak similarity to dnaJ-like heat shock proteins
5341_at	2181.2	P	hypothetical protein
5342_at	807.8	P	hypothetical protein
5343_at	14427.1	P	similarity to hypothetical protein YBR281c
5299_at	706.4	P	similarity to mitochondrial citrate transport proteins
5300_at	1232.7	P	hypothetical protein
5301_at	6669.8	P	strong similarity to human quinolinate phosphoribosyltransferase
5302_at	748.2	P	similarity to hypothetical S.pombe protein SPAC12G12.14 and to YDL001w and YDR282c
5303_at	4953.9	P	mitochondrial ribosomal protein (precursor)
5304_at	11894.8	P	proteasome subunit necessary for peptidyl glutamyl peptide hydrolyzing activity
5305_at	7536.0	P	Coatomer (COPI) complex delta subunit
5306_at	4092.6	P	cytoplasmic 32 - 34 kDa protein
5307_at	1194.9	P	Hexokinase I (PI) (also called Hexokinase A)
5308_at	88.0	P	hypothetical protein
5309_at	-53.2	A	questionable ORF
5310_at	2931.0	P	strong similarity to beta-cystathionases
5311_at	118.1	P	weak similarity to Cha4p
5312_s_at	608.6	P	hypothetical protein
5313_s_at	2843.0	P	Mob1p-like protein
5314_at	-312.4	A	hypothetical protein
5315_at	232.7	A	questionable ORF
5316_at	832.6	P	questionable ORF
5317_s_at	511.8	P	similarity to hypothetical protein YLR072w
5318_s_at	8848.4	P	bZIP (basic-leucine zipper) protein
5319_at	2189.0	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	40.6	A	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	1214.4	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 1878.7 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 43.1 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 -26.0 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 8585.2 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 869.8 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 32.3 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 -56.4 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 282.4 P

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 533.2 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 157.8 A

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 1144.9 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 832.8 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 515.9 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 437.9 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 -353.5 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 220.9 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 -76.5 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 359.8 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	1001.5	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	-103.5	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	119.8	P
ARS605 Found forward in NC_001138 between 135973 and 136029 with 100% identity.
5295_f_at	35.5	P
ARS607 Found forward in NC_001138 between 199390 and 199446 with 100% identity.
5296_i_at	32.0	P
ARS608 Found forward in NC_001138 between 216458 and 216508 with 100% identity.
5297_at	6.7	A
Protein with strong similarity to subtelomerically-encoded proteins including Cos2p, Cos4p, Cos8p, YIR040c, Cos5p, Cos9p, and Cos6p
5298_at	-81.5	A
similarity to hypothetical protein YER187w
5251_f_at	2092.8	P
strong similarity to members of the Srp1/Tip1 family
5252_at	155.2	A
GPI-anchored aspartic protease
5253_g_at	678.6	P
GPI-anchored aspartic protease
5254_i_at	27.4	P
strong similarity to hypothetical protein YOR387c
5255_s_at	125.7	A
strong similarity to hypothetical protein YOR387c
5256_at	2740.1	P
similarity to Mnn1p
5257_at	5121.1	P
alcohol dehydrogenase isoenzyme IV
5258_at	2764.1	P
high-affinity zinc transport protein
5259_at	2137.8	P
putative transcription factor, has five zinc fingers
5260_at	11984.6	P
Hexokinase II (PII) (also called Hexokinase B)
5261_at	2262.8	P
Protein involved in interorganelle communication between mitochondria, peroxisomes, and nucleus
5262_at	415.0	P
C4 zinc finger DNA-binding protein of low sequence specificity in vitro\; Probable 119 kD DNA\/RNA helicase family member
5263_at	112.5	A
hypothetical protein
5264_at	58.6	A
Required for ZIPpering up meiotic chromosomes during chromosome synapsis
5265_at	2754.3	P
3 ,5 -Cyclic-nucleotide phosphodiesterase, low affinity
5266_at	1981.2	P
similarity to hypothetical protein YHR036w
5267_at	882.2	P
weak similarity to C.elegans dom-3 protein
5268_at	10627.7	P
strong similarity to glutamine--tRNA ligase
5269_at	938.8	P
Nuclear protein

5270_at 858.9 P
tRNA-specific adenosine deaminase 1 (TAD1)\; Tad1p\/scADAT1
5271_at 4532.5 P
weak similarity to Drosophila ANK protein
5272_at 1503.0 P
similarity to Cse1p
5273_at 360.4 P
Doc1p and Cdc26p are associated with the anaphase-promoting complex and are involved in the degradation of Clb2p
5229_at 216.3 P
questionable ORF
5230_at 4800.2 P
Protein required for accurate mitotic chromosome segregation
5231_at 361.0 P
transcriptional activator protein of CYC1
5232_at 1151.4 P
strong similarity to gidA E.coli protein
5233_at -932.8 A
questionable ORF
5234_at 8894.1 P
glycinamide ribotide synthetase and aminoimidazole ribotide synthetase
5235_at 1079.4 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 537.5 P
weak similarity to P.falciparum dihydropteroate synthase
5237_at 814.9 P
weak similarity to P.falciparum dihydropteroate synthase
5238_at 4607.5 P
hypothetical protein
5239_at 97.7 A
hypothetical protein
5240_at 897.8 P
SAP4 is related to SAP155, SAP185, and SAP190, all of which associate with the SIT4 protein phosphatase
5241_at 6211.3 P
mRNA (identified by a library screen) that causes growth arrest when overexpressed
5242_at 799.6 P
TOR inhibitor
5243_at 7361.0 P
9.5-kDa zeta subunit of oligosaccharyltransferase complex
5244_at 1278.7 P
similarity to N.crassa cytochrome-c oxidase chain V
5245_at 9982.2 P
May regulate Golgi function and glycosylation in Golgi
5246_at 3106.7 P
strong similarity to hypothetical protein YER037w
5247_at 1609.0 P
weak similarity to Clostridium regulatory protein
5248_at -164.9 A
hypothetical protein
5249_at 1115.7 P
Ngg1p-interacting factor 3
5250_at 6490.8 P
weak similarity to V.alginolyticus bolA protein
5206_at 704.0 P

hypothetical protein
5207_at 78.8 A
questionable ORF
5208_at 177.8 A
questionable ORF
5209_at 1025.2 P
Kinesin-related protein
5210_at 2384.2 P
Cyclin-like protein that interacts with Pho85p in affinity chromatography
5211_at -26.5 A
questionable ORF
5212_at 2005.2 P
antiviral protein, mRNA is induced early in meiosis
5213_at 234.5 P
hydrophilic protein, heptad repeat motif
5214_at 2012.6 P
similarity to M.jannaschii hypothetical proteins MJ1157 and MJ1478
5215_at 2497.4 P
ras-like GTPase, highly homologous to YPT31
5216_at 4361.4 P
Protein containing zinc fingers very similar to zinc fingers in Mig1p
5217_at 581.9 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 7467.9 P
transcription factor
5219_at 7831.3 P
presumed vesicle coat protein
5220_at 10.6 A
fatty-acyl coenzyme A oxidase
5221_at 3521.8 P
questionable ORF
5222_at 772.3 P
carboxypeptidase B-like processing protease
5223_at 11008.5 P
aromatic amino acid aminotransferase
5224_at 457.4 P
Member of the MCM\/P1 family of proteins involved in DNA replication
5225_at 14155.0 P
type I transmemebrane protein, component of COPII-coated, ER-derived transport vesicles
5226_at 43.1 P
questionable ORF
5227_at 6818.2 P
weak similarity to Yip1p
5228_at 2332.2 P
Mck1 Dosage Suppressor 3\; negative regulator of early meiotic gene expression
5183_at 4536.3 P
hypothetical protein
5184_at 5211.3 P
translational activator of GCN4 through activation of GCN2 in response to starvation
5185_at 198.1 P
Protein with similarity to Hda1p, Rpd3p, Hos1p, and Hos3p
5186_at 1156.7 P
questionable ORF
5187_at 127.4 A
IME4 appears to activate IME1 in response to cell-type and nutritional signals and thereby regulate

meiosis
5188_at 5937.1 P
subunit VIa of cytochrome c oxidase, may specifically interact with ATP
5189_at 1061.9 P
Protein phosphatase 2A regulatory subunit B
5190_i_at 689.2 A
Ribosomal protein S26A
5191_f_at 9929.1 P
Ribosomal protein S26A
5192_at 179.4 P
hypothetical protein
5193_at 6399.5 P
subunit IV of cytochrome c oxidase
5194_at 3867.7 P
similarity to hypothetical protein Fcy21p and weak similarity to FCY2 protein
5195_at 2619.7 P
weak similarity to dehydrogenases
5196_at 1282.6 P
strong similarity to Emericella nidulans cystathionine beta-lyase
5197_at -67.6 A
hypothetical protein
5198_at 69.8 A
questionable ORF
5199_at 1160.3 P
Glycine-threonine-serine repeat protein
5200_at 553.5 P
Protein kinase
5201_at 588.2 P
ser/thr protein kinase
5202_at 822.6 P
questionable ORF
5203_at 6858.0 P
multicopy suppressor of POP2
5204_at 1161.6 P
weak similarity to Oryctolagus calcium channel BIII
5205_at 60.4 A
involved in meiotic recombination and chromosome metabolism
5161_at 817.9 P
weak similarity to C.elegans hypothetical protein R08D7.1
5162_at 7239.9 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 4533.0 P
nuclear pore complex protein with GLFG repetitive sequence motif
5164_at 5553.2 P
Contains domains found in the DEAD protein family of ATP-dependent RNA helicases\; high-copy suppressor of kem1 null mutant
5165_at 74.1 A
hypothetical protein
5166_at 890.4 P
Protein involved in translation initiation
5167_at 375.1 P
questionable ORF
5168_at 3242.1 P
Ca++-Pump, ATPase

5169_at	2129.5	P	Activator of transcription
5170_at	621.7	A	questionable ORF
5171_at	1406.9	P	similarity to S.pombe hypothetical protein SPAC31A2.10
5172_at	1025.4	P	Required for X-ray damage repair, mitotic recombination, and full meiotic recombination. mRNA increases in meiosis.
5173_at	1530.9	P	Involved in sterol uptake
5174_at	4755.9	P	hypothetical protein
5175_at	427.3	P	similarity to hypothetical protein YLR047c and Fre2p
5176_at	1907.0	P	hypothetical protein
5177_at	-15.8	A	Serine\/threonine protein kinase
5178_at	5280.2	P	similarity to V.vinifera dihydroflavonol 4-reductase
5179_at	622.3	P	vacuolar alpha mannosidase
5180_at	1522.6	P	polypeptide subunit of a yeast type 1 protein geranylgeranyltransferase
5181_at	2908.8	P	aminoadipate-semialdehyde dehydrogenase small subunit (alpha-aminoadipate reductase)
5182_at	265.1	A	questionable ORF
5137_at	1658.7	P	Peroxisomal peripheral membrane protein (peroxin) involved in import of peroxisomal matrix proteins
5138_at	678.0	P	negative regulator of URS2 of the HO promoter
5139_at	2881.7	P	Shows similarity to the Snf2p family of DNA-dependent ATPases
5140_at	359.3	P	questionable ORF
5141_at	9236.3	P	Chorismate synthase
5142_i_at	5511.0	P	Ribosomal protein L9A (L8A) (rp24) (YL11)
5143_at	289.3	P	hypothetical protein
5144_at	503.6	P	transport protein that interacts with Sec20p\; required for protein transport from the endoplasmic reticulum to the golgi apparatus
5145_at	693.6	P	strong similarity to hypothetical protein YDL109c
5146_at	679.3	P	Mitochondrial polypeptide chain release factor
5147_at	879.0	P	Most likely an alpha 1,2 mannosyltransferase utilized for the addition of the third mannose onto the GPI core structure.
5148_at	2672.0	P	similarity to human human E6-associated protein
5149_at	2463.5	P	

weak similarity to Lactobacillus putative histidine protein kinase SppK
5150_at 1108.3 P
strong similarity to hypothetical protein YPL221w
5151_at -12.3 A
hypothetical protein
5152_at 7297.7 P
encodes beta -subunit of yeast coatomer
5153_at 746.3 P
weak similarity to E.coli ftsJ protein
5154_at 695.0 P
PHO85 cyclin
5155_at 854.3 P
similarity to hypothetical protein YPL216w
5156_at 100.9 P
questionable ORF
5157_at 1042.8 P
weak similarity to S.pombe hypothetical protein C3H1.12C
5158_at 1819.3 P
mRNA guanylyltransferase (mRNA capping enzyme), alpha subunit
5159_at 439.0 P
hypothetical protein
5160_at 1036.4 P
weak similarity to rat cysteine string protein
5115_at 1322.9 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 7071.3 P
required for inositol prototrophy
5117_at 2215.5 P
putative methylenetetrahydrofolate reductase (mthfr)
5118_at 573.9 P
similarity to S.pombe hypothetical protein
5119_at 9007.4 P
Ribosomal protein S2 (S4) (rp12) (YS5)
5120_at 7017.2 P
nuclear polyadenylated RNA binding protein
5121_at 807.4 P
hypothetical protein
5122_at 8721.8 P
pre-mRNA processing factor involved in disassembly of spliceosomes after the release of mature mRNA
5123_at 1125.7 P
multicopy suppressor of a cytochrome b mRNA translation defect, essential for the electron transfer in the bc1 complex
5124_at 118.5 A
questionable ORF
5125_at 1350.0 P
hypothetical protein
5126_at 1225.0 P
beta-transducin homolog
5127_at 1844.3 P
associates with Snf1p
5128_at 2152.8 P
weak similarity to H.influenzae permease
5129_at 1396.8 P
weak similarity to YOR165w
5130_at 3080.2 P

TATA-binding protein-associated-factor
5131_at 4218.3 P
hypothetical protein
5132_at 1169.1 P
hypothetical protein
5133_at 58.3 A
questionable ORF
5134_at 1519.3 P
weak similarity to hypotetical S.pombe protein
5135_at 2387.9 P
strong similarity to hypothetical protein YBR238c
5136_at 9192.5 P
light chain for myosin Myo2p
5092_at 10152.1 P
Associated with tRNA and amino acyl-tRNA synthetases\; has affinity for quadruplex nucleic acids
5093_at 514.2 P
similarity to glucose transport proteins
5094_at 14122.1 P
Ribosomal protein L28 (L29) (rp44) (YL24)
5095_at 333.7 P
questionable ORF
5096_at 2021.9 P
strong similarity to hypothetical protein YBR242w
5097_at 3468.6 P
nuclear pore protein, homologous to sec13
5098_at 3484.3 P
similarity to putative human GTP-binding protein MMR1
5099_at 932.2 P
hypothetical protein
5100_at 6899.9 P
pheromone response pathway suppressor
5101_at 901.4 P
similarity to copper homeostasis protein Cup9p
5102_at 672.1 P
cytosolic and peripheral membrane protein
5103_at 945.8 P
135-kDa protein that is subunit of poly(A) ribonuclease
5104_at 2546.6 P
component of spindle pole
5105_at 3223.6 P
Nuclear pore complex protein with GLFG motif
5106_at 1369.6 P
35 kDa nucleotide binding protein
5107_at 162.0 P
Ligase Interacting Factor 1\; physically interacts with DNA ligase 4 protein (Lig4p)
5108_at 11350.7 P
alpha mating factor
5109_at 2894.2 P
questionable ORF
5110_at 3741.8 P
Similar to ubiquitin conjugating protein family
5111_at 804.2 P
Coiled-coil protein involved in spindle-assembly checkpoint
5112_at 1014.8 P
weak similarity to Staphylococcus aureus nuclease (SNase)
5113_at 3040.9 P

strong similarity to hypothetical protein YPL189w
5114_at 727.4 P
suppressor of GTPase mutant
5069_at 4994.3 P
strong similarity to hypothetical protein YPL191c
5070_at 296.9 P
hypothetical protein
5071_at 3687.1 P
strong similarity to C.elegans R07E5.13 protein
5072_at 1643.5 P
hypothetical protein
5073_at 5936.9 P
ATP-dependent RNA helicase CA3 of the DEAD\/DEAH box family
5074_at 7193.2 P
Transporter (permease) for choline and nitrogen mustard\; share homology with UGA4
5075_i_at 10114.3 P
Ribosomal protein L7A (L6A) (rp11) (YL8)
5076_f_at 9714.6 P
Ribosomal protein L7A (L6A) (rp11) (YL8)
5077_at 281.4 P
Mitotic Membrane Component
5078_at 0.0 A
questionable ORF
5079_at 1427.0 P
heat shock transcription factor
5080_at 113.8 P
questionable ORF
5081_at 1659.0 P
Putative transcription factor that binds the consensus site PyPuCACCCPu
5082_at 6062.9 P
RNA polymerase II subunit
5083_at -233.2 A
questionable ORF
5084_at 2492.6 P
probable ribosomal protein L12
5085_at 3500.2 P
weak similarity to H.influenzae hypothetical protein
5086_at 1750.1 P
hypothetical protein
5087_at 2953.4 P
glycosyltransferase
5088_at 915.7 P
similarity to YLR276c and YKR024c
5089_at 716.5 P
pseudouridine synthase 2
5090_at 6520.2 P
pyruvate carboxylase
5091_at 769.7 P
Death Upon Overexpression
5047_at 1761.6 P
strong similarity to hypothetical protein YBR216c
5048_at 212.5 P
similarity to rat branched-chain alpha-ketoacid dehydrogenase kinase
5049_at 2977.1 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 900.4 P
hypothetical protein
5051_at 3187.3 P
homologue of pombe SDS23\; localizes to spindle pole body
5052_at 11360.4 P
delta-9-fatty acid desaturase
5053_at 4429.3 P
strong similarity to D.melagonaster cni protein
5054_at 2314.6 P
strong similarity to hypothetical proteins YAR031w, YGL051w, YAR028w, YAR033w and YCR007c
5055_at 207.2 P
questionable ORF
5056_at 870.1 P
strong similarity to YAR033w protein
5057_at 1311.5 P
hypothetical protein
5058_at 1164.1 P
mRNA cap-binding protein (eIF-4F), 130K subunit
5059_at 10140.7 P
ATPase
5060_at 822.1 P
similarity to hypothetical S. pombe protein
5061_at 412.9 P
hypothetical protein
5062_at 737.0 P
hypothetical protein
5063_at 1531.9 P
component of the cleavage and polyadenylation factor CF I involved in pre-mRNA 3 -end processing
5064_at 1515.3 P
RNA polymerase II elongation factor
5065_at 1053.8 P
questionable ORF
5066_at 263.2 A
weak similarity to YJL109c
5067_at 7048.8 P
delta-aminolevulinate dehydratase (porphobilinogen synthase)
5068_at 4604.3 P
similarity to V. vinifera dihydroflavonol reductase
5024_at 1639.3 P
membrane-bound mannosyltransferase
5025_at 7178.5 P
similarity to E.coli hypothetical 23K protein
5026_at 1366.8 P
Mtf1 Two Hybrid Clone 2
5027_at 622.5 P
C2H2 zinc finger protein which resembles the mammalian Egr and Wilms tumour proteins
5028_at 60.8 A
questionable ORF
5029_at 49.4 A
Meiosis-specific gene required for the pairing of homologous chromosomes
5030_at 118.4 P
adhesion subunit of a-agglutinin
5031_at 11487.2 P
Ribosomal protein L24A (rp29) (YL21) (L30A)

5032_at 13372.2 P
Large ribosomal subunit protein L30 (L32) (rp73) (YL38)
5033_at 4045.9 P
weak similarity to human chromatin assembly factor I p150 chain
5034_at 4849.9 P
glucanase gene family member
5035_at 4138.8 P
glucosidase I
5036_at 13021.8 P
tryptophan synthetase
5037_at 760.6 P
Probable transcription factor, polyglutamine domain protein
5038_at 1095.4 P
questionable ORF
5039_at 3626.8 P
weak similarity to Vsp27p
5040_at 8931.0 P
required for protein glycosylation
5041_at 867.5 P
DNA damage-responsive protein
5042_at 6188.2 P
hypothetical protein
5043_at 4738.7 P
beta (38kDa) subunit of casein kinase II (CKII)
5044_at 619.9 P
Homolog of E. coli Hsc20 co-chaperone protein
5045_at 801.0 P
arginyl-tRNA-protein transferase
5046_at 1644.4 P
pleiotropic drug resistance regulatory protein
5002_at 239.2 P
hypothetical protein
5003_at 2735.5 P
similarity to Drosophila pumilio protein and Mpt5p protein
5004_at 3474.8 P
zinc-finger transcription factor of the Zn(2)-Cys(6) binuclear cluster domain type
5005_at 11057.3 P
Sterol C-24 reductase
5006_at 7432.2 P
Proteasome subunit YC7alphaVY8 (protease yscE subunit 7)
5007_at 1376.8 P
similarity to hypothetical S. pombe protein
5008_at 8681.7 P
isopropylmalate isomerase
5009_at 8557.1 P
plasma membrane H+-ATPase
5010_at 56.8 A
questionable ORF
5011_at 3707.6 P
putative vacuolar Ca2+ ATPase
5012_at 245.5 A
weak similarity to Xenopus kinesin-related protein Eg5
5013_at 1322.7 P
weak similarity to Tup1p
5014_at 700.0 P
protein required for Clb2 and Ase1 degradation

5015_at	1803.9	P	p24 protein involved in membrane trafficking
5016_at	8792.4	P	putative 3-beta-hydroxysteroid dehydrogenase
5017_at	1727.3	P	similarity to C.elegans hypothetical M142.5 protein
5018_at	2337.9	P	similarity to C.elegans hypothetical M142.5 protein
5019_at	1252.5	P	similarity to hypothetical S. pombe protein
5020_at	811.6	P	similarity to D.melanogaster lin19 protein
5021_at	1133.0	P	strong similarity to hypothetical protein YLR324w
5022_at	1467.6	P	transcription initiation factor TFIIF middle subunit
5023_at	327.4	P	RNA splicing factor associated with U5 snRNP
4979_at	5816.1	P	choline phosphate cytidylyltransferase (also called phosphoethanolamine cytidylyltransferase or phosphocholine cytidylyltransferase)
4980_at	3880.2	P	ATPase stabilizing factor
4981_at	2130.9	P	Putative t-SNARE of the plasma membrane
4982_at	1062.3	P	strong similarity to hypothetical protein YLR328w
4983_g_at	1513.6	P	strong similarity to hypothetical protein YLR328w
4984_at	1681.0	P	questionable ORF
4985_at	1406.3	P	similarity to E.nidulans cysteine synthase
4986_at	1188.2	P	Associated with U1 snRNP (no counterpart in mammalian U1 snRNP. Contains few SR-, RE- and RD-dipeptides.
4987_at	4698.9	P	putative integral membrane protein
4988_at	160.8	P	similarity to hypothetical protein YGR031w
4989_at	496.7	P	weak similarity to M.jannaschii hypothetical protein MJ1317
4990_at	1565.1	P	hypothetical protein
4991_at	273.2	A	questionable ORF
4992_at	3315.2	P	gamma-aminobutyrate (GABA) transaminase (4-aminobutyrate aminotransferase)
4993_at	8587.9	P	Vacuolar H-ATPase 14 kDa subunit (subunit F) of the catalytic (V1) sector
4994_at	710.4	P	similarity to M.leprae yfcA protein
4995_at	205.1	A	questionable ORF
4996_at	394.7	P	acts in concert with Mid2p to transduce cell wall stress signals

4997_at	3617.5	P	weak similarity to Methanobacterium thermoautotrophicum hypothetical protein MTH972
4998_at	412.9	A	questionable ORF
4999_at	4318.6	P	hypothetical protein
5000_i_at	7971.8	P	Ribosomal protein S25A (S31A) (rp45) (YS23)
5001_f_at	8008.2	P	Ribosomal protein S25A (S31A) (rp45) (YS23)
4956_at	3793.8	P	40 kDa putative membrane-spanning ATPase
4957_at	1700.4	P	integral subunit of RNase P and apparent subunit of RNase MRP
4958_at	2291.7	P	similarity to hypothetical protein YGR015c and weak similarity H.influenzae dihydrolipoamide acetyltransferase
4959_at	4570.0	P	catalytic component of 1,3-beta-D-glucan synthase
4960_at	2806.2	P	hypothetical protein
4961_at	3942.4	P	hypothetical protein
4962_at	568.1	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	16120.2	P	Acyl-CoA-binding protein (ACBP)\/Diazepam binding inhibitor (DBI)\/endozepine (EP)
4964_at	6208.2	P	strong similarity to hypothetical protein YLR350w
4965_at	161.5	P	questionable ORF
4966_at	423.1	P	MAP protein kinase homolog involved in pheromone signal transduction
4967_at	2716.8	P	Among a group of genes whose products are necessary for bud-site selection\; likely involvement in positioning the proximal pole signal
4968_at	546.5	P	hypothetical protein
4969_at	472.4	P	strong similarity to transaldolase
4970_at	2908.2	P	zinc finger protein\; negative regulator of meiosis\; directly repressed by a1-a2 regulator
4971_at	468.1	P	questionable ORF
4972_at	333.6	P	hypothetical protein
4973_at	2037.6	P	transcription factor tau (TFIIIC) subunit 131
4974_at	2351.4	P	ubiquitin fusion degradation protein
4975_at	8065.1	P	Protein that suppresses ts allele of CDC4 when overexpressed
4976_at	1239.1	P	questionable ORF
4977_at	67.4	A	

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questionable ORF
4978_at    195.0      A
similarity to ser/thr protein kinases
4934_at    -94.9      A
hypothetical protein
4935_at    4584.0     P
similarity to C.elegans E04D5.1 protein
4936_at    6844.6     P
high affinity methionine permease
4937_at    2010.8     P
Member of RSC complex
4938_at    969.8      P
Required for amino acid permease transport from the Golgi to the cell surface
4939_at    1110.5     P
similarity to mouse calcium-binding protein
4940_at    204.2      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    11776.1    P
C-4 sterol methyl oxidase
4942_at    10237.6    P                                                              5
-phosphoribosylformyl glycinamidine synthetase
4943_at    2626.8     P
Cytochrome OXidase gene 18
4944_at    6084.3     P
Zn-finger protein, transcriptional regulator
4945_at    806.0      P
questionable ORF
4946_at    1658.3     P
similarity to P.putida phthalate transporter
4947_at    37.0       M
similarity to hypothetical protein YBR105c
4948_at    657.7      P
weak similarity to transcription factors
4949_at    1098.9     P
weak similarity to Rod1p
4950_at    111.0      M
questionable ORF
4951_at    786.0      A
GDP-GTP Exchange Protein (GEP) for the Rho1p Small GTP-binding Protein
4952_at    541.1      P
similarity to hypothetical protein YLR373c
4953_at    505.9      P
factor stimulating decay of mRNAs containing premature stop codons\; acts with Nmd2p and Nam7p
4954_at    779.5      P
questionable ORF
4955_at    790.5      P
Homolog of human core snRNP protein D1, involved in snRNA maturation
4911_at    921.0      P
RNA splicing factor
4912_at    2034.8     P
Mitochondrial ribosomal protein MRPL25 (YmL25)
4913_at    3868.6     P
peroxisome associated protein containing a PTS1 signal
4914_at    4382.9     P
Polypeptide 3 of a Yeast Non-native Actin Binding Complex, homolog of a component of the bovine
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NABC complex
4915_at 2732.4 P
hypothetical protein
4916_at 3319.0 P
Twinfilin A, an actin monomer sequestering protein
4917_at 1485.4 P
weak similarity to mammalian myosin heavy chain
4918_at 7359.4 P
20 kDa mitochondrial outer membrane protein import receptor
4919_at 2152.2 P
translation initiation factor eIF2B, 71 kDa (delta) subunit\; translational repressor of GCN4 protein
4920_at 1353.8 P
35 kDa mitochondrial ribosomal small subunit protein
4921_i_at 14336.6 P
60S ribosomal protein L11B (L16B) (rp39B) (YL22)
4922_at 8218.4 P
strong similarity to hypothetical protein YPL004c
4923_at -21.8 A
Third, minor isozyme of pyruvate decarboxylase
4924_at 199.8 P
cytoplasmic catalase T
4925_at 312.3 P
weak similarity to rat tropomyosin
4926_at 4929.0 P
hypothetical protein
4927_at 1045.8 P
pre-mRNA splicing protein
4928_at 1293.6 P
Serine\/threonine protein kinase
4929_at 2226.2 P
similarity to hypothetical S.pombe protein
4930_at 11879.2 P
mitochondrial and cytoplasmic valyl-tRNA synthetase
4931_at 6481.7 P
Putative 3 ->5 exoribonuclease\; component of exosome complex of 3 ->5 exonucleases
4932_at 391.6 P
similarity to bovine Graves disease carrier protein
4933_at 5025.7 P
transcriptional activator of the SKN7 mediated two-component regulatory system
4888_at 1623.8 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 1562.7 P
involved in controlling telomere length
4890_at 821.8 P
Mac1-dependent regulator
4891_at 2584.2 P
weak similarity to B.subtilis YqgP
4892_at 1181.0 P
hypothetical protein
4893_at 4520.7 P
similarity to zebrafish essential for embryonic development gene pescadillo
4894_at 735.5 P
subunit of RNA polymerase II holoenzyme\/mediator complex
4895_at 3844.6 P

Protein involved in vacuolar H-ATPase assembly or function
4896_at 10184.4 P
hypothetical protein
4897_at 17.8 A
questionable ORF
4898_at 1094.9 P
G(sub)2-specific B-type cyclin
4899_at 113.2 A
B-type cyclin
4900_at 353.9 P
weak similarity to YLR099c and YDR125c
4901_at 968.7 P
weak similarity to mosquito carboxylesterase
4902_at 691.0 P
mitochondrial protein with homology to the mammalian SURF-1 gene
4903_at 647.7 P
Duo1 And Mps1 interacting
4904_at -213.7 A
questionable ORF
4905_g_at 1502.6 P
questionable ORF
4906_at 128.8 A
questionable ORF
4907_at 1061.2 P
transcriptional regulator, interacts with histones, primarily histone H3, possesses nucleosome assembly activity
4908_at 1768.5 P
hypothetical protein
4909_f_at 17319.5 P
Ribosomal protein S23A (S28A) (rp37) (YS14)
4910_at 796.8 P
Contains GLFG repeats in N-terminal half and heptad repeats in C-terminal half
4865_at 992.9 P
required for ER to golgi vesicle docking
4866_at 883.2 P
ammonia permease
4867_at 966.2 P
hypothetical protein
4868_at 2222.9 P
serine\/threonine phosphatase
4869_at 12412.2 P
asparagine synthetase
4870_at 3708.5 P
similarity to S.pombe hypothetical protein SPAC24H6.11c
4871_at 122.7 A
weak similarity to hypothetical protein YPR156c
4872_at 1188.6 P
weak similarity to mouse T10 protein
4873_at 3638.7 P
hypothetical protein
4874_at 504.6 P
SYnthetic lethal with cdcForty
4875_at 607.8 P
weak similarity to myosin heavy chain proteins
4876_at 595.7 P
strong similarity to Nce2p

4877_at 3593.4 P
mitochondrial protein, prohibitin homolog\; similar to S. cerevisiae Phb2p
4878_at 195.4 A
Member of ubiquitin-conjugating protein family
4879_at 1930.6 P
hypothetical protein
4880_at 7333.6 P
proteasome component Y13
4881_at 6797.3 P
weak similarity to chicken growth factor receptor-binding protein GRB2 homolog
4882_g_at 3952.8 P
weak similarity to chicken growth factor receptor-binding protein GRB2 homolog
4883_at 713.5 P
questionable ORF
4884_i_at 8277.2 P
similarity to multidrug resistance proteins
4885_at 124.3 P
questionable ORF
4886_at 657.8 P
110 kDa subunit of the centromere binding factor CBF3
4887_at 963.1 P
strong similarity to hypothetical protein YPR157w
4842_at 1933.5 P
similarity to hypothetical protein YPR158w
4843_at 4735.0 P
encodes a predicted type II membrane protein highly homologous to Kre6p
4844_at 630.2 P
component of the biosynthetic pathway producing the thiazole precursor of thiamine
4845_at 3580.3 P
similarity to C.elegans hypothetical protein
4846_at 4745.6 P
hypothetical protein
4847_at 1312.0 P N
alpha-acetyltransferase that acts on methionine termini
4848_at 8060.5 P
Ribosomal protein L24B (rp29) (YL21) (L30B)
4849_at 2018.5 P
hypothetical protein
4850_at 378.9 P
hypothetical protein
4851_i_at 6909.8 P
questionable ORF
4852_s_at 2138.6 P
questionable ORF
4853_at 626.0 P
GTP-binding protein of the ras superfamily involved in bud site selection
4854_at 360.3 P
hypothetical protein
4855_at 331.6 P
strong similarity to hypothetical proteins YKR076w and YMR251w
4856_at 12694.7 P
Cystathionine beta-synthase
4857_at 1186.9 P
hypothetical protein
4858_at 6601.5 P
Phosphatidyl-ethanolamine N-methyltransferase

4859_at 1688.4 P
involved in mRNA transport
4860_at 10285.3 P
nuclear localization sequence binding protein
4861_at 251.9 M
questionable ORF
4862_at 3909.3 P
hypothetical protein
4863_at 2977.7 P
mRNA cap-binding protein (eIF-4F), 150K subunit , highly homologous to Tif4632p, homologs of mammalian p220
4864_at 1156.2 P
GTP-binding protein
4819_at -37.1 A
questionable ORF
4820_at 1727.5 P
hypothetical protein
4821_at 1594.1 P
Involved in biosynthetic pathway for cell wall beta-glucans
4822_at 4901.2 P
Clathrin light chain
4823_at 808.6 P
hypothetical protein
4824_at 2759.2 P
similarity to Rib2p
4825_at 1787.5 P
phosphatidylserine decarboxylase located in vacuole or Golgi
4826_at 1510.6 P
mitochondrial methionyl-tRNA synthetase
4827_at 4191.0 P
Golgi membrane protein
4828_at 4996.2 P
strong similarity to human GTP-binding protein
4829_at 420.8 P
Essential for the expression and activity of ubiquinol-cytochrome c reductase
4830_at 7393.7 P
Squalene monooxygenase
4831_at -72.3 A
questionable ORF
4832_at 2753.4 P
Alcohol acetyltransferase
4833_at 7907.8 P
Poly(A)-binding protein binding protein
4834_at 797.7 P
hypothetical protein
4835_at 11994.7 P
Ribonucleotide Reductase
4836_at 7703.7 P
similarity to YHR004c-a
4837_at 5239.7 P
questionable ORF
4838_at 7541.8 P
7.3 kDa subunit 9 of the ubiquinol cytochrome c oxidoreductase complex
4839_at 2834.7 P
Ubiquitin-protein ligase
4840_at 8423.0 P

tyrosyl-tRNA synthetase, cytoplasmic
4841_at 3131.8 P
Transcription factor TFIIF large subunit
4797_at 6022.6 P
HMG1\/2 homolog
4798_at 151.7 A
Serine\/threonine protein kinase required for cell cycle arrest in response to loss of microtubule function
4799_at 10467.7 P
similarity to Aspergillus fumigatus rAsp
4800_at 114.6 A
questionable ORF
4801_at 4639.5 P
histidine permease
4802_i_at 18.1 A
Glyceraldehyde-3-phosphate dehydrogenase 3
4803_at 1965.3 P
Protein X component of mitochondrial pyruvate dehydrogenase complex
4804_at 801.7 P
xylulokinase
4805_at 4640.5 P
homolog of RNAse PH
4806_at 812.9 P
weak similarity to Tetrahymena acidic repetitive protein arp1
4807_at 2013.1 P
involved in nitrosoguanidine resistance
4808_at 3692.8 P
hypothetical protein
4809_at 3599.0 P
dolichyl phosphate-D-mannose:protein O-D-mannosyltransferase
4810_at 2532.4 P
weak similarity to rape guanine nucleotide regulatory protein
4811_at 986.3 P
strong similarity to translation elongation factor eEF1 alpha chain Cam1p
4812_at 1049.4 P
phosphorylcholine transferase\; or cholinephosphate cytidylyltransferase
4813_at 2817.6 P
weak similarity to X.laevis protein-tyrosin-phosphatase cdc homolog 2 and to hypothetical protein YPR200c
4814_at 12172.9 P
encodes the cytoplasmic trifunctional enzyme C1-tetrahydrofolate synthase
4815_at 241.0 P
similarity to S.pombe hypothetical protein D89234
4816_at 1328.7 P
similarity to Xenopus transcription factor Oct-1.17
4817_at 656.0 P
electron-transferring flavoprotein, beta chain
4818_at 3336.3 P
phosphoserine phosphatase
4774_at 8962.6 P
thioredoxin
4775_at 5101.9 P
similarity to M.jannaschii GTP-binding protein and to M.capricolum hypothetical protein SGC3
4776_at 4845.9 P
zinc finger protein
4777_at 127.8 P
weak similarity to S.pombe hypothetical protein SPAC18B11.03c

4778_at	1461.3	P	involved in 7-aminocholesterol resistance
4779_f_at	12409.4	P	Ribosomal protein S0A
4780_at	12116.8	P	Ribosomal protein S0A
4781_at	1102.9	P	strong similarity to hypothetical S. pombe protein
4782_at	1751.7	P	Participates in synthesis of N-acetylglucoaminylphosphatidylinositol, the first intermediate in synthesis of glycosylphosphatidylinositol (GPI) anchors
4783_at	1514.9	P	putative calcium channel
4784_at	606.6	P	omosome region maintenance protein
4785_at	231.8	P	questionable ORF
4786_at	3913.4	P	Mitochondrial ribosomal protein MRPL9 (YmL9) (E. coli L3) (human MRL3)
4787_at	267.8	A	similarity to hypothetical protein YHR149c
4788_at	3150.0	P	translational activator of cytochrome c oxidase subunit III
4789_at	907.8	P	weak similarity to hypothetical protein YFR021w
4790_at	526.8	P	strong similarity to drug resistance protein SGE1
4791_at	83.9	A	weak similarity to human p55CDC and Cdc20p
4792_at	-23.7	A	hypothetical protein
4793_at	2659.1	P	De-repression of ITR1 Expression
4794_at	1684.2	A	questionable ORF
4795_at	2822.6	P	57 kDa nuclear protein
4796_at	314.4	P	questionable ORF
4751_at	8281.1	P	mitochondrial protein, prohibitin homolog\; homolog of mammalian BAP37 and S. cerevisiae Phb1p
4752_at	3418.0	P	possible homolog of human 26S proteasome regulatory subunit p28
4753_at	5917.0	P	Positive regulatory protein of phosphate pathway
4754_at	10297.6	P	Flavohemoglobin
4755_at	3691.4	P	hypothetical protein
4756_at	107.0	A	questionable ORF
4757_at	1249.7	P	weak similarity to YOR019w
4758_at	1074.2	P	protein containing kelch repeats, similar to YHR158c and YPL263c
4759_at	923.0	P	

weak similarity to hypothetical protein YHR160c
4760_at 9026.4 P
phosphofructokinase alpha subunit
4761_at 2033.0 P
Yeast Assembly Polypeptide, member of AP180 protein family, binds Pan1p and clathrin
4762_at -90.3 A
questionable ORF
4763_at 897.4 P
strong similarity to hypothetical protein YHR162w
4764_at 5748.4 P
Succinate-CoA Ligase (ADP-Forming)
4765_at 3596.3 P
similarity to hypothetical S.pombe protein
4766_at 2501.8 P
RNA polymerase III transcription factor with homology to TFIIB
4767_at 650.0 P
hypothetical protein
4768_at 438.8 P
similar to SOL3
4769_at 94.7 A
Mga1p shows similarity to heat shock transcription factor
4770_at 739.0 P
weak similarity to human cleavage stimulation factor 64K chain
4771_at 2254.1 P
hypothetical protein
4772_at 1080.8 P
histone acetyltransferase
4773_at 8071.5 P
Proteasome subunit
4729_i_at 4886.3 P
enolase I
4730_s_at 7808.9 P
enolase I
4731_at 3577.3 P
COQ6 monooxygenase
4732_at 573.2 P
6-phosphogluconate dehydrogenase
4733_at 3057.0 P
similarity to C.elegans C16C10.1
4734_at 1445.9 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 521.7 P
questionable ORF
4736_at 11013.1 P
similarity to allantoate transport protein
4737_at 3025.3 P
putative beta adaptin component of the membrane-associate clathrin assembly complex
4738_at 2700.9 P
ser/thr protein kinase
4739_at 1226.4 P
weak similarity to E.coli lipase like enzyme
4740_at 9732.6 P
methionyl tRNA synthetase
4741_at -6.3 A

questionable ORF
4742_at 2707.6 P
hypothetical protein
4743_at 3624.3 P
GTP-cyclohydrolase I
4744_at 2448.5 P
weak similarity to S.pombe hypothetical protein SPAC17A5
4745_at 296.6 P
questionable ORF
4746_at 2704.9 P
Member of CDC48\/PAS1\/SEC18 family of ATPases
4747_at 531.8 P
strong similarity to S.pombe RNA helicase
4748_at 2053.5 P
similarity to hypothetical S.pombe protein SPAC12G12.02
4749_at -41.0 A
similarity to hypothetical protein YMR295c
4750_at 2943.5 P
Component of the TAFII complex required for activated transcription
4705_at 2362.6 P
hypothetical protein
4706_at 2614.2 P
ribonuclease H
4707_at 2783.6 P
similarity to hypothetical S.pombe protein
4708_at 228.3 P
similarity to C.elegans LET-858
4709_at 11016.1 P
glucanase gene family member
4710_at 7748.3 P
weak similarity to Cbf5p
4711_at 11229.1 P
ABC transporter
4712_at 13611.1 P
Cell wall endo-beta-1,3-glucanase
4713_at 1506.1 P
similarity to hypothetical protein YMR310c
4714_at 5121.7 P
similarity to mouse Surf-4 protein
4715_at 10921.3 P
Zuotin, putative Z-DNA binding protein
4716_at 3252.3 P
Biotin synthase
4717_at 173.5 P
strong similarity to maltase
4718_at 609.1 P
maltose pathway regulatory protein
4719_at 474.9 P
alpha-glucoside transporter
4720_at 320.2 A
hypothetical protein
4721_at -127.3 A
hypothetical protein
4722_s_at 235.7 P
strong similarity to hypothetical protein YBR300c
4723_f_at 1593.8 P

strong similarity to members of the Srp1p/Tip1p family
4724_i_at 5889.3 P
hypothetical protein
4725_f_at 480.3 P
hypothetical protein
4726_at 127.3 A
identified by SAGE
4727_s_at 4560.9 P
Protein essential for mitochondrial biogenesis and cell viability
4728_at 165.6 P
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 3315.2 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 5424.8 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 2370.9 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 679.8 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 3085.3 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 1545.4 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 659.4 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 26.2 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 810.6 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 387.2 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 5.8 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 75.4 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 -6.7 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 163.1 A
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 251.3 P
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 8495.9 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 1801.2 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 1637.5 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 548.7 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 325.1 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 6299.7 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 3330.9 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 127.2 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 253.6 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 1342.4 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 1051.1 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 344.0 P
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 20.1 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 10195.2 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 2045.7 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 316.3 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 -19.0 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 2566.0 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 79.2 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 165.8 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 -58.1 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 5940.3 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 722.3 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 34.7 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 94.8 A
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 161.8 A
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 1262.9 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 17.7 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 -17.4 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 -92.0 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 255.4 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 -29.4 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 -3.5 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 191.5 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 536.1 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 228.3 P

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 -241.0 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 57.9 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 50.9 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 0.1 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 81.2 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 230.5 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 1731.0 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 35.0 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 54.9 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 -0.3 A
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 60.7 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 72.3 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 79.9 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 -7.2 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 389.5 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 115.3 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 989.7 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 1582.0 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 640.3 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 81.2 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 -133.4 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 309.6 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 130.7 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 319.0 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
4609_at 393.5 P
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 -116.0 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 12.6 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 -8.8 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 542.0 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 1590.7 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 3651.6 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 565.9 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 1327.9 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 3159.8 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 551.1 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 79.1 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 605.2 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 1557.0 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 6335.0 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 223.4 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 9893.0 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 3220.1 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 1545.1 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 494.9 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 139.7 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 2136.4 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 864.9 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 219.2 P
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 774.2 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 230.9 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 663.3 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 1940.4 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 2346.3 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 -46.5 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 -64.1 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 41.4 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 353.3 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 8.9 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 252.1 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 78.9 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 354.7 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 2353.8 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 3353.0 P
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 2286.8 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 1395.8 P
snRNA
4604_i_at 586.1 P
snRNA
4605_s_at 1512.1 P
snRNA
4606_at 1591.3 P
snRNA
4607_at 1018.8 P
snRNA
4561_s_at 589.6 P
snRNA
4562_at 130.8 A
similarity to C.carbonum toxin pump
4563_f_at 2535.5 P
strong similarity to members of the Srp1p/Tip1p family
4564_at 132.8 P
similarity to subtelomeric encoded proteins
4565_at 173.2 P
ExtraCellular Mutant
4566_at 86.0 A
similarity to subtelomeric encoded proteins
4567_at 329.0 P

weak similarity to Drosophila hypothetical protein 6
4568_at 2053.7 P
similarity to C.carbonum toxin pump
4569_at 1972.0 P
weak similarity to YPL208w
4570_at 377.2 A
Cytochrome B pre-mRNA processing protein
4571_at 355.4 A
hypothetical protein
4572_at 806.4 P
very low affinity methionine permease
4573_at 1069.1 P
ABC transporter
4574_at 8580.9 P
Single-strand nucleic acid binding protein
4575_i_at 16980.7 P
Ribosomal protein L8A (rp6) (YL5) (L4A)
4576_at 815.8 P
glyerol kinase (converts glycerol to glycerol-3-phosphate
4577_at 5199.8 P
SNARE protein with a C-terminal membrane anchor
4578_at 1867.4 P
ExtraCellular Mutant
4579_at 2995.0 P
hypothetical protein
4580_at 731.7 P
Putative integral membrane protein containing novel cysteine motif. Similarity to SLG1 (WSC1), WSC2 and WSC3
4581_at 8876.3 P
Meiotic regulatory protein\; Cys-His zinc fingers
4582_at 1627.5 P
hypothetical protein
4583_at 3954.7 P
transcriptional regulator
4584_at 622.3 P
RNA binding domain (N-term) with asparagine rich region?
4539_at 842.5 P
hypothetical protein
4540_at 6.0 A
Encodes one of the earliest meiosis-specific recombination functions.
4541_at 1068.7 P
weak similarity to Pseudomonas gamma-butyrobetaine hydroxylase
4542_at 5001.6 P
negative regulator of phospholipid biosynthesis
4543_at 623.6 P
Similiar to clathrin coat proteins
4544_at 138.4 P
Dimerization cofactor of homeodomian protein NF1-alpha
4545_at 1365.1 P
Probable transmembrane protein PTM1
4546_at 913.9 P
Urea transporter
4547_at 12903.4 P
Ribosomal protein S20
4548_at 220.4 P
GTP-binding protein and glycogen phosphorylase (weak)

4549_at 4038.3 P
similarity to C.elegans hypothetical protein F21D5.2
4550_at -18.9 A
UDP Glucose pyrophosphorylase
4551_at 7606.1 P
ribose-phosphate pyrophosphokinase 3
4552_at 217.2 P
similarity to C.elegans hypothetical protein
4553_at 342.8 P
bZip DNA binding proteins
4554_at 3120.4 P
Potential formate transporter nirC
4555_at 2040.6 P
serine\/threonine protein kinase
4556_at 734.5 P
hypothetical protein
4557_at -248.4 A
hypothetical protein
4558_at 1456.8 P
mitochondrial ribosomal protein, homologous to E. coli ribosomal protein S2, component of the 37 S subunit of mitochondrial ribosomes
4559_at 1993.0 P
YKL008c
4560_at 1633.7 P
SH3 domain
4515_i_at 10867.1 P
Ribosomal protein L14B
4516_f_at 10838.8 P
Ribosomal protein L14B
4517_at 3226.8 P
60kD chaperonin (weak)
4518_at 5967.6 P
8.5 kDa subunit of the ubiqunol-cytochrome c oxidoreductase complex
4519_at 574.5 P
Mitochondrial carrier protein\/Grave s disease carrier protein
4520_at 1930.8 P
thiF, moeB, ubiquitin activating enzyme (all weak)
4521_at 646.2 P
similarity to YLL010c, YLR019w
4522_at 2140.3 P
alpha subunit of G protein coupled to mating factor receptors
4523_at 8208.5 P
May act cooperatively with Mrs5p in mitochondrial protein import or other related essential mitochondrial processes
4524_at 1562.2 P
Zinc finger (Cys(2)-His(2))
4525_at 16422.8 P
cytochrome P450 lanosterol 14a-demethylase
4526_at 3896.3 P
Manganese-containing superoxide dismutase
4527_at 4230.6 P
similarity to S.pombe hypothetical protein
4528_i_at 8160.8 P
Ribosomal protein L27A
4529_f_at 8617.7 P
Ribosomal protein L27A

4530_at 523.9 P
Seryl-tRNA synthetase
4531_at 2263.8 P
Vacuolar protein sorting
4532_at 2644.9 P
subunit of the major N alpha-acetyltransferase, complexes with the catalytic subunit of N-a-acetyltransferase (Nat1)
4533_at 179.6 P
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 334.4 P
PolyA-binding protein
4535_at 1631.1 P
SH3 domain in C-terminus
4536_at 965.3 P
strong similarity to S.douglasii YSD83
4537_at 6330.1 P
argininosuccinate lyase
4538_at 11010.0 P
Asparaginyl-tRNA synthetase
4493_at 10295.6 P
Aminoacyl tRNA-synthetase
4494_at 11308.6 P
40S Ribosomal protein S27B (rp61) (YS20)
4495_at 1.5 A
ExtraCellular Mutant
4496_at 63.9 P
RAS-related protein
4497_at 574.1 P
Class II Myosin
4498_at 1381.5 P
53 kDa subunit of the mitochondrial processing protease
4499_at 12555.4 P
homoserine kinase
4500_at 9490.3 P
proteolipid protein of the proton ATPase
4501_at 8327.5 P
Subunit of 26S Proteasome (PA700 subunit)
4502_at 2999.9 P
Dipeptidyl aminopeptidase B (DPAP B)
4503_at 3109.5 P
Thymidylate synthase (putative\; weak)
4504_at 7080.8 P
putative protein kinase
4505_at 1461.5 P
Pif1p, mitochondrial DNA repair and recombination protein
4506_at 3685.0 P
ethionine resistance protein
4507_at 1411.8 P
Pro1p (Gamma-glutamyl kinase)
4508_at 812.2 P
hypothetical protein
4509_at 168.9 P
Sec23p (weak)
4510_at 350.5 P

similarity to hypothetical protein YGL247w
4511_at 2682.9 P
delta-1-pyrroline-5-carboxylate dehydrogenase
4512_at 522.6 P
Killed in Mutagen, sensitive to Diepoxybutane and\/or Mitomycin C
4513_at 6470.4 P
Aldehyde dehydrogenases
4514_at 14651.8 P
13-kDa vacuolar H-ATPase subunit
4469_at 1372.1 P
weak similarity to Hit1p
4470_at 5002.4 P
RNA polymerase II holoenzyme\/mediator subunit
4471_at 10251.4 P
NADP-cytochrome P450 reductase
4472_s_at 3095.4 P
2-deoxyglucose-6-phosphate phosphatase
4473_i_at 124.9 P
2-deoxyglucose-6-phosphate phosphatase
4474_at 2576.8 P
hypothetical protein
4475_at 4036.8 P
Inositol monophosphatase
4476_at 7028.4 P
arginine\/alanine aminopeptidase
4477_at 695.8 P
similarity to multidrug resistance proteins
4478_at 4555.8 P
similarity to S.pombe dihydrofolate reductase and YOR280c
4479_at 353.4 P
questionable ORF
4480_at 2431.5 P
localized to mitochondrial membrane
4481_at 7909.9 P
subunit VI of cytochrome c oxidase
4482_at 3219.5 P
weak similarity to P.yoelii rhoptry protein
4483_s_at 9823.7 P
copper-binding metallothionein
4484_s_at 3818.1 P
weak similarity to YOR262w
4485_at 5089.5 P
Peptidylprolyl isomerase (cyclophilin) ER or secreted
4486_at 1008.2 P
RNA polymerase II transcriptional regulation mediator
4487_at 597.1 P
weak similarity to Ustilago hordei B east mating protein 2
4488_at 1735.2 P
required for V-ATPase activity
4489_at 1787.5 P
GTPase-interacting component 1
4490_at 2349.4 P
Protein subunit of nuclear ribonuclease P (RNase P)
4491_at 3312.3 P
weak similarity to translational activator CBS2
4492_at 12392.7 P

Hsp70 Protein
4446_at 3406.4 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 971.8 P
homologous to Ssf2p
4448_at 893.2 P
hypothetical protein
4449_at 11194.4 P
Deoxyhypusine synthase
4450_at 2017.8 P
3->5 exoribonuclease\; Component of the exosome 3->5 exonuclease complex with Rrp41p, Rrp42p, Rrp43p and Dis3p (Rrp44p).
4451_at 3394.0 P
strong similarity to N.crassa met-10+ protein
4452_at 6081.6 P
G1\/S cyclin (weak)
4453_at 6443.4 P
2,3-oxidosqualene-lanosterol cyclase
4454_at 399.5 P
Oxysterol-binding protein
4455_at 1860.5 P
weak similarity to B.subtilis spore outgrowth factor B
4456_at 573.6 P
ribosomal protein of the small subunit, mitochondrial
4457_at 1669.9 P
weak similarity to C.elegans hypothetical protein CEW09D10
4458_at 2203.8 P
hypothetical protein
4459_at 638.6 P
Ire1p is a transmembrane protein that has both serine-threonine kinase and endoribonuclease activities
4460_i_at -56.7 A
Ire1p is a transmembrane protein that has both serine-threonine kinase and endoribonuclease activities
4461_r_at -2.8 A
Ire1p is a transmembrane protein that has both serine-threonine kinase and endoribonuclease activities
4462_at 1476.1 P
similarity to hypothetical protein YDR326c, YFL042c and YLR072w
4463_at 896.5 P
weak similarity to human C1D protein
4464_at 3558.8 P
Ser\/Thr protein kinase
4465_at 2323.9 P
hypothetical protein
4466_at 2614.1 P
Transcription factor
4467_at 1892.9 P
weak similarity to fruit fly brahma transcriptional activator
4468_at 2319.3 P
putative RNA binding protein, involved in meiosis-specific splicing of the REC107 transcripts in cooperation with the Mer1 protein
4423_at 494.8 P
hypothetical protein
4424_at 2579.7 P
similarity to hypothetical protein YNL075w
4425_at 10461.5 P
small nucleolar RNP proteins

4426_at	1660.4	P	NuBbiN
4427_at	2171.8	P	Arginyl-tRNA synthetase
4428_at	280.8	P	High-affinity glucose transporter
4429_at	569.5	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	8809.7	P	High-affinity hexose (glucose) transporter
4431_at	173.2	A	hypothetical protein
4432_at	406.7	P	hexose transporter
4433_at	2017.8	P	strong similarity to hypothetical protein YDR348c
4434_at	977.6	P	strong similarity to hypothetical protein YDR348c
4435_at	5234.9	P	binds to Sed5p and Sec23p by distinct domains
4436_at	3962.7	P	ATM\/Mec1\/TOR1+2-related
4437_at	1931.2	P	hypothetical protein
4438_at	2176.0	P	Bad in glucose or big cells
4439_at	667.0	P	Bad in glucose or big cells
4440_at	1071.5	P	Ser\/Thr protein kinase
4441_at	2048.3	P	functionally redundant and similar in structure to SBE2
4442_at	3132.7	P	Aldo-keto reductase
4443_at	197.1	P	weak similarity to Mvp1p
4444_at	1871.2	P	Thioredoxin reductase
4445_at	2350.8	P	Component of 10 nm filaments of mother-bud neck (septin)
4401_at	7557.6	P	strong similarity to hypothetical protein YDR358w
4402_at	257.2	P	hypothetical protein
4403_at	3566.4	P	p24 protein involved in membrane trafficking
4404_at	1618.0	P	moeB, thiF, UBA1
4405_at	3263.1	P	Cystathionine gamma-synthase
4406_at	3466.6	P	Vacuolar aminopeptidase
4407_at	1378.2	P	SH3 domain
4408_at	2532.6	P	

strong similarity to hypothetical protein YNL116w
4409_at 536.4 P
hypothetical protein
4410_at 1409.6 P
71-kDa component of the protein translocase of the outer membrane of mitochondria
4411_at 100.9 P
50-kDa subunit of ORC
4412_at 1604.6 P
trithorax
4413_at 1034.5 P
mutS homolog involved in mitochondrial DNA repair
4414_at 2053.5 P
weak similarity to C.elegans hypothetical protein
4415_at 1903.0 P
similarity to hypothetical C. elegans protein F45G2.a
4416_at 1911.1 P
sn-1,2-diacylglycerol ethanolamine- and cholinephosphotranferase
4417_at 3270.8 P
sn-1,2-diacylglycerol ethanolamine- and cholinephosphotranferase
4418_at 170.2 P
meiosis-specific gene, mRNA is sporulation-specific
4419_at 34.6 A
questionable ORF
4420_at 93.2 A
hypothetical protein
4421_at 2690.7 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 11791.0 P
UPRTase
4378_at 439.9 P
Centractin
4379_at 965.5 P
weak similarity to T.brucei H+-transporting ATP synthase
4380_at 1141.0 P
Highly acidic C-terminus
4381_at 5776.2 P
Carboxypeptidase
4382_at 11701.5 P
similarity to hypothetical protein YNL156c
4383_at 288.8 P
hypothetical protein
4384_at 3966.7 P
membrane-bound casein kinase I homolog
4385_at 9127.7 P
17 kDa protein
4386_at 8970.7 P
aromatic amino acid aminotransferase II
4387_at 3366.4 P
hypothetical protein
4388_at 208.9 P
sporulation-specific wall maturation protein
4389_at 57.3 A
hypothetical protein
4390_at 490.2 P
hypothetical protein

4391_at	6613.0	P	weak similarity to cytochrome-c oxidases
4392_at	10111.9	P	Ser-Thr rich protein
4393_at	5001.2	P	subunit of RNA polymerase II
4394_at	3199.4	P	dCMP deaminase
4395_at	102.7	A	questionable ORF
4396_at	1867.7	P	similarity to pheromone-response G-protein Mdg1p
4397_at	1419.2	P	Mitochondrial ribosomal protein MRPL6 (YmL6)
4398_at	3640.7	P	ribosomal protein (weak similarity)
4399_at	852.1	P	similarity to hypothetical protein YGR221c
4400_at	475.2	P	weak similarity to YDR479c
4356_at	2490.9	P	hypothetical protein
4357_at	2658.6	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	109.3	P	sporulation protein
4359_at	1214.8	P	Establishes Silent omatin
4360_at	1285.0	P	Snf1-interacting protein Sip3p
4361_at	282.0	A	weak similarity to mouse kinesin KIF3B
4362_at	264.3	P	mRNA is induced early in meiosis
4363_at	1429.0	P	protein containing kelch repeats, similar to YGR238c
4364_at	105.4	A	hypothetical protein
4365_at	12.1	A	weak similarity to hypothetical protein YGR239c
4366_at	1313.4	P	Yeast Assembly Polypeptide, member of AP180 protein family, binds Pan1p and clathrin
4367_at	9306.9	P	strong similarity to hypothetical protein YGR243w
4368_at	7596.2	P	shows similarity to glucose-6-phosphate dehydrogenase non-catalytic domains\; homologous to Sol2p and Sol1p
4369_at	1145.6	P	DNA replication helicase
4370_at	3610.4	P	RNA splicing factor
4371_at	94.8	A	Cell division cycle protein
4372_at	1016.3	P	

hypothetical protein
4373_at 722.7 P
GTP-binding protein
4374_at 3635.1 P
DEAD-box protein
4375_at 6666.4 P
putative Upf1p-interacting protein
4376_at 486.7 P
autophagy
4377_at 1241.8 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 49.4 A
hypothetical protein
4334_i_at 8449.7 P
enolase
4335_at 7465.2 P
Putative low-affinity copper transport protein
4336_at 1080.5 P
Dimethylaniline monoxygenase
4337_at 518.8 P
weak similarity to Spombe pac2 protein
4338_at 858.4 P
Zinc finger (6-Cys)
4339_at 11460.8 P
NAPDH dehydrogenase (old yellow enzyme), isoform 2
4340_at 400.0 P
hypothetical protein
4341_at 5555.8 P
similarity to mouse TEG-261 protein
4342_at 916.0 P
hypothetical protein
4343_at 13903.1 P
Phosphogluconate Dehydrogenase (Decarboxylating)
4344_at 537.7 P
Involved in the control of meiotic nuclear divisions and spore formation
4345_at 70.1 P
hypothetical protein
4346_at 3016.1 P
similarity to C.elegans hypothetical protein C10C5.6
4347_at 320.9 P
confers sensitivity to killer toxin
4348_at 4849.1 P
similarity to hypothetical C. elegans proteins F17c11.7
4349_at 34.8 A
similarity to peptidyl-tRNA hydrolases
4350_at 8852.5 P
squalene synthetase
4351_at 1405.9 P
protein of unknown function
4352_at 1823.6 P
hypothetical protein
4353_at 9858.1 P
GAL4 enhancer protein, homolog of human alpha NAC subunit of the nascent-polypeptide-associated complex
4354_at 1912.3 P

similarity to hypothetical protein YOR147w
4355_at 2339.5 P
hypothetical protein
4310_at 2327.8 P
hypothetical protein
4311_at 5081.4 P
hypothetical protein
4312_at 907.8 P
strong similarity to hypothetical protein YHR199c
4313_at 5405.8 P
strong similarity to hypothetical protein YHR198c
4314_at 9268.0 P
homolog of the mammalian S5a protein, component of 26S proteasome
4315_at 2936.0 P
Cytosolic exopolyphosphatase
4316_at 1117.2 P
similarity to S.pombe hypothetical protein SPAC17G6
4317_at 3708.9 P
similarity to alpha-mannosidases
4318_at 2269.5 P
cAMP-dependent protein kinase homolog, suppressor of cdc25ts
4319_at 2552.7 P
Protein with similarity to DNA-binding region of heat shock transcription factors
4320_at 1382.7 P
weak similarity to YPL165c
4321_at 10112.2 P
branched-chain amino acid transaminase, highly similar to mammalian ECA39, which is regulated by the oncogene myc
4322_at 1440.3 P
UDP-glucose-4-epimerase (GAL10, galE)
4323_f_at 9120.0 P
IMP dehydrogenase\; probable PUR5 gene
4324_s_at 6537.2 P
gene in Y repeat region
4325_at 2.5 A
questionable ORF
4326_at 617.8 P
questionable ORF
4327_at 88.4 A
questionable ORF
4328_at 399.0 A
questionable ORF
4329_at -252.0 A
questionable ORF
4330_at 630.6 P
questionable ORF
4331_at 66.5 A
questionable ORF
4332_at 12.8 A
questionable ORF
4286_s_at 1489.1 P
Highly acidic C-terminus
4287_s_at 813.5 P
similarity to hypothetical protein YER175c
4288_at 2096.2 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 -31.0 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 323.6 P
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 -208.8 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 443.5 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 2144.0 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 419.7 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 252.4 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 346.4 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 -7.0 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 26.8 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 362.8 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 655.9 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 -8.9 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 1345.9 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 4813.5 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 211.3 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 1113.4 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 -493.9 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
4307_f_at -35.2 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 165.3 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 55.0 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 -21.5 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 19.7 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 27.7 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 390.5 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 191.8 M
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 1694.0 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 113.2 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 65.3 P
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 1922.9 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 270.1 P
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 45.9 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 5855.8 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 379.4 A
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 2861.6 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 0.1 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 62.0 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 8.8 A
Centromere

4278_at	1146.4	P	snRNA
4279_at	1043.1	P	snRNA
4280_f_at	1786.2	P	strong similarity to members of the Srp1p/Tip1p family
4281_i_at	1646.2	P	High-affinity hexose transporter
4282_f_at	62.7	A	High-affinity hexose transporter
4283_at	107.1	P	L-serine dehydratase
4284_at	-40.5	A	serine dehydratase
4285_at	630.4	P	similarity to allantoate permease Dal5p
4237_at	1203.3	P	putative pseudogene
4238_at	1840.1	P	Nit1 nitrilase
4239_at	36.0	A	questionable ORF
4240_at	2034.1	P	hypothetical protein
4241_at	121.7	A	peroxisomal 3-oxoacyl CoA thiolase
4242_at	167.0	P	Bni1p-related protein, helps regulate reorganization of the actin cytoskeleton, potential target of Rho4p
4243_at	2299.8	P	similarity to hypothetical protein YKR100c
4244_at	3495.3	P	hypothetical protein
4245_at	501.5	P	Ubiquitin-specific protease
4246_at	2231.7	P	glycerol-3-phosphate dehydrogenase, mitochondrial
4247_at	3045.3	P	transcription factor
4248_at	3028.6	P	Resistant to Rapamycin Deletion
4249_at	1139.0	P	hypothetical protein
4250_at	986.3	P	similarity to mitochondrial aldehyde dehydrogenase Ald1p
4251_at	393.1	P	Protein required for S-phase (DNA synthesis) initiation or completion
4252_at	1170.2	P	similarity to Mlp1p and myosin heavy chains
4253_i_at	12526.9	P	Ribosomal protein L40A
4254_at	3787.0	P	histidine kinase osmosensor that regulates an osmosensing MAP kinase cascade and is similar to bacterial two-component regulators
4255_at	273.8	P	ExtraCellular Mutant
4256_at	2254.3	P	

similarity to E.coli pantothenate synthetase
4257_at 125.8 P
Dmc1p interacting protein
4258_at 1291.2 P
DNA helicase homolog\; homolog of human XPBC, ERCC3
4259_at 8736.9 P
molecular chaperone
4260_at 829.6 P
questionable ORF
4215_g_at 1614.5 P
questionable ORF
4216_at 982.4 P
localizes to the plasma membrane
4217_at 298.6 P
subunit of DNA polymerase-zeta (Pol-zeta), an enzyme whose sole function appears to be translesion synthesis
4218_at 1797.6 P
Tropomyosin isoform 2
4219_at 1731.9 P
similarity to M.musculus aminopeptidase
4220_at -62.2 M
45-kDa mitochondrial outer membrane protein
4221_at 1201.5 P
similarity to Ymk1p
4222_at 725.5 P
mitochondrial inner membrane carrier protein for FAD
4223_at 10650.5 P
Ribosomal protein L16A (L21A) (rp22) (YL15)
4224_at 597.5 P
hypothetical protein
4225_at 2070.7 P
similarity to Drosophila fork head protein
4226_at 1341.3 P
similarity to Put3p and to hypothetical protein YJL206c
4227_at 5607.3 P
similarity to hypothetical human protein
4228_at 1239.4 P
Involved in nucleotide excision repair and regulation of TFIIH
4229_at 1860.6 P
weak similarity to Smy2p
4230_at 4113.4 P
helicase related protein, snf2 homolog
4231_at 6536.5 P
alpha-ketoglutarate dehydrogenase
4232_at 5765.0 P
similarity to C.perfringens nanH protein
4233_at 10171.3 P
involved in cell cycle regulation and aging
4234_at 414.8 P
hypothetical protein
4235_at 745.2 P
similarity to antibiotic resistance proteins
4236_at 1083.4 P
similarity to antibiotic resistance proteins
4192_at 424.9 P
inhibitor of ras

4193_at 2613.9 P
ras homolog--GTP binding protein
4194_at 2742.0 P
hydrophobic transmembrane domain
4195_at 4891.6 P
histidinol-phosphate aminotransferase
4196_at 3603.1 P
159-kDa nucleoporin with coiled-coil domain and repeated motifs typical of nucleoporins
4197_at 2649.0 P
voltage dependent anion channel (YVDAC2)
4198_at 481.2 P
strong similarity to dual-specificity phosphatase Msg5p
4199_at 400.5 A
similarity to ankyrin and coiled-coil proteins
4200_at 101.6 A
Cytochrome-c oxidase chain Vb
4201_at 1402.8 P
weak similarity to hypothetical C.elegans protein
4202_at 5660.8 P
The Sec23p-Sec24p complex is one of three cytoplamic COPII factors involved in ER to Golgi transport
4203_at 2544.2 P
similarity to hypothetical S. pombe protein
4204_at 357.3 P
6-Phosphofructose-2-kinase
4205_at 709.6 P
weak similarity to probable transcription factor Ask10p
4206_at 842.0 P
similarity to hypothetical S. pombe protein
4207_at 3441.1 P
weak similarity to Dph2 protein
4208_at -73.1 A
strong similarity to YIL014c-a
4209_at 116.7 P
DNA-binding transcriptional repressor
4210_at 6.9 A
similarity to mouse Gcap1 protein and fruit fly Bkm-like sex-determining region hypothetical protein CS314
4211_at 818.2 P
intracellular glucoamylase
4212_g_at -28.5 A
intracellular glucoamylase
4213_at 884.9 P
Formation of Mitochondrial Cytochromes 1
4214_at 494.6 P
hypothetical protein
4170_at 2917.8 P
hypothetical protein
4171_at 119.0 P
probable serine\/threonine-protein kinase
4172_at 9644.3 P
Homo-isocitrate dehydrogenase
4173_at 278.6 P
weak similarity to S.pombe hypothetical protein SPBC16A3
4174_at 529.8 P
hypothetical protein
4175_at 2074.8 P

weak similarity to spt5p
4176_at 3003.9 P
similarity to hypothetical S. pombe protein
4177_at 979.8 P
similarity to hypothetical protein YLR036c
4178_at 3873.1 P
weak similarity to A.thaliana aminoacid permease AAP4
4179_at 3005.6 P
hypothetical protein
4180_at 101.3 M
hypothetical protein
4181_at 1292.1 P
Putative mannosyltransferase of the KRE2 family
4182_at 238.4 P
Functions are similar to those of SIN3 and RPD3
4183_at 3790.3 P
hypothetical protein
4184_s_at 2971.7 P
Ty3-2 orf C fragment
4185_at 1282.7 P
strong similarity to hypothetical protein YDL175c
4186_at 9656.2 P
Threonyl-tRNA synthetase, cytoplasmic
4187_at 735.7 P
hypothetical protein
4188_at 4815.1 P
epsilon-COP coatomer subunit Sec28p
4189_at 7571.7 P
RPN2p is a component of the 26S proteosome
4190_at 3732.8 P
strong similarity to E.coli phosphoglycerate dehydrogenase
4191_at 79.4 A
weak similarity to mouse polycystic kidney disease-related protein
4147_at -346.1 A
Meiosis-specific protein involved in homologous chromosome synapsis and chiasmata formation
4148_at 196.2 P
hypothetical protein
4149_at 5262.5 P
mitochondrial acidic matrix protein
4150_at 2496.2 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 2221.3 P
hypothetical protein
4152_at 2572.8 P
similarity to C.elegans hypothetical protein
4153_at 1254.4 P
weak similarity to fowlpox virus major core protein
4154_at 1433.6 P
nuclear protein, interacts with Gsp1p and Crm1p
4155_at 9323.2 P
Arp Complex Subunit
4156_at 191.0 P
U1snRNP 70K protein homolog
4157_at 201.1 M
questionable ORF

4158_at 536.0 P
hypothetical protein
4159_at 325.4 A
hypothetical protein
4160_at 285.0 A
strong similarity to YER067w
4161_at 6197.7 P
similarity to YER064c
4162_at 411.9 P
hypothetical protein
4163_at 252.9 P
weak similarity to fruit fly NADH dehydrogenase
4164_at 8001.0 P
DL-glycerol-3-phosphatase
4165_i_at 14971.7 P
Ribosomal protein L34B
4166_at 10285.7 P
Maintenance of Mitochondrial DNA 1
4167_at 1796.2 P
PHO85 cyclin
4168_at 4277.8 P
Protein required for filamentous growth, cell polarity, and cellular elongation
4169_at 3479.3 P
ATPase that leads to neomycin-resistant protein when overexpressed
4124_at 7588.4 P
plasma membrane protein
4125_at 1147.9 P
Met30p contains five copies of WD40 motif and interacts with and regulates Met4p
4126_at 221.6 P
Protein with 30\%% identity to protein corresponding to YER054
4127_at 1635.6 P
weak similarity to zinc finger protein Gcs1p
4128_at 8867.4 P
cytochrome b reductase
4129_at 1219.1 P
similarity to rat branched-chain alpha-ketoacid dehydrogenase kinase
4130_at 8979.7 P
similarity to S.pombe hypothetical protein
4131_at 2717.1 P
weak similarity to T.brucei NADH dehydrogenase
4132_at 6958.8 P
hypothetical protein
4133_at 1601.0 P
General negative regulator of transcription\; may inhibit RNA polymerase II transcription machinery
4134_at 167.0 A
hypothetical protein
4135_at 1330.0 P
weak similarity to human cAMP responce element-binding protein
4136_at 2702.0 P
alpha subunit of casein kinase II
4137_at 2946.9 P
beta subunit of capping protein
4138_at 6898.7 P
regulatory subunit of cAMP-dependent protein kinase
4139_at 567.3 A
hypothetical protein

4140_at	789.6	P	Suppressor of Mif Two
4141_at	4032.9	P	integral nuclear membrane protein
4142_at	91.1	P	strong similarity to hypothetical protein YPR071w
4143_at	328.1	P	putative pseudogene
4144_at	6783.7	P	hypothetical protein
4145_at	447.5	P	Irregular
4146_at	-1.4	A	weak similarity to E.gracilis RNA polymerase subunit
4101_at	536.9	P	hypothetical protein
4102_at	4036.2	P	similarity to mouse MHC H-2K/t-w5-linked ORF precursor
4103_at	4526.4	P	48.8 kDa protein involved in mitochondrial protein import
4104_at	2840.4	P	45 kDa subunit of RNA polymerase II
4105_at	1333.1	P	phosphoribosyl-5-amino-1-phosphoribosyl-4-imidazolecarboxiamide isomerase
4106_at	799.8	P	weak similarity to S.pombe hypothetical protein SPAC3F10
4107_at	513.2	P	hypothetical protein
4108_at	1436.7	P	18.3 kD integral membrane protein
4109_at	57.3	A	encodes a-cell barrier activity on alpha factor
4110_at	-44.1	A	strong similarity to hypothetical protein YIL102c
4111_at	1514.9	P	similarity to Mnn1p
4112_at	481.5	P	Putative member of the ABC family of membrane transporters
4113_at	198.3	A	hypothetical protein
4114_at	4538.8	P	strong similarity to members of the Srp1p/Tip1p family
4115_at	5319.4	P	Derepression Of Telomeric silencing
4116_at	1944.6	P	181aa protein - 20.5 kD
4117_at	1119.3	P	181aa protein - 20.5 kD
4118_at	2319.7	P	Acyl CoA synthase
4119_at	3655.2	P	hypothetical protein
4120_at	553.1	P	similarity to C.elegans hypothetical protein
4121_at	540.6	P	similarity to Flx1p

4122_at	3093.6	P	similarity to protein disulfide isomerases
4123_at	1411.5	P	Synaptobrevin (t-SNARE) homolog present on ER vesicles recycling from Golgi
4079_at	2285.2	P	strong similarity to Nbp35p and human nucleotide-binding protein
4080_at	1204.4	P	phosphatidylinositol 4,5-bisphosphate 5-phosphatase
4081_at	959.5	P	similarity to S.pombe hypothetical protein, weak similarity to human ankyrin
4082_at	719.3	P	similarity to D.melanogaster RNA binding protein
4083_at	1199.5	P	weak similarity to ATP-dependent RNA helicases
4084_at	2886.6	P	weak similarity to mammalian neurofilament triplet H proteins
4085_at	1981.2	P	DnaJ-like protein required for Peroxisome biogenesis\; Djp1p is located in the cytosol
4086_at	526.2	P	similarity to RNA-binding proteins
4087_at	9663.8	P	polyA-specific ribonuclease
4088_at	443.4	P	hypothetical protein
4089_at	2073.6	P	p48 polypeptide of DNA primase
4090_at	832.3	P	encodes YU2B, a component of yeast U2 snRNP
4091_at	1410.4	P	hypothetical protein
4092_at	3362.4	P	restores protein transport when overexpressed and rRNA stability to a sec23 mutation
4093_at	8958.8	P	contains multiple WD repeats and interacts with Qsr1p in two hybrid
4094_at	202.8	A	strong similarity to YLR013w, similarity to YMR136w
4095_at	873.4	P	hypothetical protein
4096_at	448.2	P	an integral subunit of RNase P but not RNase MRP
4097_at	1868.9	P	weak similarity to YOL036w
4098_at	796.8	P	Transcriptional activator of sulfur amino acid metabolism
4099_at	1572.3	P	bZIP protein\; transcription factor
4100_at	2117.4	P	cell surface flocculin with structure similar to serine\/threonine-rich GPI-anchored cell wall proteins
4056_at	692.2	P	hypothetical protein
4057_at	2101.2	P	mitochondrial RNA splicing
4058_at	3565.1	P	signal peptidase subunit
4059_at	1389.3	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 765.1 P
G1 Factor needed for normal G1 phase
4061_at 468.3 P
hypothetical protein
4062_at 2397.4 P
nitrogen starvation-induced protein phosphatase
4063_at 180.6 P
allantoinase
4064_at 287.0 P
allantoin permease
4065_at -54.6 A
allantoicase
4066_at 873.3 P
involved in nitrogen-catabolite metabolism
4067_at 314.2 A
Malate synthase 2
4068_at 68.6 A
ureidoglycolate hydrolase
4069_at 1075.2 P
may be involved in the remodeling chromatin structure
4070_at 5741.3 P
saccharopine dehydrogenase
4071_at 5286.9 P
similarity to human corticosteroid 11-beta-dehydrogenase
4072_at 3280.9 P
similarity to E.coli fabD
4073_at 8710.0 P
putative glutathione-peroxidase
4074_at 2138.6 P
Glutathione transferase
4075_at 357.0 P
GPI-anchored aspartic protease
4076_f_at 272.8 P
similarity to members of the Srp1p/Tip1p family
4077_at 721.0 P
weak similarity to B.licheniformi hypothetical protein P20
4078_i_at 215.4 P
putative pseudogene
4032_f_at 82.8 P
putative pseudogene
4033_f_at 7567.9 P
putative pseudogene
4034_at 76.4 A
hypothetical protein
4035_at 17.0 A
questionable ORF
4036_at 758.4 P
questionable ORF
4037_at 77.8 A
questionable ORF
4038_at 518.0 P
questionable ORF
4039_at 3.0 A
questionable ORF
4040_at 93.0 P

questionable ORF
4041_at 38.1 A
hypothetical protein
4042_at 606.8 A
questionable ORF
4043_s_at 275.6 A
invertase (sucrose hydrolyzing enzyme)
4044_s_at 1832.9 P
Mps One Binder
4045_s_at 228.8 A
Ribonucleotide reductase (ribonucleoside-diphosphate reductase) large subunit
4046_at -7.5 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 195.9 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 -64.9 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 445.9 A
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 864.7 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 132.6 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 -58.1 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 3445.3 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 4371.7 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 -264.5 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 8934.0 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 73.1 P
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 1671.8 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 533.0 P
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 9.1 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 1135.6 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 503.3 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 561.5 P
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 397.7 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 314.2 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 1877.2 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 2211.5 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 210.1 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 121.4 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 211.6 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 406.6 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 844.2 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 808.4 P
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 978.5 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 390.9 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 1634.3 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 1637.1 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 1446.3 P
snRNA
3983_at 50.4 A
cytochrome-c oxidase subunit II
3984_r_at 17.0 A

questionable ORF Found forward in NC_001224 between 74495 and 74804 with 99.677419% identity.
3985_i_at 85.9 P
questionable ORF Found forward in NC_001224 between 74495 and 74804 with 99.677419% identity.
3986_f_at 145.4 P
questionable ORF Found forward in NC_001224 between 74495 and 74804 with 99.677419% identity.
3987_at 6.9 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 108.6 A
cytochrome-c oxidase chain III
3989_at -5.6 A
strong similarity to maturase-related hypothetical protein RF2
3990_i_at 24.3 A
similarity to hypothetical protein Sgc2p Found forward in NC_001224 between 75041 and 75472 with 64.392324% identity.
3991_r_at -85.8 A
similarity to hypothetical protein Sgc2p Found forward in NC_001224 between 75041 and 75472 with 64.392324% identity.
3992_f_at -98.3 A
similarity to hypothetical protein Sgc2p Found forward in NC_001224 between 75041 and 75472 with 64.392324% identity.
3993_at -15.7 A
strong similarity to Yeast (S.uvarum) mitochondria RF2 gene and maturase-related hypothetical protein RF2
3994_at 613.6 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 51.8 A
RF2 protein Found forward in NC_001224 between 8526 and 8736 with 84.489796% identity.
3996_s_at 1661.9 P
cytochrome-c oxidase subunit I Found forward in NC_001224 between 13818 and 13988 with 100% identity.
3997_at 3003.7 P
questionable ORF Found reverse in NC_001224 between 13748 and 14122 with 100% identity.
3998_at 450.0 P
COX1 intron 1 protein Found forward in NC_001224 between 13818 and 16322 with 99.92016% identity.
3999_at 705.9 P
COX1 intron 2 protein Found forward in NC_001224 between 16473 and 18830 with 99.872774% identity.
4000_at 697.5 P
COX1 intron 3 protein Found forward in NC_001224 between 18992 and 19996 with 98.308458% identity.
4001_at 6849.7 P
cytochrome-c oxidase subunit I Found forward in NC_001224 between 20508 and 20984 with 99.790356% identity.
4002_at 103.5 P
DNA endonuclease I-SceII Found forward in NC_001224 between 20985 and 21935 with 99.684543% identity.
4003_s_at 1520.5 P
cytochrome-c oxidase subunit I Found forward in NC_001224 between 21995 and 22246 with 97.222222% identity.
4004_at 940.7 P
probable mRNA maturase aI5-alpha Found forward in NC_001224 between 21995 and 23167 with 99.40324% identity.
4005_at 10002.5 P
cytochrome-c oxidase subunit I Found forward in NC_001224 between 23612 and 23746 with 100%

identity.

4006_at 63.5 P

COX1 intron protein aI5-beta Found forward in NC_001224 between 24120 and 25151 with 96.317829% identity.

4007_at 944.8 P

cytochrome-c oxidase subunit I Found forward in NC_001224 between 26228 and 26530 with 99.339934% identity.

4008_at 301.1 P

cytochrome-c oxidase subunit I Found forward in NC_001224 between 26627 and 26701 with 100% identity.

3956_i_at 1553.3 P

F1F0-ATPase complex, F0 subunit 8 Found forward in NC_001224 between 27666 and 27812 with 99.319728% identity.

3957_r_at 840.8 P

F1F0-ATPase complex, F0 subunit 8 Found forward in NC_001224 between 27666 and 27812 with 99.319728% identity.

3958_r_at 167.4 A

similarity to mouse Gcap1 Found forward in NC_001224 between 28122 and 28444 with 88.588589% identity.

3959_at 422.6 P

F1F0-ATPase complex, FO A subunit Found forward in NC_001224 between 28487 and 29266 with 97.564103% identity.

3960_at -32.4 A

endonuclease SCEI, small subunit Found forward in NC_001224 between 46046 and 46361 with 69.393939% identity.

3961_i_at -18.6 A

endonuclease SCEI, small subunit Found forward in NC_001224 between 8238 and 8509 with 72.463768% identity.

3962_f_at 539.2 P

endonuclease SCEI, small subunit Found forward in NC_001224 between 8238 and 8509 with 72.463768% identity.

3963_at 11.9 A

endonuclease SCEI, small subunit Found forward in NC_001224 between 11057 and 11551 with 65.530303% identity.

3964_at -19.2 A

endonuclease SCEI, small subunit Found forward in NC_001224 between 77067 and 77606 with 61.663653% identity.

3965_i_at -219.1 A

ORF5 Found forward in NC_001224 between 30874 and 31014 with 100% identity.

3966_i_at -69.5 A

similarity to T.brucei mitochondrion protein SGC6 Found reverse in NC_001224 between 34032 and 34430 with 88.279302% identity.

3967_r_at -38.5 A

similarity to T.brucei mitochondrion protein SGC6 Found reverse in NC_001224 between 34032 and 34430 with 88.279302% identity.

3968_s_at 626.7 P

ubiquinol--cytochrome-c reductase subunit (cytochrome B) Found forward in NC_001224 between 36540 and 36954 with 100% identity.

3969_at 20.1 A

mRNA maturase bI2 Found forward in NC_001224 between 37723 and 38579 with 99.883314% identity.

3970_s_at 567.6 P

ubiquinol--cytochrome-c reductase subunit (cytochrome B) Found forward in NC_001224 between 39141 and 39217 with 100% identity.

3971_at -35.0 A

mRNA maturase bI3 Found forward in NC_001224 between 39141 and 40265 with 98.577778% identity.

3972_s_at 686.8 P

ubiquinol--cytochrome-c reductase subunit (cytochrome B) Found forward in NC_001224 between 40841 and 41093 with 100% identity.
3973_at 105.7 P
mRNA maturase bI4 Found forward in NC_001224 between 40815 and 42251 with 99.860821% identity.
3974_at 346.2 P
ubiquinol--cytochrome-c reductase subunit (cytochrome B) Found forward in NC_001224 between 42508 and 42561 with 100% identity.
3975_at 1068.1 P
ubiquinol--cytochrome-c reductase subunit (cytochrome B) Found forward in NC_001224 between 43297 and 43647 with 100% identity.
3976_at 11878.6 P
F1F0-ATPase complex, F0 subunit 9 Found forward in NC_001224 between 46723 and 46953 with 100% identity.
3977_i_at 102.6 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 -52.4 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 207.2 A
mitochondrial ribosomal protein Found forward in NC_001224 between 48901 and 50097 with 98.436214% identity.
3980_r_at -6.7 A
mitochondrial ribosomal protein Found forward in NC_001224 between 48901 and 50097 with 98.436214% identity.
3981_at 352.6 P
probable mRNA maturase in 21S rRNA intron Found forward in NC_001224 between 61193 and 61729 with 100% identity.
3982_at -75.5 A
kanamycin resistance casette
3932_at -61.4 A
MAL-activator 23 (MAL23) gene
3933_s_at 1059.8 P
Required for the catabolism of melibiose and regulated by several GAL genes
3934_at 2361.1 P
Protein that confers resistance to molasses
3935_at -120.9 A
Tropomyosin-related protein with transmembrane domain and basic C-terminal
3936_at 469.3 P
invertase (sucrose hydrolyzing enzyme)
3937_g_at 1971.3 P
invertase (sucrose hydrolyzing enzyme)
3938_at 2141.8 P
Protein involved in targeting of plasma membrane [H+]ATPase
3939_at 541.8 P
Probable aldehyde dehydrogenase (EC 1.2.1.-)
3940_at 418.0 P
Degradation in the Endoplasmic Reticulum
3941_at 878.6 P
Ser\/Thr protein kinase
3942_at 7382.3 P
bZIP (basic-leucine zipper) protein
3943_i_at 12225.0 P
bZIP (basic-leucine zipper) protein
3944_f_at 5305.2 P
bZIP (basic-leucine zipper) protein

3945_at 1181.2 P
Protein essential for mitochondrial biogenesis and cell viability
3946_at 1818.7 P
Protein essential for mitochondrial biogenesis and cell viability
3947_at 7823.9 P
strong similarity to holacid-halidohydrolase
3948_s_at 1250.1 P
probable serine\/threonine-specific protein kinase (EC 2.7.1.-)
3949_i_at 3033.4 P
protein of unknown function
3950_at 1494.7 P
Rho family GTPase
3951_at 3023.5 P 2
micron plasmid recombinase
3952_at 6569.9 P 2
micron plasmid rep1 protein
3953_at 8027.7 P 2
micron plasmid D protein
3954_at 7371.3 P 2
micron plasmid rep2 protein
3955_at 458.4 P 2
micron plasmid recombinase
3907_f_at 1640.4 P
strong similarity to subtelomeric encoded proteins
3908_i_at 22.5 A
Ty1 LTR
3909_f_at 15.1 A
Ty1 LTR
3910_at 158.4 P
Ty1 LTR
3911_at -1.9 A
Ty1 LTR
3912_f_at 9252.2 P
Ty1 LTR
3913_s_at 5861.0 A
Full length Ty1
3914_s_at 15144.5 P
Full length Ty1
3915_s_at 11569.1 P
Full length Ty1
3916_s_at 13299.6 P
Full length Ty1
3917_f_at 9234.8 P
Full length Ty1
3918_f_at 12283.3 P
Full length Ty1
3919_f_at 11034.2 P
Saccharomyces cerevisiae chromosome I, complete chromosome sequence. Found reverse in NC_001133 between 160593 and 164183 with 100% identity.
3920_f_at 12527.9 P
Saccharomyces cerevisiae chromosome I, complete chromosome sequence. Found reverse in NC_001133 between 160593 and 164183 with 100% identity.
3921_s_at 12480.0 P
Saccharomyces cerevisiae chromosome I, complete chromosome sequence. Found reverse in NC_001133 between 164540 and 165862 with 100% identity.
3922_f_at 9619.4 P

Ty1 LTR		
3923_f_at	997.3	P
tRNA-Ala		
3924_f_at	1540.7	P
tRNA-Ser		
3925_f_at	8105.8	P
Ty3 LTR Found forward in NC_001133 between 182610 and 182949 with 100% identity.		
3926_f_at	3855.8	P
Ty1 LTR		
3927_f_at	4534.7	P
Ty2 LTR		
3928_f_at	73.0	P
Ty1 LTR		
3929_s_at	495.1	P
tRNA-Thr		
3930_i_at	74.3	P
Ty1 LTR		
3931_f_at	747.7	P
Ty1 LTR		
3884_f_at	1089.6	P
tRNA-Glu		
3885_f_at	2612.1	P
tRNA-Ala		
3886_f_at	131.6	P
Ty3 LTR		
3887_f_at	1406.9	P
Ty4 LTR		
3888_s_at	97.8	P
Saccharomyces cerevisiae chromosome X, complete chromosome sequence. Found forward in NC_001142 between 197614 and 198699 with 100% identity.		
3889_s_at	535.4	P
Saccharomyces cerevisiae chromosome X, complete chromosome sequence. Found forward in NC_001142 between 197614 and 198699 with 100% identity.		
3890_s_at	35.8	A
Saccharomyces cerevisiae chromosome X, complete chromosome sequence. Found forward in NC_001142 between 197614 and 198858 with 100% identity.		
3891_s_at	27.8	A
Saccharomyces cerevisiae chromosome X, complete chromosome sequence. Found forward in NC_001142 between 198701 and 203026 with 100% identity.		
3892_s_at	177.7	A
Saccharomyces cerevisiae chromosome X, complete chromosome sequence. Found forward in NC_001142 between 198701 and 203026 with 100% identity.		
3893_s_at	-93.9	A
Saccharomyces cerevisiae chromosome X, complete chromosome sequence. Found forward in NC_001142 between 198701 and 203026 with 100% identity.		
3894_s_at	-17.3	A
Saccharomyces cerevisiae chromosome X, complete chromosome sequence. Found forward in NC_001142 between 198701 and 203026 with 100% identity.		
3895_s_at	427.7	P
Saccharomyces cerevisiae chromosome X, complete chromosome sequence. Found forward in NC_001142 between 198701 and 203026 with 100% identity.		
3896_s_at	-61.5	A
Full length Ty4		
3897_s_at	-1.1	A
Full length Ty4		
3898_s_at	-32.1	A

Full length Ty4	3899_s_at	123.5	P
Full length Ty4	3900_f_at	2391.0	P
Full length Ty4	3901_f_at	1537.1	P
Ty4 LTR	3902_f_at	4103.0	P
Ty1 LTR	3903_i_at	18.0	A
Ty1 LTR	3904_f_at	1904.6	P
Ty1 LTR	3905_s_at	886.1	P
tRNA-Asp	3906_f_at	1659.3	P
tRNA-Arg	3859_i_at	7.7	A
Ty1 LTR	3860_f_at	7221.6	P
Ty1 LTR	3861_f_at	6565.4	P
Ty1 LTR	3862_f_at	949.5	P
tRNA-Arg	3863_f_at	1005.4	P
tRNA-Arg	3864_i_at	-66.7	A
Ty1 LTR	3865_f_at	-14.3	A
Ty1 LTR	3866_at	90.4	P
Ty1 LTR	3867_s_at	4368.8	P
tRNA-Val	3868_s_at	140.7	P
tRNA-Met	3869_f_at	-1795.7	A
tRNA-Gly	3870_s_at	1819.0	P
tRNA-Lys	3871_at	-62.2	A
Ty4 LTR	3872_i_at	110.4	P
Ty1 LTR	3873_f_at	1.7	A
Ty1 LTR	3874_i_at	-5.8	A
Ty1 LTR	3875_f_at	90.1	P
Ty1 LTR	3876_at	918.9	P
Ty4 LTR	3877_at	606.0	P
Ty1 LTR	3878_s_at	1063.5	P

tRNA-Leu
3879_f_at 8951.5 P
Ty1 LTR
3880_f_at 10143.6 P
Saccharomyces cerevisiae chromosome X, complete chromosome sequence. Found forward in NC_001142 between 473751 and 477716 with 100% identity.
3881_f_at 10770.9 P
Full length Ty1
3882_f_at 10277.0 P
Full length Ty1
3883_f_at 5666.7 P
Ty1 LTR
3835_s_at 18538.3 P
Saccharomyces cerevisiae chromosome X, complete chromosome sequence. Found forward in NC_001142 between 479334 and 483300 with 100% identity.
3836_f_at 8245.2 P
Full length Ty1
3837_f_at 10176.7 P
Ty1 LTR
3838_s_at 440.8 P
tRNA-Met
3839_at -8.3 A
Ty1 LTR
3840_f_at 1418.4 P
tRNA-Ser
3841_at 311.3 A
Ty1 LTR
3842_f_at -2049.4 A
tRNA-Gly
3843_at 262.5 P
Ty1 LTR
3844_f_at 8772.9 P
Ty1 LTR
3845_i_at -180.4 A
tRNA-Arg
3846_f_at 21.8 A
tRNA-Arg
3847_i_at -420.2 A
Ty1 LTR
3848_f_at 4513.8 P
Ty1 LTR
3849_f_at 153.0 A
Ty1 LTR
3850_at 706.6 P
Ty1 LTR
3851_s_at 8467.0 P
Protein with similarity to members of the Ybr302p\/Ycr007p\/Cos8p\/Cos9p family, coded from subtelomeric region
3852_f_at 3709.5 P
Protein with similarity to members of the Ybr302p\/Ycr007p\/Cos8p\/Cos9p family, coded from subtelomeric region
3853_f_at 496.8 P
strong similarity to subtelomeric encoded proteins
3854_f_at 121.5 P
strong similarity to Gin11p, YKL225w and other subtelomeric encoded proteins
3855_s_at -14.8 A

strong similarity to subtelomeric encoded proteins
3856_at -53.0 A
tRNA-Thr
3857_at -79.0 A
Ty1 LTR
3858_s_at 464.3 P
tRNA-Asn
3812_at 159.9 A
Ty1 LTR
3813_f_at 924.3 P
tRNA-Glu
3814_f_at 906.7 P
tRNA-Arg
3815_i_at -13.7 A
Ty1 LTR
3816_f_at 27.7 A
Ty1 LTR
3817_f_at 7933.6 P
Ty3 LTR
3818_at 23.7 A
Ty1 LTR
3819_f_at 2944.4 P
tRNA-Ala
3820_f_at 1120.7 P
Ty1 LTR
3821_f_at 1043.4 P
tRNA-His
3822_f_at 2930.0 P
Ty1 LTR
3823_f_at 2894.6 P
Ty1 LTR
3824_f_at 8994.0 P
Ty1 LTR
3825_at -33.7 A
Ty1 LTR
3826_at -43.6 A
Ty1 LTR
3827_f_at 2492.7 P
tRNA-Arg
3828_f_at 1104.3 P
Ty1 LTR
3829_f_at 10707.7 P
Ty1 LTR
3830_f_at 2912.3 P
tRNA-Ala
3831_s_at 86.1 A
strong similarity to subtelomeric encoded proteins
3832_s_at 129.0 A
strong similarity to subtelomeric encoded proteins
3833_f_at -28.8 A
Ty5 LTR
3834_s_at 10754.4 P
strong similarity to subtelomeric encoded proteins
3789_s_at 11452.4 P
strong similarity to subtelomeric encoded proteins
3790_s_at 9808.8 P

strong similarity to subtelomeric encoded proteins
3791_s_at 1552.3 P
strong similarity to subtelomeric encoded proteins
3792_s_at 9198.8 P
strong similarity to subtelomeric encoded proteins
3793_f_at 994.0 P
Ty1 LTR
3794_f_at 1367.9 P
tRNA-Ser
3795_at -65.1 A
Ty3 LTR
3796_f_at 934.1 P
tRNA-Ala
3797_f_at 8822.5 P
Ty1 LTR
3798_s_at 15805.4 P
Saccharomyces cerevisiae chromosome XII, complete chromosome sequence. Found reverse in NC_001144 between 215441 and 219403 with 100% identity.
3799_f_at 8146.3 P
Ty1 LTR
3800_at 12.0 A
Ty1 LTR
3801_f_at 647.9 A
Ty1 LTR
3802_f_at 3733.3 P
Ty3 LTR
3803_f_at 1932.3 P
tRNA-Arg
3804_f_at 5409.5 P
tRNA-Gln
3805_f_at 4535.4 P
Ty1 LTR
3806_s_at 9229.0 P
35S ribosomal RNA
3807_s_at 737.5 P
35S ribosomal RNA
3808_s_at 10673.1 P
35S ribosomal RNA
3809_s_at 9992.3 P
35S ribosomal RNA
3810_s_at 48.3 A
35S ribosomal RNA
3811_s_at -158.0 A
35S ribosomal RNA
3764_s_at 194.1 P
35S ribosomal RNA
3765_s_at 2187.1 P
25S ribosomal RNA
3766_s_at 2291.3 P
25S ribosomal RNA
3767_s_at -45.2 A
18S ribosomal RNA
3768_i_at 1237.6 A
5S ribosomal RNA
3769_s_at 712.1 P
5S ribosomal RNA

3770_i_at 1502.0 P
5S ribosomal RNA
3771_f_at 9526.4 P
Ty1 LTR
3772_f_at 9177.1 P
Full length Ty1
3773_f_at 12022.3 P
Full length Ty1
3774_f_at 10367.7 P
Saccharomyces cerevisiae chromosome XII, complete chromosome sequence. Found reverse in NC_001144 between 476334 and 480296 with 100% identity.
3775_f_at 8858.8 P
Ty1 LTR
3776_i_at -195.5 A
Ty1 LTR
3777_f_at 269.8 A
Ty1 LTR
3778_f_at 5980.6 P
Ty1 LTR
3779_f_at 10296.5 P
Saccharomyces cerevisiae chromosome XII, complete chromosome sequence. Found forward in NC_001144 between 594749 and 598706 with 100% identity.
3780_f_at 7379.0 P
Full length Ty1
3781_f_at 10584.2 P
Full length Ty1
3782_f_at 6905.9 P
Ty1 LTR
3783_at 152.8 A
Ty1 LTR
3784_at -48.9 A
Ty4 LTR
3785_f_at 8095.8 P
Ty1 LTR
3786_s_at 14046.0 P
TY1B protein Found forward in NC_001144 between 652918 and 653385 with 100% identity.
3787_f_at 9505.8 P
Saccharomyces cerevisiae chromosome XII, complete chromosome sequence. Found forward in NC_001144 between 654177 and 656387 with 100% identity.
3788_f_at 14306.3 P
Saccharomyces cerevisiae chromosome XII, complete chromosome sequence. Found forward in NC_001144 between 654177 and 656387 with 100% identity.
3740_f_at 8080.3 P
Full length Ty1
3741_f_at 9473.0 P
Full length Ty1
3742_f_at 6564.9 P
Ty1 LTR
3743_f_at 3418.6 P
tRNA-Ala
3744_i_at 3897.4 P
Ty3 LTR
3745_f_at 1866.2 P
Ty3 LTR
3746_at 576.5 P
Ty1 LTR

3747_at	-81.0	A	Ty1 LTR
3748_i_at	-23.5	A	Ty1 LTR
3749_r_at	-17.9	A	Ty1 LTR
3750_f_at	112.1	A	Ty1 LTR
3751_f_at	7373.2	P	Ty2 LTR
3752_f_at	2208.1	P	Ty1 LTR
3753_s_at	287.2	P	tRNA-Ile
3754_s_at	1302.0	P	tRNA-Ser
3755_f_at	254.3	A	Ty3 LTR
3756_i_at	31.3	A	Ty1 LTR
3757_f_at	5792.4	P	Ty1 LTR
3758_f_at	895.3	P	tRNA-Glu
3759_f_at	2939.0	P	Ty1 LTR
3760_at	682.0	M	tRNA-Arg
3761_f_at	8585.8	P	Ty2 LTR
3762_s_at	8201.7	P	Saccharomyces cerevisiae chromosome XII, complete chromosome sequence. Found forward in NC_001144 between 941478 and 942778 with 100% identity.
3763_s_at	4038.8	P	Saccharomyces cerevisiae chromosome XII, complete chromosome sequence. Found forward in NC_001144 between 941478 and 942778 with 100% identity.
3717_s_at	12342.4	P	Saccharomyces cerevisiae chromosome XII, complete chromosome sequence. Found forward in NC_001144 between 942777 and 946791 with 100% identity.
3718_s_at	15662.6	P	Saccharomyces cerevisiae chromosome XII, complete chromosome sequence. Found forward in NC_001144 between 942777 and 946791 with 100% identity.
3719_s_at	8810.5	P	Saccharomyces cerevisiae chromosome XII, complete chromosome sequence. Found forward in NC_001144 between 942777 and 946791 with 100% identity.
3720_f_at	12704.1	P	Saccharomyces cerevisiae chromosome XII, complete chromosome sequence. Found forward in NC_001144 between 942777 and 946791 with 100% identity.
3721_s_at	9667.8	P	Full length Ty2
3722_s_at	11110.1	P	Full length Ty2
3723_f_at	11914.2	P	Full length Ty2
3724_f_at	8083.9	P	Ty2 LTR

3725_at 1100.9 P
Ty1 LTR
3726_f_at 5776.6 P
Ty2 LTR
3727_f_at 5041.4 P
Full length Ty2
3728_f_at 9312.8 P
Saccharomyces cerevisiae chromosome XII, complete chromosome sequence. Found reverse in NC_001144 between 976606 and 980109 with 100% identity.
3729_f_at 4139.8 P
Ty2 LTR
3730_at 847.1 P
Ty1 LTR
3731_s_at 1597.7 P
strong similarity to subtelomeric encoded proteins
3732_s_at 393.3 P
strong similarity to subtelomeric encoded proteins
3733_s_at 2105.0 P
strong similarity to subtelomeric encoded proteins
3734_s_at 4319.7 P
strong similarity to subtelomeric encoded proteins
3735_f_at 11473.7 P
strong similarity to subtelomeric encoded proteins
3736_s_at 2677.2 P
strong similarity to subtelomeric encoded proteins
3737_s_at 2151.2 P
strong similarity to subtelomeric encoded proteins
3738_s_at 9869.9 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 9222.2 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 956.4 P
tRNA-Arg
3696_at 56.1 M
Ty1 LTR
3697_f_at 7581.2 P
Ty2 LTR
3698_f_at -2029.8 A
tRNA-Gly
3699_f_at 10783.0 P
Ty1 LTR
3700_f_at 7053.6 P
Full length Ty1
3701_f_at 10217.9 P
Ty1 LTR
3702_f_at 9398.5 P
Ty1 LTR
3703_f_at 10540.9 P
Saccharomyces cerevisiae chromosome XIII, complete chromosome sequence. Found forward in NC_001145 between 197939 and 201896 with 100% identity.
3704_f_at 9725.8 P
Full length Ty1
3705_f_at 10396.7 P
Full length Ty1

3706_f_at	8384.3	P	Ty1 LTR
3707_f_at	1433.2	P	tRNA-Ser
3708_at	39.8	A	Ty4 LTR
3709_f_at	991.2	P	tRNA-Glu
3710_f_at	2951.2	P	tRNA-Ala
3711_f_at	8482.9	P	Ty1 LTR
3712_s_at	7463.7	P	Full length Ty1
3713_s_at	8416.5	P	Full length Ty1
3714_f_at	8361.5	P	Full length Ty1
3715_f_at	8602.2	P	Ty1 LTR
3716_f_at	1121.7	P	tRNA-His
3671_f_at	8826.6	P	Ty1 LTR
3672_f_at	8719.1	P	Full length Ty1
3673_f_at	8918.0	P	Ty1 LTR
3674_i_at	621.6	A	Ty1 LTR
3675_r_at	53.6	A	Ty1 LTR
3676_f_at	193.3	P	Ty1 LTR
3677_f_at	270.0	A	Ty1 LTR
3678_at	-3.4	A	Ty1 LTR
3679_at	105.7	P	Ty1 LTR
3680_i_at	-73.1	A	Ty1 LTR
3681_s_at	34.2	A	Ty1 LTR
3682_i_at	5.9	A	Ty1 LTR
3683_f_at	35.7	A	Ty1 LTR
3684_f_at	1403.8	P	Ty4 LTR
3685_f_at	2419.6	P	Ty1 LTR
3686_f_at	128.8	A	Ty1 LTR
3687_f_at	1012.9	P	tRNA-Arg

3688_f_at 2705.9 P
tRNA-Ala
3689_f_at 6040.4 P
Ty2 LTR
3690_f_at 1654.3 A
tRNA-Gln
3691_f_at 1971.3 P
Ty4 LTR
3692_at 121.4 P
Ty1 LTR
3693_f_at 133.4 P
Ty1 LTR
3694_at 114.7 A
strong similarity to subtelomeric encoded proteins
3646_s_at 557.3 P
strong similarity to subtelomeric encoded proteins
3647_f_at 1096.4 P
strong similarity to subtelomeric encoded proteins
3648_f_at 9886.7 P
Protein with similarity to subtelomerically-encoded proteins such as Cos5p, Ybr302p, Cos3p, Cos1p, Cos4p, Cos8p, Cos6p, Cos9p
3649_f_at 64.3 A
tRNA-Gly
3650_f_at 2521.3 P
Ty4 LTR
3651_f_at 9953.3 P
Ty1 LTR
3652_f_at 8845.9 P
Full length Ty1
3653_f_at 10096.9 P
Ty1 LTR
3654_i_at 110.0 P
Ty3 LTR
3655_f_at 105.0 A
Ty3 LTR
3656_f_at 6611.6 P
Ty1 LTR
3657_f_at 8804.5 P
Saccharomyces cerevisiae chromosome XIV, complete chromosome sequence. Found forward in NC_001146 between 520758 and 524702 with 100% identity.
3658_f_at 8806.3 P
Full length Ty1
3659_f_at 7434.6 P
Full length Ty1
3660_f_at 6385.1 P
Ty1 LTR
3661_at 3104.9 P
Ty3 LTR
3662_f_at 7875.1 P
Ty3 LTR
3663_f_at 1572.8 P
Ty4 LTR
3664_f_at 7681.9 P
Ty2 LTR
3665_f_at 8909.9 P
Full length Ty2

3666_f_at 8749.6 P
Saccharomyces cerevisiae chromosome XIV, complete chromosome sequence. Found reverse in NC_001146 between 562383 and 566402 with 100% identity.
3667_f_at 7570.0 P
Ty2 LTR
3668_f_at 2470.8 P
tRNA-Pro
3669_f_at 4860.7 P
Ty1 LTR
3670_f_at 1065.1 P
Ty4 LTR
3621_i_at -41.7 A
Ty3 LTR
3622_f_at 8395.4 P
Ty3 LTR
3623_f_at 6142.3 P
Ty1 LTR
3624_at 1312.5 P
Ty1 LTR
3625_at 718.3 P
Protein with strong similarity to subtelomerically-encoded proteins such as Cos5p, Ybr302p, Cos3p, Cos1p, Cos4p, Cos8p, Cos6p, Cos9p
3626_i_at 789.0 P
Protein with strong similarity to subtelomerically-encoded proteins such as Cos5p, Ybr302p, Cos3p, Cos1p, Cos4p, Cos8p, Cos6p, Cos9p
3627_r_at 692.9 P
Protein with strong similarity to subtelomerically-encoded proteins such as Cos5p, Ybr302p, Cos3p, Cos1p, Cos4p, Cos8p, Cos6p, Cos9p
3628_f_at 68.3 A
Protein with strong similarity to subtelomerically-encoded proteins such as Cos5p, Ybr302p, Cos3p, Cos1p, Cos4p, Cos8p, Cos6p, Cos9p
3629_f_at 517.0 P
strong similarity to subtelomeric encoded proteins
3630_at -61.4 A
Ty1 LTR
3631_s_at 1188.5 P
Ty4 LTR
3632_at -31.0 A
Ty1 LTR
3633_f_at 20.9 A
tRNA-Gly
3634_f_at 575.3 P
Ty1 LTR
3635_f_at 9841.6 P
Ty1 LTR
3636_f_at 10883.3 P
Saccharomyces cerevisiae chromosome XV, complete chromosome sequence. Found forward in NC_001147 between 119305 and 123267 with 100% identity.
3637_f_at 9082.5 P
Full length Ty1
3638_f_at 10121.3 P
Full length Ty1
3639_f_at 11300.5 P
Ty1 LTR
3640_f_at -1254.0 A
tRNA-Gly

3641_f_at	102.5	A	Ty3 LTR
3642_at	26.1	A	Ty1 LTR
3643_i_at	-905.9	A	Ty1 LTR
3644_f_at	1051.3	A	Ty1 LTR
3645_f_at	-1917.3	A	tRNA-Gly
3597_at	27.6	A	Ty1 LTR
3598_f_at	2353.0	P	tRNA-Arg
3599_at	-57.3	A	Ty1 LTR
3600_i_at	-179.6	A	Ty3 LTR
3601_f_at	151.2	A	Ty3 LTR
3602_at	257.2	A	Ty1 LTR
3603_at	175.2	P	Ty1 LTR
3604_f_at	32.3	A	tRNA-Gly
3605_f_at	7.3	P	Ty1 LTR
3606_f_at	8312.4	P	Ty1 LTR
3607_f_at	6443.5	P	Full length Ty1
3608_f_at	8875.4	P	Ty1 LTR
3609_i_at	33.6	A	Ty1 LTR
3610_f_at	75.2	A	Ty1 LTR
3611_f_at	165.0	A	Ty1 LTR
3612_f_at	7811.3	P	Ty2 LTR
3613_i_at	225.9	P	Ty1 LTR
3614_f_at	88.8	A	Ty1 LTR
3615_i_at	-6.6	A	Ty1 LTR
3616_f_at	145.7	P	Ty1 LTR
3617_f_at	1793.6	P	Ty4 LTR
3618_f_at	6644.9	P	Ty2 LTR
3619_f_at	9480.4	P	Full length Ty2

3620_f_at	11329.7	P	Saccharomyces cerevisiae chromosome XV, complete chromosome sequence. Found reverse in NC_001147 between 704417 and 708436 with 100% identity.
3572_f_at	6142.8	P	Ty2 LTR
3573_f_at	1577.4	P	Ty4 LTR
3574_f_at	941.6	P	tRNA-Ala
3575_f_at	5688.6	P	Ty3 LTR
3576_f_at	1331.7	A	Ty3 LTR
3577_at	118.4	P	Ty1 LTR
3578_f_at	5575.2	P	Ty2 LTR
3579_f_at	10960.4	P	Saccharomyces cerevisiae chromosome XV, complete chromosome sequence. Found forward in NC_001147 between 971863 and 975882 with 100% identity.
3580_f_at	10512.7	P	Full length Ty2
3581_f_at	5628.7	P	Ty2 LTR
3582_f_at	6946.8	P	Ty1 LTR
3583_i_at	500.1	P	Ty1 LTR
3584_f_at	60.1	P	Ty1 LTR
3585_f_at	-43.5	A	Ty3 LTR
3586_f_at	7563.8	P	Ty1 LTR
3587_f_at	9762.4	P	Saccharomyces cerevisiae chromosome XVI, complete chromosome sequence. Found forward in NC_001148 between 58054 and 62016 with 100% identity.
3588_f_at	9513.6	P	Full length Ty1
3589_f_at	11157.1	P	Full length Ty1
3590_f_at	8845.5	P	Ty1 LTR
3591_f_at	4985.0	P	Ty2 LTR
3592_i_at	-889.6	A	Ty1 LTR
3593_f_at	1841.8	P	Ty1 LTR
3594_f_at	1004.7	P	tRNA-Glu
3595_at	15.7	A	Ty1 LTR
3596_f_at	5463.9	P	Ty2 LTR
3548_s_at	860.9	P	

			tRNA-Cys
3549_f_at	28.1	A	Ty1 LTR
3550_i_at	-69.1	A	Ty1 LTR
3551_f_at	1076.7	P	Ty1 LTR
3552_f_at	4.9	A	Ty1 LTR
3553_f_at	1541.4	P	Ty4 LTR
3554_f_at	2282.4	P	Full length Ty4
3555_s_at	356.8	P	Saccharomyces cerevisiae chromosome XVI, complete chromosome sequence. Found reverse in NC_001148 between 437328 and 439490 with 100% identity.
3556_s_at	344.7	A	Saccharomyces cerevisiae chromosome XVI, complete chromosome sequence. Found reverse in NC_001148 between 437328 and 439490 with 100% identity.
3557_s_at	14.9	A	Saccharomyces cerevisiae chromosome XVI, complete chromosome sequence. Found reverse in NC_001148 between 439423 and 442737 with 100% identity.
3558_f_at	1486.2	P	Ty4 LTR
3559_f_at	10362.8	P	Ty1 LTR
3560_at	175.5	P	Ty1 LTR
3561_f_at	-692.1	A	tRNA-Gly
3562_f_at	857.4	P	tRNA-Ser
3563_s_at	302.2	P	tRNA-Thr
3564_f_at	9602.3	P	Ty3 LTR
3565_at	332.9	P	Ty1 LTR
3566_i_at	74.4	A	Ty1 LTR
3567_r_at	-4.3	A	Ty1 LTR
3568_f_at	1359.1	P	Ty1 LTR
3569_at	423.4	A	Ty1 LTR
3570_f_at	820.6	P	Ty1 LTR
3571_f_at	6319.5	P	Ty1 LTR
3524_f_at	6453.6	P	Full length Ty1
3525_f_at	10322.3	P	Full length Ty1
3526_f_at	10098.2	P	Saccharomyces cerevisiae chromosome XVI, complete chromosome sequence. Found reverse in

NC_001148 between 804996 and 808958 with 100% identity.		
3527_f_at	6422.2	P
Ty1 LTR		
3528_f_at	8857.9	P
Ty1 LTR		
3529_f_at	10202.2	P
Full length Ty3		
3530_f_at	8944.5	P
Ty1 LTR		
3531_at	131.0	P
Ty1 LTR		
3532_f_at	11881.9	P
Ty1 LTR		
3533_f_at	10064.6	P
Full length Ty1		
3534_f_at	9868.4	P
Ty1 LTR		
3535_i_at	17.9	M
Ty3 LTR		
3536_f_at	6549.8	P
Ty3 LTR		
3537_f_at	3143.6	P
tRNA-Ala		
3538_f_at	-1878.5	A
tRNA-Gly		
3539_f_at	2719.2	P
Ty3 LTR		
3540_at	63.8	A
Ty4 LTR		
3541_at	407.1	A
Ty4 LTR		
3542_f_at	9428.0	P
strong similarity to subtelomeric encoded proteins		
3543_s_at	12377.1	P
strong similarity to subtelomeric encoded proteins		
3544_at	89.6	A
strong similarity to subtelomeric encoded proteins		
3545_i_at	27.5	A
Ty1 LTR		
3546_f_at	9.3	A
Ty1 LTR		
3547_f_at	4069.8	P
Ty2 LTR		
3500_f_at	-66.6	A
Ty1 LTR		
3501_f_at	5027.8	P
Ty2 LTR		
3502_f_at	10558.5	P
Saccharomyces cerevisiae chromosome II, complete chromosome sequence. Found forward in NC_001134 between 31221 and 35240 with 100% identity.		
3503_f_at	5010.8	P
Full length Ty2		
3504_f_at	3850.6	P
Ty2 LTR		
3505_s_at	1061.9	A
Ty1 LTR		

3506_s_at	1854.1	P
Ty4 LTR		
3507_at	35.8	A
Ty1 LTR		
3508_f_at	-1898.8	A
tRNA-Gly		
3509_f_at	5080.2	P
Ty3 LTR		
3510_s_at	708.1	P
Ty1 LTR		
3511_f_at	8543.7	P
Ty1 LTR		
3512_f_at	9023.2	P
Full length Ty1		
3513_f_at	8507.8	P
Ty1 LTR		
3514_f_at	1391.4	P
tRNA-Ser		
3515_at	560.5	P
Ty1 LTR		
3516_f_at	7833.3	P
Ty1 LTR		
3517_f_at	6761.1	P
Full length Ty1		
3518_f_at	7230.1	P
Ty1 LTR		
3519_f_at	7.9	A
Ty1 LTR		
3520_s_at	495.1	P
tRNA-Val		
3521_i_at	-4.7	A
Ty1 LTR		
3522_f_at	1928.0	P
Ty1 LTR		
3523_at	248.8	A
Ty1 LTR		
3477_at	41.9	A
Ty1 LTR		
3478_f_at	7352.7	P
tRNA-Gln		
3479_f_at	984.6	P
tRNA-Arg		
3480_at	-5.5	A
Ty1 LTR		
3481_at	273.0	A
Ty1 LTR		
3482_f_at	970.7	P
tRNA-Glu		
3483_f_at	8692.7	P
Protein with similarity to members of the Cos3\/Cos5\/Cos1\/Cos4\/Cos8\/Cos6\/Cos9 family, coded from subtelomeric region		
3484_f_at	14.5	A
Ty5 LTR		
3485_at	-340.8	A
Full length Ty5		
3486_at	60.3	A

Full length Ty5
3487_g_at 157.7 A
Full length Ty5
3488_at 39.4 A
Full length Ty5
3489_f_at 17.7 A
Full length Ty5
3490_f_at 1.3 A
Ty5 LTR
3491_f_at 957.4 P
tRNA-Glu
3492_f_at 1701.8 P
Ty1 LTR
3493_f_at 3582.2 P
Ty1 LTR
3494_f_at 6142.4 P
Ty1 LTR
3495_f_at 1339.0 P
Ty1 LTR
3496_f_at 7739.6 P
Ty2 LTR
3497_f_at 10395.2 P
Saccharomyces cerevisiae chromosome III, complete chromosome sequence. Found forward in NC_001135 between 86005 and 90030 with 100% identity.
3498_f_at 12072.1 P
Full length Ty2
3499_f_at 7575.6 P
Ty2 LTR
3451_f_at 2232.0 P
tRNA-Pro
3452_f_at 7167.5 P
Ty1 LTR
3453_at 240.0 P
strong similarity to subtelomeric encoded proteins
3454_s_at 602.8 P
tRNA-Asn
3455_f_at -1785.6 A
tRNA-Gly
3456_i_at 76.2 P
Ty1 LTR
3457_f_at 4469.1 P
Ty1 LTR
3458_f_at 541.1 P
Ty1 LTR
3459_at 110.1 A
Ty1 LTR
3460_at 32.2 A
Ty4 LTR
3461_f_at 7832.4 P
Ty1 LTR
3462_f_at 6010.4 P
tRNA-Gln
3463_at 155.2 P
Ty1 LTR
3464_at 587.5 P
Ty1 LTR

3465_at	43.2	A	Ty5 LTR
3466_i_at	54.8	A	Ty1 LTR
3467_f_at	3899.1	P	Ty1 LTR
3468_i_at	-42.2	A	Ty1 LTR
3469_f_at	53.8	A	Ty1 LTR
3470_i_at	1857.0	P	Protein with strong similarity to other subtelomerically-encoded proteins such as Cos5p, Ybr302p, Cos3p, Cos1p, Cos4p, Cos8p, Cos6p, Cos9p
3471_f_at	3766.0	P	Protein with strong similarity to other subtelomerically-encoded proteins such as Cos5p, Ybr302p, Cos3p, Cos1p, Cos4p, Cos8p, Cos6p, Cos9p
3472_f_at	-1797.3	A	tRNA-Gly
3473_f_at	2670.5	P	tRNA-Ala
3474_f_at	1587.2	P	Ty1 LTR
3475_f_at	1676.1	P	Ty4 LTR
3476_f_at	1313.4	P	tRNA-Ser
3427_at	143.7	A	Ty1 LTR
3428_f_at	3403.1	P	Ty1 LTR
3429_f_at	7472.9	P	Ty2 LTR
3430_f_at	12234.6	P	Full length Ty2
3431_f_at	10970.1	P	Saccharomyces cerevisiae chromosome IV, complete chromosome sequence. Found reverse in NC_001136 between 514037 and 518056 with 100% identity.
3432_f_at	6229.7	P	Ty2 LTR
3433_i_at	20.9	A	Ty1 LTR
3434_f_at	301.4	P	Ty1 LTR
3435_f_at	2449.6	P	Ty1 LTR
3436_f_at	5270.6	P	tRNA-Gln
3437_f_at	933.2	P	tRNA-Arg
3438_f_at	1824.7	P	tRNA-Arg
3439_f_at	5446.9	P	tRNA-Gln
3440_f_at	6534.0	P	Ty1 LTR
3441_f_at	8219.0	P	

Full length Ty1
3442_f_at 10205.9 P
Full length Ty1
3443_f_at 11957.3 P
Saccharomyces cerevisiae chromosome IV, complete chromosome sequence. Found reverse in NC_001136 between 645851 and 649813 with 100% identity.
3444_f_at 7225.9 P
Ty1 LTR
3445_f_at 1847.0 P
Ty3 LTR
3446_i_at -119.8 A
Ty1 LTR
3447_f_at 544.7 A
Ty1 LTR
3448_s_at 2922.2 P
Ty3 LTR
3449_i_at 216.9 P
Ty1 LTR
3450_r_at 13.5 A
Ty1 LTR
3404_f_at 1930.7 P
Ty1 LTR
3405_f_at 6376.8 P
tRNA-Gln
3406_f_at 8815.5 P
Ty1 LTR
3407_at 352.6 P
Saccharomyces cerevisiae chromosome IV, complete chromosome sequence. Found forward in NC_001136 between 804494 and 805681 with 100% identity.
3408_f_at 5605.8 P
Ty1 LTR
3409_f_at 14135.7 P
Saccharomyces cerevisiae chromosome IV, complete chromosome sequence. Found forward in NC_001136 between 873398 and 877417 with 100% identity.
3410_f_at 5190.8 P
Full length Ty2
3411_f_at 4975.7 P
Ty1 LTR
3412_f_at 8347.7 P
Full length Ty1
3413_f_at 10416.8 P
Full length Ty1
3414_f_at 10616.1 P
Saccharomyces cerevisiae chromosome IV, complete chromosome sequence. Found reverse in NC_001136 between 878651 and 882613 with 100% identity.
3415_i_at 46.7 A
Ty1 LTR
3416_s_at 4496.2 P
Ty1 LTR
3417_f_at 6010.9 P
Ty3 LTR
3418_f_at 1419.0 P
tRNA-Ser
3419_f_at 4825.9 P
Ty1 LTR
3420_f_at 12160.8 P

Saccharomyces cerevisiae chromosome IV, complete chromosome sequence. Found forward in NC_001136 between 982747 and 986766 with 100% identity.

3421_f_at 8736.6 P
Full length Ty2
3422_f_at 7458.8 P
Ty1 LTR
3423_f_at 6782.6 P
Ty1 LTR
3424_f_at 7674.8 P
Full length Ty1
3425_f_at 8196.5 P
Full length Ty1
3426_f_at 7867.3 P

Saccharomyces cerevisiae chromosome IV, complete chromosome sequence. Found reverse in NC_001136 between 987525 and 991034 with 100% identity.

3379_f_at 6092.2 P
Ty1 LTR
3380_i_at 120.9 P
Ty3 LTR
3381_f_at 24.8 P
Ty3 LTR
3382_f_at -1656.3 A
tRNA-Gly
3383_f_at 519.3 P
tRNA-Glu
3384_f_at 5411.2 P
Ty3 LTR
3385_s_at 3631.4 P
tRNA-Val
3386_f_at 9473.7 P
Ty1 LTR
3387_f_at 6908.5 P
Full length Ty1
3388_f_at 9954.9 P
Ty1 LTR
3389_f_at 2999.3 P
Ty1 LTR
3390_at 70.6 A
Ty3 LTR
3391_f_at 4373.5 P
Ty1 LTR
3392_f_at 9795.7 P
Ty1 LTR
3393_f_at 13548.5 P

Saccharomyces cerevisiae chromosome IV, complete chromosome sequence. Found forward in NC_001136 between 1208292 and 1212254 with 100% identity.

3394_f_at 7686.6 P
Full length Ty1
3395_f_at 10096.4 P
Full length Ty1
3396_f_at 7050.0 P
Ty1 LTR
3397_f_at 216.9 A
tRNA-Gly
3398_f_at 567.3 A
tRNA-Ser

3399_f_at 5178.6 P
Ty1 LTR
3400_i_at 75.7 P
Ty1 LTR
3401_f_at -8.3 A
Ty1 LTR
3402_at 14.2 A
Ty1 LTR
3403_f_at 1214.5 P
strong similarity to subtelomeric encoded proteins
3356_f_at 848.5 P
strong similarity to subtelomeric encoded proteins
3357_at 200.6 A
strong similarity to subtelomeric encoded proteins
3358_f_at -1848.9 A
tRNA-Gly
3359_f_at 7350.1 P
Ty1 LTR
3360_at -20.0 A
Ty1 LTR
3361_f_at 1275.9 P
tRNA-Ser
3362_at -87.6 A
Ty1 LTR
3363_at -44.5 A
Ty4 LTR
3364_f_at 5695.6 P
tRNA-Gln
3365_f_at 7233.1 P
Ty1 LTR
3366_at 11.4 A
Ty1 LTR
3367_f_at 1286.6 P
Ty1 LTR
3368_f_at 929.5 P
tRNA-Arg
3369_i_at 11.9 A
Ty1 LTR
3370_f_at 438.0 P
Ty1 LTR
3371_f_at 938.1 P
tRNA-Glu
3372_f_at 1122.8 P
tRNA-His
3373_at 492.8 P
Ty1 LTR
3374_at 352.4 P
Ty1 LTR
3375_f_at 6814.4 P
Ty3 LTR
3376_f_at 6086.2 P
tRNA-Gln
3377_at 84.5 A
Ty1 LTR
3378_f_at 849.1 P
tRNA-Ser

3332_i_at	21.3	A	Ty1 LTR
3333_f_at	4300.5	P	Ty1 LTR
3334_at	77.4	A	Ty1 LTR
3335_at	83.9	A	Ty1 LTR
3336_f_at	1599.0	P	Ty4 LTR
3337_i_at	506.2	P	Ty3 LTR
3338_f_at	16.1	A	Ty3 LTR
3340_f_at	7512.5	P	Ty1 LTR
3342_f_at	7178.4	P	Ty3 LTR
3343_i_at	1465.6	P	Ty1 LTR
3344_f_at	1922.7	P	Ty1 LTR
3345_f_at	2378.5	P	Ty1 LTR
3346_at	365.6	A	Ty4 LTR
3347_s_at	2609.3	P	Ty1 LTR
3348_f_at	5964.8	P	Ty1 LTR
3350_f_at	10078.7	P	Full length Ty1
3352_s_at	10204.3	P	Ty1 LTR
3354_s_at	554.9	P	Ty1 LTR
3355_s_at	905.6	P	Ty1 LTR
3307_s_at	252.0	A	Ty1 LTR
3308_s_at	823.4	P	Ty1 LTR
3309_s_at	169.6	P	Ty1 LTR
3310_s_at	522.1	P	Ty1 LTR
3311_f_at	6598.9	P	Ty1 LTR
3313_f_at	3884.4	P	Ty1 LTR
3315_f_at	11712.8	P	Ty3 LTR
3316_f_at	12881.8	P	Ty3 LTR
3317_f_at	12481.3	P	Ty1 LTR

3319_f_at	12667.6	P	Ty1 LTR
3320_i_at	-50.5	A	Ty1 LTR
3321_f_at	148.7	A	Ty1 LTR
3322_at	-17.3	A	Ty1 LTR
3323_i_at	-258.0	A	Ty5 LTR
3324_at	319.1	P	Ty5 LTR
3325_f_at	1727.4	P	strong similarity to subtelomeric encoded proteins
3326_at	289.5	P	strong similarity to subtelomeric encoded proteins
3327_f_at	9876.2	P	Protein with strong similarity to subtelomerically-encoded proteins such as Cos5p, Ybr302p, Cos3p, Cos1p, Cos4p, Cos8p, Cos6p, Cos9p
3328_at	62.8	A	Ty1 LTR
3329_f_at	3458.5	P	Ty1 LTR
3330_f_at	7211.2	P	Ty2 LTR
3283_f_at	11305.2	P	Saccharomyces cerevisiae chromosome VI, complete chromosome sequence. Found forward in NC_001138 between 139492 and 143511 with 100% identity.
3284_f_at	9423.7	P	Full length Ty2
3285_f_at	6213.1	P	Ty2 LTR
3286_f_at	1964.8	P	Ty1 LTR
3287_s_at	238.3	P	Ty4 LTR
3288_at	61.2	A	Ty1 LTR
3289_i_at	83.9	A	Ty1 LTR
3290_f_at	208.4	A	Ty1 LTR
3291_f_at	2838.8	P	Ty1 LTR
3294_at	23.2	A	Ty1 LTR
3296_at	-21.6	A	Ty1 LTR
3297_i_at	-48.7	A	Ty5 LTR
3298_f_at	-68.5	A	Ty5 LTR
3299_f_at	3.1	A	strong similarity to subtelomeric encoded proteins
3301_f_at	1415.1	P	Ty4 LTR

3302_f_at	5325.7	P	Ty1 LTR
3303_f_at	561.0	P	Ty1 LTR
3304_f_at	495.5	A	Ty1 LTR
3305_at	-60.8	A	Ty4 LTR
3306_i_at	931.9	P	Ty1 LTR
3258_f_at	835.6	P	Ty1 LTR
3259_at	3886.7	P	Ty1 LTR
3260_f_at	7660.5	P	Ty3 LTR
3262_at	15.3	A	Ty4 LTR
3263_i_at	2973.2	P	Ty1 LTR
3264_f_at	258.0	P	Ty1 LTR
3267_f_at	2177.1	P	Ty3 LTR
3268_f_at	9545.8	P	Ty1 LTR
3269_f_at	1404.2	P	Ty1 LTR
3270_f_at	6883.7	P	Ty1 LTR
3271_i_at	30.1	A	Ty3 LTR
3272_f_at	3761.0	P	Ty3 LTR
3274_at	119.9	A	Ty1 LTR
3276_i_at	-14.1	A	Ty1 LTR
3277_f_at	108.5	A	Ty1 LTR
3279_f_at	6787.2	P	Full length Ty1
3235_f_at	5504.0	P	Ty1 LTR
3236_f_at	7699.4	P	Full length Ty1
3237_f_at	10588.9	P	Full length Ty1
3239_f_at	8391.0	P	Ty1 LTR
3240_f_at	6887.5	P	Ty2 LTR
3241_f_at	7364.7	P	Full length Ty2
3243_at	457.5	P	tRNA-Leu

3244_i_at	66.1	P	Ty1 LTR
3245_f_at	366.0	P	Ty1 LTR
3247_s_at	497.9	P	TY3B protein Found forward in NC_001139 between 707604 and 708461 with 100% identity.
3248_s_at	1784.0	P	Saccharomyces cerevisiae chromosome VII, complete chromosome sequence. Found forward in NC_001139 between 708460 and 712248 with 100% identity.
3249_s_at	4697.8	P	Saccharomyces cerevisiae chromosome VII, complete chromosome sequence. Found forward in NC_001139 between 708460 and 712248 with 100% identity.
3250_s_at	2175.0	P	Saccharomyces cerevisiae chromosome VII, complete chromosome sequence. Found forward in NC_001139 between 708460 and 712248 with 100% identity.
3251_s_at	276.0	P	Full length Ty3
3252_s_at	3539.3	P	Full length Ty3
3253_f_at	9182.0	P	Full length Ty3
3255_at	892.1	P	Ty1 LTR
3256_at	36.1	A	Ty1 LTR
3257_f_at	7024.7	P	Ty3 LTR
3212_f_at	1184.3	P	Ty1 LTR
3214_at	311.2	P	Ty1 LTR
3215_f_at	312.2	P	Ty1 LTR
3216_at	14.8	A	Ty1 LTR
3218_at	31.7	A	Ty1 LTR
3222_f_at	9092.0	P	Full length Ty2
3223_f_at	6464.7	P	Ty2 LTR
3225_f_at	8106.1	P	Full length Ty1
3226_f_at	8773.2	P	Ty1 LTR
3228_at	165.7	P	Ty3 LTR
3230_f_at	4520.8	P	Ty1 LTR
3232_f_at	2175.3	P	Ty4 LTR
3233_f_at	10282.1	P	Ty1 LTR
3234_at	6526.0	P	Protein with strong similarity to other subtelomerically-encoded proteins such as Cos5p, Ybr302p, Cos3p, Cos1p, Cos4p, Cos8p, Cos6p, Cos9p

3187_s_at 5905.4 P
strong similarity to subtelomeric encoded proteins
3188_at 814.0 A
Protein with similarity to subtelomerically-encoded proteins such as Cos5p, Ybr302p, Cos3p, Cos1p, Cos4p, Cos8p, Cos6p, Cos9p
3189_i_at -294.9 A
Protein with similarity to subtelomerically-encoded proteins such as Cos5p, Ybr302p, Cos3p, Cos1p, Cos4p, Cos8p, Cos6p, Cos9p
3190_f_at 251.3 P
Protein with similarity to subtelomerically-encoded proteins such as Cos5p, Ybr302p, Cos3p, Cos1p, Cos4p, Cos8p, Cos6p, Cos9p
3191_i_at 30.7 A
Ty5 LTR
3192_f_at 8.3 A
Ty5 LTR
3193_at 1308.1 A
strong similarity to subtelomeric encoded proteins
3195_f_at 8732.5 P
Ty3 LTR
3196_f_at 1540.7 P
Ty4 LTR
3199_f_at 6186.8 P
Ty1 LTR
3200_i_at 123.6 P
Ty1 LTR
3201_r_at 11.8 A
Ty1 LTR
3202_f_at -1.0 A
Ty1 LTR
3203_f_at 9610.3 P
Ty1 LTR
3204_at 677.5 P
Ty1 LTR
3206_at 0.8 A
Ty1 LTR
3207_i_at 323.5 P
Ty1 LTR
3208_f_at 161.0 P
Ty1 LTR
3209_f_at 7252.7 P
Ty1 LTR
3161_f_at 5082.9 P
Ty3 LTR
3162_at 1107.1 P
Ty4 LTR
3163_i_at 33.4 P
Ty1 LTR
3164_f_at 36.7 A
Ty1 LTR
3165_at 3.9 A
Ty4 LTR
3166_i_at 52.0 A
Ty1 LTR
3167_r_at 17.2 A
Ty1 LTR
3168_f_at 38.1 A

Ty1 LTR
3169_f_at 8574.3 P
Ty2 LTR
3170_i_at 24.7 A
Ty1 LTR
3171_r_at -2.2 A
Ty1 LTR
3172_f_at 172.6 P
Ty1 LTR
3173_i_at 8.3 A
Ty1 LTR
3174_f_at 93.3 A
Ty1 LTR
3175_i_at 323.8 P
Ty1 LTR
3176_f_at 967.0 P
Ty1 LTR
3177_f_at 311.0 P
Ty3 LTR
3178_f_at 56.8 A
Ty1 LTR
3180_f_at 9331.5 P
Full length Ty1
3181_f_at 10081.7 P
Ty1 LTR
3182_i_at 165.3 A
strong similarity to subtelomeric encoded YDR544c
3183_f_at 10417.1 P
strong similarity to subtelomeric encoded proteins
3184_s_at 374.5 P
strong similarity to subtelomeric encoded proteins
3185_s_at 189.4 A
strong similarity to subtelomeric encoded proteins
3133_f_at 2981.2 P
Ty1 LTR
3136_s_at 4525.8 P
Saccharomyces cerevisiae chromosome IX, complete chromosome sequence. Found forward in NC_001141 between 206488 and 210129 with 100% identity.
3137_s_at 1677.1 P
Full length Ty3
3139_f_at 197.3 P
Ty2 LTR
3141_i_at 54.8 P
Ty1 LTR
3142_f_at 3397.7 P
Ty1 LTR
3143_f_at 949.9 P
Ty3 LTR
3144_f_at 1171.6 P
Ty1 LTR
3145_at 409.6 P
Ty1 LTR
3147_at -8.6 M
Ty1 LTR
3148_s_at 3815.9 P
mating hormone a2

3149_at 1307.6 P
Saccharomyces cerevisiae chromosome I, complete chromosome sequence. Found forward in NC_001133 between 13744 and 14743 with 100% identity.

3150_at 1798.3 P
Saccharomyces cerevisiae chromosome I, complete chromosome sequence. Found forward in NC_001133 between 14744 and 15743 with 100% identity.
3151_g_at 773.6 P
Saccharomyces cerevisiae chromosome I, complete chromosome sequence. Found forward in NC_001133 between 14744 and 15743 with 100% identity.
3152_at 2561.0 P
Saccharomyces cerevisiae chromosome I, complete chromosome sequence. Found forward in NC_001133 between 15744 and 16743 with 100% identity.
3153_at 192.9 P
Saccharomyces cerevisiae chromosome I, complete chromosome sequence. Found forward in NC_001133 between 16744 and 17743 with 100% identity.
3154_at 487.0 P
Saccharomyces cerevisiae chromosome I, complete chromosome sequence. Found forward in NC_001133 between 17744 and 18743 with 100% identity.
3155_at -460.5 A
Saccharomyces cerevisiae chromosome I, complete chromosome sequence. Found forward in NC_001133 between 18744 and 19729 with 100% identity.
3156_at 123.8 P
Saccharomyces cerevisiae chromosome I, complete chromosome sequence. Found forward in NC_001133 between 88357 and 89356 with 100% identity.
3157_at 266.0 P
Saccharomyces cerevisiae chromosome I, complete chromosome sequence. Found forward in NC_001133 between 89357 and 90356 with 100% identity.
3158_at 282.5 P
Saccharomyces cerevisiae chromosome I, complete chromosome sequence. Found forward in NC_001133 between 90357 and 91356 with 100% identity.
3159_at 374.4 A
Saccharomyces cerevisiae chromosome I, complete chromosome sequence. Found forward in NC_001133 between 91357 and 92356 with 100% identity.
3088_at 88.2 A
Saccharomyces cerevisiae chromosome I, complete chromosome sequence. Found forward in NC_001133 between 92357 and 93356 with 100% identity.
3089_g_at 533.9 A
Saccharomyces cerevisiae chromosome I, complete chromosome sequence. Found forward in NC_001133 between 92357 and 93356 with 100% identity.
3090_s_at 20.0 A
Saccharomyces cerevisiae chromosome I, complete chromosome sequence. Found forward in NC_001133 between 93357 and 93988 with 100% identity.
3091_at -271.7 A
Saccharomyces cerevisiae chromosome I, complete chromosome sequence. Found forward in NC_001133 between 159789 and 160788 with 100% identity.
3092_f_at 51.4 P
Saccharomyces cerevisiae chromosome I, complete chromosome sequence. Found forward in NC_001133 between 160789 and 161788 with 100% identity.
3093_f_at -90.1 P
Saccharomyces cerevisiae chromosome I, complete chromosome sequence. Found forward in NC_001133 between 161789 and 162788 with 100% identity.
3096_f_at 131.2 P
Saccharomyces cerevisiae chromosome I, complete chromosome sequence. Found forward in NC_001133 between 164789 and 165788 with 100% identity.
3097_at 115.7 P

Saccharomyces cerevisiae chromosome I, complete chromosome sequence. Found forward in NC_001133 between 165789 and 166468 with 100% identity.
3098_at 1045.6 P
Saccharomyces cerevisiae chromosome I, complete chromosome sequence. Found forward in NC_001133 between 208649 and 209648 with 100% identity.
3099_at 334.2 P
Saccharomyces cerevisiae chromosome I, complete chromosome sequence. Found forward in NC_001133 between 209649 and 210648 with 100% identity.
3100_s_at 896.3 P
Saccharomyces cerevisiae chromosome I, complete chromosome sequence. Found forward in NC_001133 between 210649 and 211648 with 100% identity.
3101_at 317.6 P
Saccharomyces cerevisiae chromosome I, complete chromosome sequence. Found forward in NC_001133 between 211649 and 212648 with 100% identity.
3102_s_at 879.2 P
Saccharomyces cerevisiae chromosome I, complete chromosome sequence. Found forward in NC_001133 between 212649 and 213648 with 100% identity.
3103_at 258.7 P
Saccharomyces cerevisiae chromosome I, complete chromosome sequence. Found forward in NC_001133 between 213649 and 214648 with 100% identity.
3104_at 262.9 P
Saccharomyces cerevisiae chromosome I, complete chromosome sequence. Found forward in NC_001133 between 214649 and 215648 with 100% identity.
3105_g_at 455.4 A
Saccharomyces cerevisiae chromosome I, complete chromosome sequence. Found forward in NC_001133 between 214649 and 215648 with 100% identity.
3106_s_at 462.2 P
Saccharomyces cerevisiae chromosome I, complete chromosome sequence. Found forward in NC_001133 between 215649 and 216648 with 100% identity.
3107_s_at 3662.9 P
Saccharomyces cerevisiae chromosome I, complete chromosome sequence. Found forward in NC_001133 between 216649 and 217143 with 100% identity.
3108_at 155.8 P
Saccharomyces cerevisiae chromosome X, complete chromosome sequence. Found forward in NC_001142 between 9138 and 10137 with 100% identity.
3109_at -372.7 P
Saccharomyces cerevisiae chromosome X, complete chromosome sequence. Found forward in NC_001142 between 10138 and 11137 with 100% identity.
3110_s_at -244.7 A
Saccharomyces cerevisiae chromosome X, complete chromosome sequence. Found forward in NC_001142 between 11138 and 12137 with 100% identity.
3111_s_at 223.8 P
Saccharomyces cerevisiae chromosome X, complete chromosome sequence. Found forward in NC_001142 between 12138 and 13137 with 100% identity.
3112_s_at 74.5 P
Saccharomyces cerevisiae chromosome X, complete chromosome sequence. Found forward in NC_001142 between 13138 and 14137 with 100% identity.
3113_s_at 1575.0 P
Saccharomyces cerevisiae chromosome X, complete chromosome sequence. Found forward in NC_001142 between 14138 and 15137 with 100% identity.
3114_s_at 2302.4 P
Saccharomyces cerevisiae chromosome X, complete chromosome sequence. Found forward in NC_001142 between 15138 and 15624 with 100% identity.
3115_at -153.9 P
Saccharomyces cerevisiae chromosome X, complete chromosome sequence. Found forward in NC_001142 between 41889 and 42888 with 100% identity.

3116_at 1474.9 A
Saccharomyces cerevisiae chromosome X, complete chromosome sequence. Found forward in NC_001142 between 42889 and 43888 with 100% identity.
3117_at -227.9 P
Saccharomyces cerevisiae chromosome X, complete chromosome sequence. Found forward in NC_001142 between 43889 and 44888 with 100% identity.
3118_at -2118.7 P
Saccharomyces cerevisiae chromosome X, complete chromosome sequence. Found forward in NC_001142 between 44889 and 45888 with 100% identity.
3119_at -329.3 A
Saccharomyces cerevisiae chromosome X, complete chromosome sequence. Found forward in NC_001142 between 45889 and 46888 with 100% identity.
3120_at 303.3 P
Saccharomyces cerevisiae chromosome X, complete chromosome sequence. Found forward in NC_001142 between 46889 and 47659 with 100% identity.
3121_at 1452.2 A
Saccharomyces cerevisiae chromosome X, complete chromosome sequence. Found forward in NC_001142 between 165921 and 166920 with 100% identity.
3122_at 928.5 P
Saccharomyces cerevisiae chromosome X, complete chromosome sequence. Found forward in NC_001142 between 166921 and 167920 with 100% identity.
3123_at -573.7 P
Saccharomyces cerevisiae chromosome X, complete chromosome sequence. Found forward in NC_001142 between 167921 and 168920 with 100% identity.
3124_at 707.7 P
Saccharomyces cerevisiae chromosome X, complete chromosome sequence. Found forward in NC_001142 between 168921 and 169920 with 100% identity.
3125_at 1506.4 P
Saccharomyces cerevisiae chromosome X, complete chromosome sequence. Found forward in NC_001142 between 169921 and 170920 with 100% identity.
3126_at 168.4 P
Saccharomyces cerevisiae chromosome X, complete chromosome sequence. Found forward in NC_001142 between 170921 and 171920 with 100% identity.
3127_at 356.9 A
Saccharomyces cerevisiae chromosome X, complete chromosome sequence. Found forward in NC_001142 between 171921 and 172694 with 100% identity.
3128_at 445.4 P
Saccharomyces cerevisiae chromosome X, complete chromosome sequence. Found forward in NC_001142 between 196825 and 197824 with 100% identity.
3129_at -453.6 A
Saccharomyces cerevisiae chromosome X, complete chromosome sequence. Found forward in NC_001142 between 203825 and 204824 with 100% identity.
3130_at 56.0 P
Saccharomyces cerevisiae chromosome X, complete chromosome sequence. Found forward in NC_001142 between 204825 and 205824 with 100% identity.
3131_g_at 773.8 P
Saccharomyces cerevisiae chromosome X, complete chromosome sequence. Found forward in NC_001142 between 204825 and 205824 with 100% identity.
3045_s_at 862.6 P
Saccharomyces cerevisiae chromosome X, complete chromosome sequence. Found forward in NC_001142 between 205825 and 206646 with 100% identity.
3046_at -66.7 A
Saccharomyces cerevisiae chromosome X, complete chromosome sequence. Found forward in NC_001142 between 212197 and 213196 with 100% identity.
3047_at 621.6 P
Saccharomyces cerevisiae chromosome X, complete chromosome sequence. Found forward in

NC_001142 between 213197 and 214196 with 100% identity.
3048_at 697.7 A
Saccharomyces cerevisiae chromosome X, complete chromosome sequence. Found forward in NC_001142 between 214197 and 215196 with 100% identity.
3049_at 25.5 A
Saccharomyces cerevisiae chromosome X, complete chromosome sequence. Found forward in NC_001142 between 215197 and 216196 with 100% identity.
3050_at 433.5 P
Saccharomyces cerevisiae chromosome X, complete chromosome sequence. Found forward in NC_001142 between 216197 and 217196 with 100% identity.
3051_at 187.0 P
Saccharomyces cerevisiae chromosome X, complete chromosome sequence. Found forward in NC_001142 between 217197 and 217402 with 100% identity.
3052_at -96.3 A
Saccharomyces cerevisiae chromosome X, complete chromosome sequence. Found forward in NC_001142 between 254933 and 255932 with 100% identity.
3053_at -1437.6 A
Saccharomyces cerevisiae chromosome X, complete chromosome sequence. Found forward in NC_001142 between 255933 and 256932 with 100% identity.
3054_at -441.9 A
Saccharomyces cerevisiae chromosome X, complete chromosome sequence. Found forward in NC_001142 between 256933 and 257932 with 100% identity.
3055_g_at 469.7 P
Saccharomyces cerevisiae chromosome X, complete chromosome sequence. Found forward in NC_001142 between 256933 and 257932 with 100% identity.
3056_s_at 314.7 A
Saccharomyces cerevisiae chromosome X, complete chromosome sequence. Found forward in NC_001142 between 257933 and 258932 with 100% identity.
3057_s_at 2976.3 P
Saccharomyces cerevisiae chromosome X, complete chromosome sequence. Found forward in NC_001142 between 258933 and 259932 with 100% identity.
3058_s_at 1523.0 P
Saccharomyces cerevisiae chromosome X, complete chromosome sequence. Found forward in NC_001142 between 259933 and 260143 with 100% identity.
3059_at 55.2 A
Saccharomyces cerevisiae chromosome X, complete chromosome sequence. Found forward in NC_001142 between 368944 and 369943 with 100% identity.
3060_at 1102.1 P
Saccharomyces cerevisiae chromosome X, complete chromosome sequence. Found forward in NC_001142 between 369944 and 370943 with 100% identity.
3061_at -329.9 A
Saccharomyces cerevisiae chromosome X, complete chromosome sequence. Found forward in NC_001142 between 370944 and 371943 with 100% identity.
3062_at 987.6 A
Saccharomyces cerevisiae chromosome X, complete chromosome sequence. Found forward in NC_001142 between 371944 and 372943 with 100% identity.
3063_at -213.2 A
Saccharomyces cerevisiae chromosome X, complete chromosome sequence. Found forward in NC_001142 between 372944 and 373943 with 100% identity.
3064_at 2383.3 A
Saccharomyces cerevisiae chromosome X, complete chromosome sequence. Found forward in NC_001142 between 373944 and 374811 with 100% identity.
3065_g_at 629.2 A
Saccharomyces cerevisiae chromosome X, complete chromosome sequence. Found forward in NC_001142 between 373944 and 374811 with 100% identity.
3066_at -8.6 M

Saccharomyces cerevisiae chromosome X, complete chromosome sequence. Found forward in NC_001142 between 424301 and 425300 with 100% identity.
3067_g_at 17.7 M
Saccharomyces cerevisiae chromosome X, complete chromosome sequence. Found forward in NC_001142 between 424301 and 425300 with 100% identity.
3068_s_at 923.4 P
Saccharomyces cerevisiae chromosome X, complete chromosome sequence. Found forward in NC_001142 between 425301 and 426300 with 100% identity.
3069_s_at -291.2 A
Saccharomyces cerevisiae chromosome X, complete chromosome sequence. Found forward in NC_001142 between 426301 and 427300 with 100% identity.
3070_s_at -882.3 P
Saccharomyces cerevisiae chromosome X, complete chromosome sequence. Found forward in NC_001142 between 427301 and 428300 with 100% identity.
3071_s_at 1972.6 P
Saccharomyces cerevisiae chromosome X, complete chromosome sequence. Found forward in NC_001142 between 428301 and 429300 with 100% identity.
3072_s_at 4326.3 P
Saccharomyces cerevisiae chromosome X, complete chromosome sequence. Found forward in NC_001142 between 429301 and 430300 with 100% identity.
3073_s_at 171.3 P
Saccharomyces cerevisiae chromosome X, complete chromosome sequence. Found forward in NC_001142 between 430301 and 430425 with 100% identity.
3074_at -3.4 M
Saccharomyces cerevisiae chromosome X, complete chromosome sequence. Found forward in NC_001142 between 510427 and 511426 with 100% identity.
3075_at 381.0 M
Saccharomyces cerevisiae chromosome X, complete chromosome sequence. Found forward in NC_001142 between 511427 and 512426 with 100% identity.
3076_at -34.9 A
Saccharomyces cerevisiae chromosome X, complete chromosome sequence. Found forward in NC_001142 between 512427 and 513426 with 100% identity.
3077_at 261.3 A
Saccharomyces cerevisiae chromosome X, complete chromosome sequence. Found forward in NC_001142 between 513427 and 514426 with 100% identity.
3078_g_at 1037.6 P
Saccharomyces cerevisiae chromosome X, complete chromosome sequence. Found forward in NC_001142 between 513427 and 514426 with 100% identity.
3079_s_at 2303.7 P
Saccharomyces cerevisiae chromosome X, complete chromosome sequence. Found forward in NC_001142 between 514427 and 515426 with 100% identity.
3080_f_at 3052.5 P
Saccharomyces cerevisiae chromosome X, complete chromosome sequence. Found forward in NC_001142 between 515427 and 515477 with 100% identity.
3081_at 1333.2 P
Saccharomyces cerevisiae chromosome X, complete chromosome sequence. Found forward in NC_001142 between 557997 and 558996 with 100% identity.
3082_at -107.6 A
Saccharomyces cerevisiae chromosome X, complete chromosome sequence. Found forward in NC_001142 between 558997 and 559996 with 100% identity.
3083_g_at -141.4 A
Saccharomyces cerevisiae chromosome X, complete chromosome sequence. Found forward in NC_001142 between 558997 and 559996 with 100% identity.
3084_s_at 352.1 A
Saccharomyces cerevisiae chromosome X, complete chromosome sequence. Found forward in NC_001142 between 559997 and 560996 with 100% identity.

3085_s_at 771.7 P
Saccharomyces cerevisiae chromosome X, complete chromosome sequence. Found forward in NC_001142 between 560997 and 561996 with 100% identity.
3086_s_at 438.4 P
Saccharomyces cerevisiae chromosome X, complete chromosome sequence. Found forward in NC_001142 between 561997 and 562996 with 100% identity.
3087_s_at -58.1 A
Saccharomyces cerevisiae chromosome X, complete chromosome sequence. Found forward in NC_001142 between 562997 and 563996 with 100% identity.
3003_s_at 2108.1 P
Saccharomyces cerevisiae chromosome X, complete chromosome sequence. Found forward in NC_001142 between 563997 and 564996 with 100% identity.
3004_s_at 2647.8 P
Saccharomyces cerevisiae chromosome X, complete chromosome sequence. Found forward in NC_001142 between 564997 and 565996 with 100% identity.
3005_at 416.3 A
Saccharomyces cerevisiae chromosome X, complete chromosome sequence. Found forward in NC_001142 between 595249 and 596248 with 100% identity.
3006_at 306.0 P
Saccharomyces cerevisiae chromosome X, complete chromosome sequence. Found forward in NC_001142 between 596249 and 597248 with 100% identity.
3007_at 390.1 M
Saccharomyces cerevisiae chromosome X, complete chromosome sequence. Found forward in NC_001142 between 597249 and 598248 with 100% identity.
3008_at 383.6 P
Saccharomyces cerevisiae chromosome X, complete chromosome sequence. Found forward in NC_001142 between 598249 and 599248 with 100% identity.
3009_g_at 1166.6 P
Saccharomyces cerevisiae chromosome X, complete chromosome sequence. Found forward in NC_001142 between 598249 and 599248 with 100% identity.
3010_s_at -61.4 A
Saccharomyces cerevisiae chromosome X, complete chromosome sequence. Found forward in NC_001142 between 599249 and 600248 with 100% identity.
3011_s_at 789.8 P
Saccharomyces cerevisiae chromosome X, complete chromosome sequence. Found forward in NC_001142 between 600249 and 601248 with 100% identity.
3012_s_at 1260.3 P
Saccharomyces cerevisiae chromosome X, complete chromosome sequence. Found forward in NC_001142 between 601249 and 602248 with 100% identity.
3013_at 225.4 A
Saccharomyces cerevisiae chromosome X, complete chromosome sequence. Found forward in NC_001142 between 629774 and 630773 with 100% identity.
3014_at 96.1 A
Saccharomyces cerevisiae chromosome X, complete chromosome sequence. Found forward in NC_001142 between 630774 and 631773 with 100% identity.
3015_at 436.6 P
Saccharomyces cerevisiae chromosome X, complete chromosome sequence. Found forward in NC_001142 between 631774 and 632773 with 100% identity.
3016_at 184.1 A
Saccharomyces cerevisiae chromosome X, complete chromosome sequence. Found forward in NC_001142 between 632774 and 633773 with 100% identity.
3017_g_at 720.6 P
Saccharomyces cerevisiae chromosome X, complete chromosome sequence. Found forward in NC_001142 between 632774 and 633773 with 100% identity.
3018_s_at 574.3 P
Saccharomyces cerevisiae chromosome X, complete chromosome sequence. Found forward in

NC_001142 between 633774 and 634773 with 100% identity.
3019_at -608.8 A
Saccharomyces cerevisiae chromosome X, complete chromosome sequence. Found forward in NC_001142 between 690939 and 691938 with 100% identity.
3020_at 219.0 A
Saccharomyces cerevisiae chromosome X, complete chromosome sequence. Found forward in NC_001142 between 691939 and 692938 with 100% identity.
3021_at -353.1 A
Saccharomyces cerevisiae chromosome X, complete chromosome sequence. Found forward in NC_001142 between 692939 and 693938 with 100% identity.
3022_at -258.5 A
Saccharomyces cerevisiae chromosome X, complete chromosome sequence. Found forward in NC_001142 between 693939 and 694938 with 100% identity.
3023_at -119.0 A
Saccharomyces cerevisiae chromosome X, complete chromosome sequence. Found forward in NC_001142 between 694939 and 695938 with 100% identity.
3024_g_at 1692.5 P
Saccharomyces cerevisiae chromosome X, complete chromosome sequence. Found forward in NC_001142 between 694939 and 695938 with 100% identity.
3025_s_at 1118.0 P
Saccharomyces cerevisiae chromosome X, complete chromosome sequence. Found forward in NC_001142 between 695939 and 696138 with 100% identity.
3026_at -27.0 A
Saccharomyces cerevisiae chromosome X, complete chromosome sequence. Found forward in NC_001142 between 712444 and 713443 with 100% identity.
3027_at 92.1 P
Saccharomyces cerevisiae chromosome X, complete chromosome sequence. Found forward in NC_001142 between 713444 and 714443 with 100% identity.
3028_at 441.3 A
Saccharomyces cerevisiae chromosome X, complete chromosome sequence. Found forward in NC_001142 between 714444 and 715443 with 100% identity.
3029_at 57.7 P
Saccharomyces cerevisiae chromosome X, complete chromosome sequence. Found forward in NC_001142 between 715444 and 716443 with 100% identity.
3030_at -1378.0 P
Saccharomyces cerevisiae chromosome X, complete chromosome sequence. Found forward in NC_001142 between 716444 and 717443 with 100% identity.
3031_at -240.7 P
Saccharomyces cerevisiae chromosome X, complete chromosome sequence. Found forward in NC_001142 between 717444 and 718443 with 100% identity.
3032_at 340.0 P
Saccharomyces cerevisiae chromosome X, complete chromosome sequence. Found forward in NC_001142 between 718444 and 719443 with 100% identity.
3033_s_at -2990.2 A
Saccharomyces cerevisiae chromosome X, complete chromosome sequence. Found forward in NC_001142 between 719444 and 720443 with 100% identity.
3034_at -35.7 P
Saccharomyces cerevisiae chromosome XI, complete chromosome sequence. Found forward in NC_001143 between 9592 and 10591 with 100% identity.
3035_at 700.9 P
Saccharomyces cerevisiae chromosome XI, complete chromosome sequence. Found forward in NC_001143 between 10592 and 11591 with 100% identity.
3036_at 1225.7 P
Saccharomyces cerevisiae chromosome XI, complete chromosome sequence. Found forward in NC_001143 between 11592 and 12591 with 100% identity.
3037_at 89.0 A

Saccharomyces cerevisiae chromosome XI, complete chromosome sequence. Found forward in NC_001143 between 12592 and 13591 with 100% identity.
3038_at 215.6 A
Saccharomyces cerevisiae chromosome XI, complete chromosome sequence. Found forward in NC_001143 between 13592 and 14591 with 100% identity.
3039_s_at 3463.8 P
Saccharomyces cerevisiae chromosome XI, complete chromosome sequence. Found forward in NC_001143 between 14592 and 15208 with 100% identity.
3040_at 630.9 P
Saccharomyces cerevisiae chromosome XI, complete chromosome sequence. Found forward in NC_001143 between 56435 and 57434 with 100% identity.
3041_at 220.5 A
Saccharomyces cerevisiae chromosome XI, complete chromosome sequence. Found forward in NC_001143 between 57435 and 58434 with 100% identity.
3042_at -136.7 A
Saccharomyces cerevisiae chromosome XI, complete chromosome sequence. Found forward in NC_001143 between 58435 and 59434 with 100% identity.
3043_at -89.5 A
Saccharomyces cerevisiae chromosome XI, complete chromosome sequence. Found forward in NC_001143 between 59435 and 60434 with 100% identity.
3044_at 62.7 A
Saccharomyces cerevisiae chromosome XI, complete chromosome sequence. Found forward in NC_001143 between 60435 and 61434 with 100% identity.
2960_at 33.5 P
Saccharomyces cerevisiae chromosome XI, complete chromosome sequence. Found forward in NC_001143 between 61435 and 62434 with 100% identity.
2961_at 614.0 P
Saccharomyces cerevisiae chromosome XI, complete chromosome sequence. Found forward in NC_001143 between 62435 and 63434 with 100% identity.
2962_at 1124.2 P
Saccharomyces cerevisiae chromosome XI, complete chromosome sequence. Found forward in NC_001143 between 63435 and 63899 with 100% identity.
2963_at 411.1 A
Saccharomyces cerevisiae chromosome XI, complete chromosome sequence. Found forward in NC_001143 between 99643 and 100642 with 100% identity.
2964_at 13981.2 P
Saccharomyces cerevisiae chromosome XI, complete chromosome sequence. Found forward in NC_001143 between 100643 and 101642 with 100% identity.
2965_g_at 7643.8 P
Saccharomyces cerevisiae chromosome XI, complete chromosome sequence. Found forward in NC_001143 between 100643 and 101642 with 100% identity.
2966_s_at 12524.3 P
Saccharomyces cerevisiae chromosome XI, complete chromosome sequence. Found forward in NC_001143 between 101643 and 102642 with 100% identity.
2967_s_at 8039.8 P
Saccharomyces cerevisiae chromosome XI, complete chromosome sequence. Found forward in NC_001143 between 102643 and 103642 with 100% identity.
2968_s_at 9504.1 P
Saccharomyces cerevisiae chromosome XI, complete chromosome sequence. Found forward in NC_001143 between 103643 and 104642 with 100% identity.
2969_s_at 8993.1 P
Saccharomyces cerevisiae chromosome XI, complete chromosome sequence. Found forward in NC_001143 between 104643 and 105642 with 100% identity.
2970_s_at 15350.3 P
Saccharomyces cerevisiae chromosome XI, complete chromosome sequence. Found forward in NC_001143 between 105643 and 106328 with 100% identity.

2971_at -1304.0 M
Saccharomyces cerevisiae chromosome XI, complete chromosome sequence. Found forward in NC_001143 between 411757 and 412756 with 100% identity.
2972_at 370.6 P
Saccharomyces cerevisiae chromosome XI, complete chromosome sequence. Found forward in NC_001143 between 412757 and 413756 with 100% identity.
2973_at 177.6 P
Saccharomyces cerevisiae chromosome XI, complete chromosome sequence. Found forward in NC_001143 between 413757 and 414756 with 100% identity.
2974_at -834.8 A
Saccharomyces cerevisiae chromosome XI, complete chromosome sequence. Found forward in NC_001143 between 414757 and 415756 with 100% identity.
2975_at 414.7 P
Saccharomyces cerevisiae chromosome XI, complete chromosome sequence. Found forward in NC_001143 between 415757 and 416756 with 100% identity.
2976_at 74.9 P
Saccharomyces cerevisiae chromosome XI, complete chromosome sequence. Found forward in NC_001143 between 416757 and 417146 with 100% identity.
2977_at -237.0 A
Saccharomyces cerevisiae chromosome XI, complete chromosome sequence. Found forward in NC_001143 between 535784 and 536783 with 100% identity.
2978_at 273.5 P
Saccharomyces cerevisiae chromosome XI, complete chromosome sequence. Found forward in NC_001143 between 536784 and 537783 with 100% identity.
2979_at 1858.7 A
Saccharomyces cerevisiae chromosome XI, complete chromosome sequence. Found forward in NC_001143 between 537784 and 538783 with 100% identity.
2980_at 230.5 P
Saccharomyces cerevisiae chromosome XI, complete chromosome sequence. Found forward in NC_001143 between 538784 and 539783 with 100% identity.
2981_at 146.7 A
Saccharomyces cerevisiae chromosome XI, complete chromosome sequence. Found forward in NC_001143 between 539784 and 540783 with 100% identity.
2982_at 130.5 P
Saccharomyces cerevisiae chromosome XI, complete chromosome sequence. Found forward in NC_001143 between 540784 and 541783 with 100% identity.
2983_at -237.9 A
Saccharomyces cerevisiae chromosome XI, complete chromosome sequence. Found forward in NC_001143 between 541784 and 542783 with 100% identity.
2984_at 10.5 A
Saccharomyces cerevisiae chromosome XI, complete chromosome sequence. Found forward in NC_001143 between 542784 and 543783 with 100% identity.
2985_at -158.0 A
Saccharomyces cerevisiae chromosome XI, complete chromosome sequence. Found forward in NC_001143 between 543784 and 544783 with 100% identity.
2986_at 137.3 A
Saccharomyces cerevisiae chromosome XI, complete chromosome sequence. Found forward in NC_001143 between 544784 and 545783 with 100% identity.
2987_at 544.4 P
Saccharomyces cerevisiae chromosome XI, complete chromosome sequence. Found forward in NC_001143 between 545784 and 546783 with 100% identity.
2988_at -1808.8 A
Saccharomyces cerevisiae chromosome XI, complete chromosome sequence. Found forward in NC_001143 between 546784 and 547783 with 100% identity.
2989_at 235.1 P
Saccharomyces cerevisiae chromosome XI, complete chromosome sequence. Found forward in

NC_001143 between 547784 and 548228 with 100% identity.
2990_g_at 1178.8 P
Saccharomyces cerevisiae chromosome XI, complete chromosome sequence. Found forward in NC_001143 between 547784 and 548228 with 100% identity.
2991_at 477.8 P
Saccharomyces cerevisiae chromosome XI, complete chromosome sequence. Found forward in NC_001143 between 619375 and 620374 with 100% identity.
2992_g_at 397.0 P
Saccharomyces cerevisiae chromosome XI, complete chromosome sequence. Found forward in NC_001143 between 619375 and 620374 with 100% identity.
2993_s_at 496.4 P
Saccharomyces cerevisiae chromosome XI, complete chromosome sequence. Found forward in NC_001143 between 620375 and 621374 with 100% identity.
2994_s_at 542.3 P
Saccharomyces cerevisiae chromosome XI, complete chromosome sequence. Found forward in NC_001143 between 621375 and 622374 with 100% identity.
2995_s_at 848.7 P
Saccharomyces cerevisiae chromosome XI, complete chromosome sequence. Found forward in NC_001143 between 622375 and 623374 with 100% identity.
2996_s_at 1260.7 P
Saccharomyces cerevisiae chromosome XI, complete chromosome sequence. Found forward in NC_001143 between 623375 and 624374 with 100% identity.
2997_s_at 2382.9 P
Saccharomyces cerevisiae chromosome XI, complete chromosome sequence. Found forward in NC_001143 between 624375 and 624566 with 100% identity.
2998_at 516.0 P
Saccharomyces cerevisiae chromosome XI, complete chromosome sequence. Found forward in NC_001143 between 642133 and 643132 with 100% identity.
2999_at 3319.9 P
Saccharomyces cerevisiae chromosome XI, complete chromosome sequence. Found forward in NC_001143 between 643133 and 644132 with 100% identity.
3000_at 151.4 P
Saccharomyces cerevisiae chromosome XI, complete chromosome sequence. Found forward in NC_001143 between 644133 and 645132 with 100% identity.
3001_at 623.2 P
Saccharomyces cerevisiae chromosome XI, complete chromosome sequence. Found forward in NC_001143 between 645133 and 646132 with 100% identity.
3002_g_at 128.4 A
Saccharomyces cerevisiae chromosome XI, complete chromosome sequence. Found forward in NC_001143 between 645133 and 646132 with 100% identity.
2917_s_at 448.4 A
Saccharomyces cerevisiae chromosome XI, complete chromosome sequence. Found forward in NC_001143 between 646133 and 647132 with 100% identity.
2918_s_at 333.4 P
Saccharomyces cerevisiae chromosome XI, complete chromosome sequence. Found forward in NC_001143 between 647133 and 648132 with 100% identity.
2919_s_at 2066.9 P
Saccharomyces cerevisiae chromosome XI, complete chromosome sequence. Found forward in NC_001143 between 648133 and 648994 with 100% identity.
2920_at 1807.1 P
Saccharomyces cerevisiae chromosome XI, complete chromosome sequence. Found forward in NC_001143 between 649494 and 650493 with 100% identity.
2921_at 1023.6 P
Saccharomyces cerevisiae chromosome XI, complete chromosome sequence. Found forward in NC_001143 between 650494 and 651493 with 100% identity.
2922_at 809.0 P

Saccharomyces cerevisiae chromosome XI, complete chromosome sequence. Found forward in NC_001143 between 651494 and 652493 with 100% identity.
2923_at 1186.8 P
Saccharomyces cerevisiae chromosome XI, complete chromosome sequence. Found forward in NC_001143 between 652494 and 653493 with 100% identity.
2924_g_at -461.1 P
Saccharomyces cerevisiae chromosome XI, complete chromosome sequence. Found forward in NC_001143 between 652494 and 653493 with 100% identity.
2925_s_at 1047.1 P
Saccharomyces cerevisiae chromosome XI, complete chromosome sequence. Found forward in NC_001143 between 653494 and 654493 with 100% identity.
2926_s_at 414.6 P
Saccharomyces cerevisiae chromosome XI, complete chromosome sequence. Found forward in NC_001143 between 654494 and 655493 with 100% identity.
2927_s_at 450.9 P
Saccharomyces cerevisiae chromosome XI, complete chromosome sequence. Found forward in NC_001143 between 655494 and 655865 with 100% identity.
2928_at 946.6 A
Saccharomyces cerevisiae chromosome XI, complete chromosome sequence. Found forward in NC_001143 between 662918 and 663917 with 100% identity.
2929_at 424.9 M
Saccharomyces cerevisiae chromosome XI, complete chromosome sequence. Found forward in NC_001143 between 663918 and 664917 with 100% identity.
2930_at 490.0 P
Saccharomyces cerevisiae chromosome XI, complete chromosome sequence. Found forward in NC_001143 between 664918 and 665917 with 100% identity.
2931_at -30.1 A
Saccharomyces cerevisiae chromosome XI, complete chromosome sequence. Found forward in NC_001143 between 665918 and 666445 with 100% identity.
2932_at 61.7 A
Saccharomyces cerevisiae chromosome XII, complete chromosome sequence. Found forward in NC_001144 between 54710 and 55709 with 100% identity.
2933_at 578.7 P
Saccharomyces cerevisiae chromosome XII, complete chromosome sequence. Found forward in NC_001144 between 55710 and 56709 with 100% identity.
2934_at 179.8 A
Saccharomyces cerevisiae chromosome XII, complete chromosome sequence. Found forward in NC_001144 between 56710 and 57709 with 100% identity.
2935_at 2581.3 P
Saccharomyces cerevisiae chromosome XII, complete chromosome sequence. Found forward in NC_001144 between 57710 and 58709 with 100% identity.
2936_at 169.3 A
Saccharomyces cerevisiae chromosome XII, complete chromosome sequence. Found forward in NC_001144 between 58710 and 59709 with 100% identity.
2937_at -24.2 A
Saccharomyces cerevisiae chromosome XII, complete chromosome sequence. Found forward in NC_001144 between 59710 and 60709 with 100% identity.
2938_at -14.4 A
Saccharomyces cerevisiae chromosome XII, complete chromosome sequence. Found forward in NC_001144 between 60710 and 61709 with 100% identity.
2939_at -74.4 A
Saccharomyces cerevisiae chromosome XII, complete chromosome sequence. Found forward in NC_001144 between 61710 and 62709 with 100% identity.
2940_at 194.4 A
Saccharomyces cerevisiae chromosome XII, complete chromosome sequence. Found forward in NC_001144 between 62710 and 63709 with 100% identity.

2941_at -227.2 A
Saccharomyces cerevisiae chromosome XII, complete chromosome sequence. Found forward in NC_001144 between 63710 and 64061 with 100% identity.
2942_at -1053.7 A
Saccharomyces cerevisiae chromosome XII, complete chromosome sequence. Found forward in NC_001144 between 99543 and 100542 with 100% identity.
2943_at 1117.5 P
Saccharomyces cerevisiae chromosome XII, complete chromosome sequence. Found forward in NC_001144 between 100543 and 101542 with 100% identity.
2944_g_at 2371.5 P
Saccharomyces cerevisiae chromosome XII, complete chromosome sequence. Found forward in NC_001144 between 100543 and 101542 with 100% identity.
2945_s_at 760.0 P
Saccharomyces cerevisiae chromosome XII, complete chromosome sequence. Found forward in NC_001144 between 101543 and 102542 with 100% identity.
2946_s_at 1557.2 A
Saccharomyces cerevisiae chromosome XII, complete chromosome sequence. Found forward in NC_001144 between 102543 and 103542 with 100% identity.
2947_s_at 5103.3 P
Saccharomyces cerevisiae chromosome XII, complete chromosome sequence. Found forward in NC_001144 between 103543 and 104542 with 100% identity.
2948_s_at 1664.3 P
Saccharomyces cerevisiae chromosome XII, complete chromosome sequence. Found forward in NC_001144 between 104543 and 104846 with 100% identity.
2949_at 334.6 P
Saccharomyces cerevisiae chromosome XII, complete chromosome sequence. Found forward in NC_001144 between 188164 and 189163 with 100% identity.
2950_at 543.4 P
Saccharomyces cerevisiae chromosome XII, complete chromosome sequence. Found forward in NC_001144 between 189164 and 190163 with 100% identity.
2951_at 464.0 A
Saccharomyces cerevisiae chromosome XII, complete chromosome sequence. Found forward in NC_001144 between 190164 and 191163 with 100% identity.
2952_at 245.5 A
Saccharomyces cerevisiae chromosome XII, complete chromosome sequence. Found forward in NC_001144 between 191164 and 192163 with 100% identity.
2953_at 335.5 A
Saccharomyces cerevisiae chromosome XII, complete chromosome sequence. Found forward in NC_001144 between 192164 and 193163 with 100% identity.
2954_at 193.7 A
Saccharomyces cerevisiae chromosome XII, complete chromosome sequence. Found forward in NC_001144 between 193164 and 194163 with 100% identity.
2955_at -541.9 A
Saccharomyces cerevisiae chromosome XII, complete chromosome sequence. Found forward in NC_001144 between 194164 and 194675 with 100% identity.
2956_g_at 2146.6 P
Saccharomyces cerevisiae chromosome XII, complete chromosome sequence. Found forward in NC_001144 between 194164 and 194675 with 100% identity.
2957_at 1602.2 P
Saccharomyces cerevisiae chromosome XII, complete chromosome sequence. Found forward in NC_001144 between 307356 and 308355 with 100% identity.
2958_at -12.0 P
Saccharomyces cerevisiae chromosome XII, complete chromosome sequence. Found forward in NC_001144 between 308356 and 309355 with 100% identity.
2959_at 3667.4 P
Saccharomyces cerevisiae chromosome XII, complete chromosome sequence. Found forward in NC_001144 between 309356 and 310355 with 100% identity.

2875_at -1453.5 A
Saccharomyces cerevisiae chromosome XII, complete chromosome sequence. Found forward in NC_001144 between 310356 and 311355 with 100% identity.
2876_at -870.3 A
Saccharomyces cerevisiae chromosome XII, complete chromosome sequence. Found forward in NC_001144 between 311356 and 312355 with 100% identity.
2877_at -567.1 A
Saccharomyces cerevisiae chromosome XII, complete chromosome sequence. Found forward in NC_001144 between 312356 and 313355 with 100% identity.
2878_at 358.1 A
Saccharomyces cerevisiae chromosome XII, complete chromosome sequence. Found forward in NC_001144 between 313356 and 314355 with 100% identity.
2879_at 479.7 A
Saccharomyces cerevisiae chromosome XII, complete chromosome sequence. Found forward in NC_001144 between 314356 and 315355 with 100% identity.
2880_at 504.2 P
Saccharomyces cerevisiae chromosome XII, complete chromosome sequence. Found forward in NC_001144 between 315356 and 315877 with 100% identity.
2881_at 1236.4 P
Saccharomyces cerevisiae chromosome XII, complete chromosome sequence. Found forward in NC_001144 between 330178 and 331177 with 100% identity.
2882_at 1352.7 A
Saccharomyces cerevisiae chromosome XII, complete chromosome sequence. Found forward in NC_001144 between 331178 and 332177 with 100% identity.
2883_at -809.2 A
Saccharomyces cerevisiae chromosome XII, complete chromosome sequence. Found forward in NC_001144 between 332178 and 333177 with 100% identity.
2884_g_at 1451.2 P
Saccharomyces cerevisiae chromosome XII, complete chromosome sequence. Found forward in NC_001144 between 332178 and 333177 with 100% identity.
2885_s_at 1767.7 P
Saccharomyces cerevisiae chromosome XII, complete chromosome sequence. Found forward in NC_001144 between 333178 and 334177 with 100% identity.
2886_s_at 2430.3 P
Saccharomyces cerevisiae chromosome XII, complete chromosome sequence. Found forward in NC_001144 between 334178 and 335177 with 100% identity.
2887_s_at 3345.1 P
Saccharomyces cerevisiae chromosome XII, complete chromosome sequence. Found forward in NC_001144 between 335178 and 335534 with 100% identity.
2888_at 1280.9 P
Saccharomyces cerevisiae chromosome XII, complete chromosome sequence. Found forward in NC_001144 between 349507 and 350506 with 100% identity.
2889_at 781.2 P
Saccharomyces cerevisiae chromosome XII, complete chromosome sequence. Found forward in NC_001144 between 350507 and 351506 with 100% identity.
2890_at -139.5 A
Saccharomyces cerevisiae chromosome XII, complete chromosome sequence. Found forward in NC_001144 between 351507 and 352506 with 100% identity.
2891_at 406.1 P
Saccharomyces cerevisiae chromosome XII, complete chromosome sequence. Found forward in NC_001144 between 352507 and 353506 with 100% identity.
2892_at -1377.7 A
Saccharomyces cerevisiae chromosome XII, complete chromosome sequence. Found forward in NC_001144 between 353507 and 354506 with 100% identity.
2893_at -148.7 A
Saccharomyces cerevisiae chromosome XII, complete chromosome sequence. Found forward in

NC_001144 between 354507 and 355506 with 100% identity.
2894_at -671.9 A
Saccharomyces cerevisiae chromosome XII, complete chromosome sequence. Found forward in NC_001144 between 355507 and 356506 with 100% identity.
2895_at 5.5 A
Saccharomyces cerevisiae chromosome XII, complete chromosome sequence. Found forward in NC_001144 between 356507 and 357506 with 100% identity.
2896_at -47.6 A
Saccharomyces cerevisiae chromosome XII, complete chromosome sequence. Found forward in NC_001144 between 357507 and 358506 with 100% identity.
2897_at -209.4 A
Saccharomyces cerevisiae chromosome XII, complete chromosome sequence. Found forward in NC_001144 between 358507 and 359506 with 100% identity.
2898_at -45.2 A
Saccharomyces cerevisiae chromosome XII, complete chromosome sequence. Found forward in NC_001144 between 359507 and 360506 with 100% identity.
2899_at 625.1 M
Saccharomyces cerevisiae chromosome XII, complete chromosome sequence. Found forward in NC_001144 between 360507 and 361506 with 100% identity.
2900_at -155.7 A
Saccharomyces cerevisiae chromosome XII, complete chromosome sequence. Found forward in NC_001144 between 361507 and 362506 with 100% identity.
2901_at 110.0 A
Saccharomyces cerevisiae chromosome XII, complete chromosome sequence. Found forward in NC_001144 between 362507 and 363506 with 100% identity.
2902_at -98.0 A
Saccharomyces cerevisiae chromosome XII, complete chromosome sequence. Found forward in NC_001144 between 363507 and 364506 with 100% identity.
2903_g_at 1798.9 A
Saccharomyces cerevisiae chromosome XII, complete chromosome sequence. Found forward in NC_001144 between 363507 and 364506 with 100% identity.
2904_s_at 2102.7 P
Saccharomyces cerevisiae chromosome XII, complete chromosome sequence. Found forward in NC_001144 between 364507 and 364831 with 100% identity.
2905_at -329.1 A
Saccharomyces cerevisiae chromosome XII, complete chromosome sequence. Found forward in NC_001144 between 629184 and 630183 with 100% identity.
2906_at 144.9 P
Saccharomyces cerevisiae chromosome XII, complete chromosome sequence. Found forward in NC_001144 between 630184 and 631183 with 100% identity.
2907_at -207.3 A
Saccharomyces cerevisiae chromosome XII, complete chromosome sequence. Found forward in NC_001144 between 631184 and 632183 with 100% identity.
2908_at 26.5 M
Saccharomyces cerevisiae chromosome XII, complete chromosome sequence. Found forward in NC_001144 between 632184 and 633183 with 100% identity.
2909_at -110.7 A
Saccharomyces cerevisiae chromosome XII, complete chromosome sequence. Found forward in NC_001144 between 633184 and 634183 with 100% identity.
2910_at -4.5 A
Saccharomyces cerevisiae chromosome XII, complete chromosome sequence. Found forward in NC_001144 between 634184 and 635183 with 100% identity.
2911_s_at 4862.1 P
Saccharomyces cerevisiae chromosome XII, complete chromosome sequence. Found forward in NC_001144 between 635184 and 635584 with 100% identity.
2912_at 301.5 A

Saccharomyces cerevisiae chromosome XII, complete chromosome sequence. Found forward in NC_001144 between 769817 and 770816 with 100% identity.
2913_at 2482.9 P
Saccharomyces cerevisiae chromosome XII, complete chromosome sequence. Found forward in NC_001144 between 770817 and 771816 with 100% identity.
2914_at -95.7 A
Saccharomyces cerevisiae chromosome XII, complete chromosome sequence. Found forward in NC_001144 between 771817 and 772816 with 100% identity.
2915_g_at 278.4 P
Saccharomyces cerevisiae chromosome XII, complete chromosome sequence. Found forward in NC_001144 between 771817 and 772816 with 100% identity.
2916_s_at 143.0 A
Saccharomyces cerevisiae chromosome XII, complete chromosome sequence. Found forward in NC_001144 between 772817 and 773816 with 100% identity.
2832_s_at 767.7 P
Saccharomyces cerevisiae chromosome XII, complete chromosome sequence. Found forward in NC_001144 between 773817 and 774816 with 100% identity.
2833_s_at 695.5 P
Saccharomyces cerevisiae chromosome XII, complete chromosome sequence. Found forward in NC_001144 between 774817 and 775803 with 100% identity.
2834_at -123.7 A
Saccharomyces cerevisiae chromosome XII, complete chromosome sequence. Found forward in NC_001144 between 808817 and 809816 with 100% identity.
2835_at 3269.4 P
Saccharomyces cerevisiae chromosome XII, complete chromosome sequence. Found forward in NC_001144 between 809817 and 810816 with 100% identity.
2836_g_at 7518.4 P
Saccharomyces cerevisiae chromosome XII, complete chromosome sequence. Found forward in NC_001144 between 809817 and 810816 with 100% identity.
2837_s_at 3646.7 P
Saccharomyces cerevisiae chromosome XII, complete chromosome sequence. Found forward in NC_001144 between 810817 and 811816 with 100% identity.
2838_s_at 7055.3 P
Saccharomyces cerevisiae chromosome XII, complete chromosome sequence. Found forward in NC_001144 between 811817 and 812816 with 100% identity.
2839_s_at 10576.2 P
Saccharomyces cerevisiae chromosome XII, complete chromosome sequence. Found forward in NC_001144 between 812817 and 813816 with 100% identity.
2840_s_at 11717.1 P
Saccharomyces cerevisiae chromosome XII, complete chromosome sequence. Found forward in NC_001144 between 813817 and 814816 with 100% identity.
2841_s_at 13375.8 P
Saccharomyces cerevisiae chromosome XII, complete chromosome sequence. Found forward in NC_001144 between 814817 and 815126 with 100% identity.
2842_at 866.0 A
Saccharomyces cerevisiae chromosome XII, complete chromosome sequence. Found forward in NC_001144 between 934909 and 935908 with 100% identity.
2843_at 947.1 P
Saccharomyces cerevisiae chromosome XII, complete chromosome sequence. Found forward in NC_001144 between 935909 and 936908 with 100% identity.
2844_at -34.9 M
Saccharomyces cerevisiae chromosome XII, complete chromosome sequence. Found forward in NC_001144 between 936909 and 937908 with 100% identity.
2845_g_at 1222.3 P
Saccharomyces cerevisiae chromosome XII, complete chromosome sequence. Found forward in NC_001144 between 936909 and 937908 with 100% identity.

2846_s_at 2647.8 P

Saccharomyces cerevisiae chromosome XII, complete chromosome sequence. Found forward in NC_001144 between 937909 and 938908 with 100% identity.

2847_s_at 3948.3 P

Saccharomyces cerevisiae chromosome XII, complete chromosome sequence. Found forward in NC_001144 between 938909 and 939908 with 100% identity.

2848_s_at 5151.8 P

Saccharomyces cerevisiae chromosome XII, complete chromosome sequence. Found forward in NC_001144 between 939909 and 940476 with 100% identity.

2849_at 848.7 P

Saccharomyces cerevisiae chromosome XII, complete chromosome sequence. Found forward in NC_001144 between 965554 and 966553 with 100% identity.

2850_g_at 879.9 P

Saccharomyces cerevisiae chromosome XII, complete chromosome sequence. Found forward in NC_001144 between 965554 and 966553 with 100% identity.

2851_s_at 1291.2 P

Saccharomyces cerevisiae chromosome XII, complete chromosome sequence. Found forward in NC_001144 between 966554 and 967553 with 100% identity.

2852_s_at 1144.1 P

Saccharomyces cerevisiae chromosome XII, complete chromosome sequence. Found forward in NC_001144 between 967554 and 968553 with 100% identity.

2853_s_at 281.5 A

Saccharomyces cerevisiae chromosome XII, complete chromosome sequence. Found forward in NC_001144 between 968554 and 969553 with 100% identity.

2854_s_at 864.1 P

Saccharomyces cerevisiae chromosome XII, complete chromosome sequence. Found forward in NC_001144 between 969554 and 970553 with 100% identity.

2855_s_at 2693.3 P

Saccharomyces cerevisiae chromosome XII, complete chromosome sequence. Found forward in NC_001144 between 970554 and 971189 with 100% identity.

2856_at 1204.4 P

Saccharomyces cerevisiae chromosome XII, complete chromosome sequence. Found forward in NC_001144 between 979430 and 980429 with 100% identity.

2857_at 1007.6 P

Saccharomyces cerevisiae chromosome XII, complete chromosome sequence. Found forward in NC_001144 between 980430 and 981429 with 100% identity.

2858_at 13.9 A

Saccharomyces cerevisiae chromosome XII, complete chromosome sequence. Found forward in NC_001144 between 981430 and 982429 with 100% identity.

2859_at 1786.6 P

Saccharomyces cerevisiae chromosome XII, complete chromosome sequence. Found forward in NC_001144 between 982430 and 983429 with 100% identity.

2860_g_at -251.7 P

Saccharomyces cerevisiae chromosome XII, complete chromosome sequence. Found forward in NC_001144 between 982430 and 983429 with 100% identity.

2861_s_at 211.8 A

Saccharomyces cerevisiae chromosome XII, complete chromosome sequence. Found forward in NC_001144 between 983430 and 984429 with 100% identity.

2862_s_at 638.2 P

Saccharomyces cerevisiae chromosome XII, complete chromosome sequence. Found forward in NC_001144 between 984430 and 985429 with 100% identity.

2863_s_at 291.2 P

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

2864_at 452.5 P

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

NC_001144 between 992726 and 993725 with 100% identity.
2865_g_at 401.7 P
Saccharomyces cerevisiae chromosome XII, complete chromosome sequence. Found forward in NC_001144 between 992726 and 993725 with 100% identity.
2866_s_at 610.7 P
Saccharomyces cerevisiae chromosome XII, complete chromosome sequence. Found forward in NC_001144 between 993726 and 994725 with 100% identity.
2867_s_at 1391.9 P
Saccharomyces cerevisiae chromosome XII, complete chromosome sequence. Found forward in NC_001144 between 994726 and 995725 with 100% identity.
2868_s_at -1149.9 A
Saccharomyces cerevisiae chromosome XII, complete chromosome sequence. Found forward in NC_001144 between 995726 and 996725 with 100% identity.
2869_s_at 753.1 P
Saccharomyces cerevisiae chromosome XII, complete chromosome sequence. Found forward in NC_001144 between 996726 and 997725 with 100% identity.
2870_s_at -497.4 P
Saccharomyces cerevisiae chromosome XII, complete chromosome sequence. Found forward in NC_001144 between 997726 and 998725 with 100% identity.
2871_s_at 3576.8 P
Saccharomyces cerevisiae chromosome XII, complete chromosome sequence. Found forward in NC_001144 between 998726 and 999623 with 100% identity.
2872_at 142.3 A
Saccharomyces cerevisiae chromosome XII, complete chromosome sequence. Found forward in NC_001144 between 1042294 and 1043293 with 100% identity.
2873_at 260.5 A
Saccharomyces cerevisiae chromosome XII, complete chromosome sequence. Found forward in NC_001144 between 1043294 and 1044293 with 100% identity.
2874_g_at 139.7 A
Saccharomyces cerevisiae chromosome XII, complete chromosome sequence. Found forward in NC_001144 between 1043294 and 1044293 with 100% identity.
2789_s_at 229.8 M
Saccharomyces cerevisiae chromosome XII, complete chromosome sequence. Found forward in NC_001144 between 1044294 and 1045293 with 100% identity.
2790_s_at 464.0 P
Saccharomyces cerevisiae chromosome XII, complete chromosome sequence. Found forward in NC_001144 between 1045294 and 1046293 with 100% identity.
2791_s_at 398.4 A
Saccharomyces cerevisiae chromosome XII, complete chromosome sequence. Found forward in NC_001144 between 1046294 and 1047293 with 100% identity.
2792_s_at 132.1 A
Saccharomyces cerevisiae chromosome XII, complete chromosome sequence. Found forward in NC_001144 between 1047294 and 1048293 with 100% identity.
2793_s_at 690.8 P
Saccharomyces cerevisiae chromosome XII, complete chromosome sequence. Found forward in NC_001144 between 1048294 and 1049293 with 100% identity.
2794_s_at 2274.3 P
Saccharomyces cerevisiae chromosome XII, complete chromosome sequence. Found forward in NC_001144 between 1049294 and 1050293 with 100% identity.
2795_s_at 2676.5 P
Saccharomyces cerevisiae chromosome XII, complete chromosome sequence. Found forward in NC_001144 between 1050294 and 1051293 with 100% identity.
2796_f_at 4998.9 P
Saccharomyces cerevisiae chromosome XII, complete chromosome sequence. Found forward in NC_001144 between 1051294 and 1051379 with 100% identity.
2797_at 394.6 P

Saccharomyces cerevisiae chromosome XII, complete chromosome sequence. Found forward in NC_001144 between 1071425 and 1072424 with 100% identity.
2798_g_at 292.0 P
Saccharomyces cerevisiae chromosome XII, complete chromosome sequence. Found forward in NC_001144 between 1071425 and 1072424 with 100% identity.
2799_at 25.7 A
Saccharomyces cerevisiae chromosome XIII, complete chromosome sequence. Found forward in NC_001145 between 63082 and 64081 with 100% identity.
2800_at 479.2 A
Saccharomyces cerevisiae chromosome XIII, complete chromosome sequence. Found forward in NC_001145 between 64082 and 65081 with 100% identity.
2801_at 194.3 A
Saccharomyces cerevisiae chromosome XIII, complete chromosome sequence. Found forward in NC_001145 between 65082 and 66081 with 100% identity.
2802_at 479.9 A
Saccharomyces cerevisiae chromosome XIII, complete chromosome sequence. Found forward in NC_001145 between 66082 and 67081 with 100% identity.
2803_at -497.0 P
Saccharomyces cerevisiae chromosome XIII, complete chromosome sequence. Found forward in NC_001145 between 67082 and 68081 with 100% identity.
2804_at 496.6 P
Saccharomyces cerevisiae chromosome XIII, complete chromosome sequence. Found forward in NC_001145 between 68082 and 69081 with 100% identity.
2805_g_at 2573.0 P
Saccharomyces cerevisiae chromosome XIII, complete chromosome sequence. Found forward in NC_001145 between 68082 and 69081 with 100% identity.
2806_s_at 2685.7 P
Saccharomyces cerevisiae chromosome XIII, complete chromosome sequence. Found forward in NC_001145 between 69082 and 69200 with 100% identity.
2807_at 1128.0 P
Saccharomyces cerevisiae chromosome XIII, complete chromosome sequence. Found forward in NC_001145 between 153719 and 154718 with 100% identity.
2808_at -1303.2 A
Saccharomyces cerevisiae chromosome XIII, complete chromosome sequence. Found forward in NC_001145 between 154719 and 155718 with 100% identity.
2809_at -68.8 A
Saccharomyces cerevisiae chromosome XIII, complete chromosome sequence. Found forward in NC_001145 between 155719 and 156718 with 100% identity.
2810_at 278.3 A
Saccharomyces cerevisiae chromosome XIII, complete chromosome sequence. Found forward in NC_001145 between 156719 and 157718 with 100% identity.
2811_at 351.3 P
Saccharomyces cerevisiae chromosome XIII, complete chromosome sequence. Found forward in NC_001145 between 157719 and 158718 with 100% identity.
2812_at 150.6 A
Saccharomyces cerevisiae chromosome XIII, complete chromosome sequence. Found forward in NC_001145 between 183363 and 184362 with 100% identity.
2813_at 830.6 P
Saccharomyces cerevisiae chromosome XIII, complete chromosome sequence. Found forward in NC_001145 between 189363 and 190244 with 100% identity.
2814_at -187.3 A
Saccharomyces cerevisiae chromosome XIII, complete chromosome sequence. Found forward in NC_001145 between 195413 and 196412 with 100% identity.
2815_at 2048.8 P
Saccharomyces cerevisiae chromosome XIII, complete chromosome sequence. Found forward in NC_001145 between 201413 and 202412 with 100% identity.

2816_at 5934.0 P
Saccharomyces cerevisiae chromosome XIII, complete chromosome sequence. Found forward in NC_001145 between 202413 and 202775 with 100% identity.
2817_at 3251.0 P
Saccharomyces cerevisiae chromosome XIII, complete chromosome sequence. Found forward in NC_001145 between 356810 and 357809 with 100% identity.
2818_at 765.7 P
Saccharomyces cerevisiae chromosome XIII, complete chromosome sequence. Found forward in NC_001145 between 357810 and 358809 with 100% identity.
2819_s_at 1641.7 P
Saccharomyces cerevisiae chromosome XIII, complete chromosome sequence. Found forward in NC_001145 between 358810 and 359809 with 100% identity.
2821_at -276.9 A
Saccharomyces cerevisiae chromosome XIII, complete chromosome sequence. Found forward in NC_001145 between 360810 and 361809 with 100% identity.
2822_at 1089.7 A
Saccharomyces cerevisiae chromosome XIII, complete chromosome sequence. Found forward in NC_001145 between 361810 and 362701 with 100% identity.
2823_at 154.4 P
Saccharomyces cerevisiae chromosome XIII, complete chromosome sequence. Found forward in NC_001145 between 368593 and 369592 with 100% identity.
2824_at 1723.6 P
Saccharomyces cerevisiae chromosome XIII, complete chromosome sequence. Found forward in NC_001145 between 369593 and 370592 with 100% identity.
2825_at 310.3 P
Saccharomyces cerevisiae chromosome XIII, complete chromosome sequence. Found forward in NC_001145 between 370593 and 371592 with 100% identity.
2826_at 16.3 M
Saccharomyces cerevisiae chromosome XIII, complete chromosome sequence. Found forward in NC_001145 between 371593 and 372592 with 100% identity.
2827_g_at 235.8 A
Saccharomyces cerevisiae chromosome XIII, complete chromosome sequence. Found forward in NC_001145 between 371593 and 372592 with 100% identity.
2828_at 50.5 A
Saccharomyces cerevisiae chromosome XIII, complete chromosome sequence. Found forward in NC_001145 between 372593 and 373592 with 100% identity.
2829_f_at 3347.3 P
Saccharomyces cerevisiae chromosome XIII, complete chromosome sequence. Found forward in NC_001145 between 373593 and 374592 with 100% identity.
2748_at 10.2 A
Saccharomyces cerevisiae chromosome XIII, complete chromosome sequence. Found forward in NC_001145 between 378593 and 379592 with 100% identity.
2749_s_at 746.4 P
Saccharomyces cerevisiae chromosome XIII, complete chromosome sequence. Found forward in NC_001145 between 379593 and 379699 with 100% identity.
2750_at 10.2 A
Saccharomyces cerevisiae chromosome XIII, complete chromosome sequence. Found forward in NC_001145 between 677692 and 678691 with 100% identity.
2751_at 687.1 A
Saccharomyces cerevisiae chromosome XIII, complete chromosome sequence. Found forward in NC_001145 between 678692 and 679691 with 100% identity.
2752_at 34.5 A
Saccharomyces cerevisiae chromosome XIII, complete chromosome sequence. Found forward in NC_001145 between 679692 and 680691 with 100% identity.
2753_at 169.6 M
Saccharomyces cerevisiae chromosome XIII, complete chromosome sequence. Found forward in

NC_001145 between 680692 and 681691 with 100% identity.
2754_at -80.5 A
Saccharomyces cerevisiae chromosome XIII, complete chromosome sequence. Found forward in NC_001145 between 681692 and 682691 with 100% identity.
2755_at -81.9 A
Saccharomyces cerevisiae chromosome XIII, complete chromosome sequence. Found forward in NC_001145 between 682692 and 683691 with 100% identity.
2756_at -324.1 P
Saccharomyces cerevisiae chromosome XIII, complete chromosome sequence. Found forward in NC_001145 between 683692 and 684691 with 100% identity.
2757_g_at 7882.9 P
Saccharomyces cerevisiae chromosome XIII, complete chromosome sequence. Found forward in NC_001145 between 683692 and 684691 with 100% identity.
2758_s_at 9328.4 P
Saccharomyces cerevisiae chromosome XIII, complete chromosome sequence. Found forward in NC_001145 between 684692 and 685297 with 100% identity.
2759_at -303.4 A
Saccharomyces cerevisiae chromosome XIII, complete chromosome sequence. Found forward in NC_001145 between 704078 and 705077 with 100% identity.
2760_at 807.3 P
Saccharomyces cerevisiae chromosome XIII, complete chromosome sequence. Found forward in NC_001145 between 705078 and 706077 with 100% identity.
2761_at 628.4 A
Saccharomyces cerevisiae chromosome XIII, complete chromosome sequence. Found forward in NC_001145 between 706078 and 707077 with 100% identity.
2762_at 29.1 A
Saccharomyces cerevisiae chromosome XIII, complete chromosome sequence. Found forward in NC_001145 between 707078 and 708077 with 100% identity.
2763_s_at 15.9 A
Saccharomyces cerevisiae chromosome XIII, complete chromosome sequence. Found forward in NC_001145 between 708078 and 709077 with 100% identity.
2764_s_at 558.9 P
Saccharomyces cerevisiae chromosome XIII, complete chromosome sequence. Found forward in NC_001145 between 709078 and 710077 with 100% identity.
2765_s_at -540.6 A
Saccharomyces cerevisiae chromosome XIII, complete chromosome sequence. Found forward in NC_001145 between 710078 and 711077 with 100% identity.
2766_s_at 2533.9 P
Saccharomyces cerevisiae chromosome XIII, complete chromosome sequence. Found forward in NC_001145 between 711078 and 711608 with 100% identity.
2767_at 740.7 P
Saccharomyces cerevisiae chromosome XIII, complete chromosome sequence. Found forward in NC_001145 between 726433 and 727432 with 100% identity.
2768_at 480.7 A
Saccharomyces cerevisiae chromosome XIII, complete chromosome sequence. Found forward in NC_001145 between 727433 and 728432 with 100% identity.
2769_at -640.4 A
Saccharomyces cerevisiae chromosome XIII, complete chromosome sequence. Found forward in NC_001145 between 728433 and 729432 with 100% identity.
2770_at 105.9 P
Saccharomyces cerevisiae chromosome XIII, complete chromosome sequence. Found forward in NC_001145 between 729433 and 730432 with 100% identity.
2771_at 397.4 A
Saccharomyces cerevisiae chromosome XIII, complete chromosome sequence. Found forward in NC_001145 between 730433 and 731432 with 100% identity.
2772_at 701.1 P

Saccharomyces cerevisiae chromosome XIII, complete chromosome sequence. Found forward in NC_001145 between 731433 and 731964 with 100% identity.
2773_at -131.8 P
Saccharomyces cerevisiae chromosome XIII, complete chromosome sequence. Found forward in NC_001145 between 827528 and 828527 with 100% identity.
2774_at 468.0 P
Saccharomyces cerevisiae chromosome XIII, complete chromosome sequence. Found forward in NC_001145 between 828528 and 829527 with 100% identity.
2775_at 491.1 A
Saccharomyces cerevisiae chromosome XIII, complete chromosome sequence. Found forward in NC_001145 between 829528 and 830527 with 100% identity.
2776_at -944.7 A
Saccharomyces cerevisiae chromosome XIII, complete chromosome sequence. Found forward in NC_001145 between 830528 and 831527 with 100% identity.
2777_at 150.3 A
Saccharomyces cerevisiae chromosome XIII, complete chromosome sequence. Found forward in NC_001145 between 831528 and 832527 with 100% identity.
2778_g_at 841.0 P
Saccharomyces cerevisiae chromosome XIII, complete chromosome sequence. Found forward in NC_001145 between 831528 and 832527 with 100% identity.
2779_s_at 1664.5 P
Saccharomyces cerevisiae chromosome XIII, complete chromosome sequence. Found forward in NC_001145 between 832528 and 832753 with 100% identity.
2780_at 637.5 P
Saccharomyces cerevisiae chromosome XIII, complete chromosome sequence. Found forward in NC_001145 between 842936 and 843935 with 100% identity.
2781_at 345.4 P
Saccharomyces cerevisiae chromosome XIII, complete chromosome sequence. Found forward in NC_001145 between 843936 and 844935 with 100% identity.

2782_at 271.6 A
Saccharomyces cerevisiae chromosome XIII, complete chromosome sequence. Found forward in NC_001145 between 844936 and 845935 with 100% identity.
2783_g_at 884.2 P
Saccharomyces cerevisiae chromosome XIII, complete chromosome sequence. Found forward in NC_001145 between 844936 and 845935 with 100% identity.
2784_s_at 418.2 A
Saccharomyces cerevisiae chromosome XIII, complete chromosome sequence. Found forward in NC_001145 between 845936 and 846935 with 100% identity.
2785_s_at 1119.6 P
Saccharomyces cerevisiae chromosome XIII, complete chromosome sequence. Found forward in NC_001145 between 846936 and 847935 with 100% identity.
2786_s_at 4021.7 P
Saccharomyces cerevisiae chromosome XIII, complete chromosome sequence. Found forward in NC_001145 between 847936 and 847986 with 100% identity.
2787_at 330.9 A
Saccharomyces cerevisiae chromosome XIII, complete chromosome sequence. Found forward in NC_001145 between 879563 and 880562 with 100% identity.
2788_at 335.6 P
Saccharomyces cerevisiae chromosome XIII, complete chromosome sequence. Found forward in NC_001145 between 880563 and 881562 with 100% identity.
2703_g_at -37.6 A
Saccharomyces cerevisiae chromosome XIII, complete chromosome sequence. Found forward in NC_001145 between 880563 and 881562 with 100% identity.
2704_s_at 487.7 P
Saccharomyces cerevisiae chromosome XIII, complete chromosome sequence. Found forward in

NC_001145 between 881563 and 882562 with 100% identity.
2705_s_at -608.3 A
Saccharomyces cerevisiae chromosome XIII, complete chromosome sequence. Found forward in NC_001145 between 882563 and 883562 with 100% identity.
2706_s_at 394.7 A
Saccharomyces cerevisiae chromosome XIII, complete chromosome sequence. Found forward in NC_001145 between 883563 and 884562 with 100% identity.
2707_s_at 407.9 A
Saccharomyces cerevisiae chromosome XIII, complete chromosome sequence. Found forward in NC_001145 between 884563 and 885562 with 100% identity.
2708_s_at 707.6 P
Saccharomyces cerevisiae chromosome XIII, complete chromosome sequence. Found forward in NC_001145 between 885563 and 886016 with 100% identity.
2709_s_at 1078.4 P
Saccharomyces cerevisiae chromosome XIV, complete chromosome sequence. Found forward in NC_001146 between 871 and 1870 with 100% identity.
2710_s_at 569.9 P
Saccharomyces cerevisiae chromosome XIV, complete chromosome sequence. Found forward in NC_001146 between 1871 and 2870 with 100% identity.
2711_s_at 1110.1 P
Saccharomyces cerevisiae chromosome XIV, complete chromosome sequence. Found forward in NC_001146 between 2871 and 3870 with 100% identity.
2712_s_at 512.9 P
Saccharomyces cerevisiae chromosome XIV, complete chromosome sequence. Found forward in NC_001146 between 3871 and 4870 with 100% identity.
2713_s_at 495.2 A
Saccharomyces cerevisiae chromosome XIV, complete chromosome sequence. Found forward in NC_001146 between 4871 and 5870 with 100% identity.
2714_s_at 6192.8 P
Saccharomyces cerevisiae chromosome XIV, complete chromosome sequence. Found forward in NC_001146 between 5871 and 6080 with 100% identity.
2715_at 87.7 A
Saccharomyces cerevisiae chromosome XIV, complete chromosome sequence. Found forward in NC_001146 between 130021 and 131020 with 100% identity.
2716_at 549.5 A
Saccharomyces cerevisiae chromosome XIV, complete chromosome sequence. Found forward in NC_001146 between 131021 and 132020 with 100% identity.
2717_at 1201.1 P
Saccharomyces cerevisiae chromosome XIV, complete chromosome sequence. Found forward in NC_001146 between 132021 and 133020 with 100% identity.
2718_at 1883.6 M
Saccharomyces cerevisiae chromosome XIV, complete chromosome sequence. Found forward in NC_001146 between 133021 and 134020 with 100% identity.
2719_at -670.2 A
Saccharomyces cerevisiae chromosome XIV, complete chromosome sequence. Found forward in NC_001146 between 134021 and 135020 with 100% identity.
2720_at 39.4 A
Saccharomyces cerevisiae chromosome XIV, complete chromosome sequence. Found forward in NC_001146 between 135021 and 135939 with 100% identity.
2721_at 385.6 A
Saccharomyces cerevisiae chromosome XIV, complete chromosome sequence. Found forward in NC_001146 between 147395 and 148394 with 100% identity.
2722_g_at 326.1 P
Saccharomyces cerevisiae chromosome XIV, complete chromosome sequence. Found forward in NC_001146 between 147395 and 148394 with 100% identity.
2723_s_at -1645.8 A

Saccharomyces cerevisiae chromosome XIV, complete chromosome sequence. Found forward in NC_001146 between 148395 and 149394 with 100% identity.
2724_s_at 877.2 P
Saccharomyces cerevisiae chromosome XIV, complete chromosome sequence. Found forward in NC_001146 between 149395 and 150394 with 100% identity.
2725_s_at -120.7 A
Saccharomyces cerevisiae chromosome XIV, complete chromosome sequence. Found forward in NC_001146 between 150395 and 151394 with 100% identity.
2726_s_at 501.3 P
Saccharomyces cerevisiae chromosome XIV, complete chromosome sequence. Found forward in NC_001146 between 151395 and 152394 with 100% identity.
2727_s_at 1920.2 P
Saccharomyces cerevisiae chromosome XIV, complete chromosome sequence. Found forward in NC_001146 between 152395 and 153394 with 100% identity.
2728_s_at 1348.6 P
Saccharomyces cerevisiae chromosome XIV, complete chromosome sequence. Found forward in NC_001146 between 153395 and 154379 with 100% identity.
2729_at 231.1 A
Saccharomyces cerevisiae chromosome XIV, complete chromosome sequence. Found forward in NC_001146 between 161130 and 162129 with 100% identity.
2730_at -78.2 A
Saccharomyces cerevisiae chromosome XIV, complete chromosome sequence. Found forward in NC_001146 between 162130 and 163129 with 100% identity.
2731_at 1439.5 P
Saccharomyces cerevisiae chromosome XIV, complete chromosome sequence. Found forward in NC_001146 between 163130 and 164129 with 100% identity.
2732_at 136.6 A
Saccharomyces cerevisiae chromosome XIV, complete chromosome sequence. Found forward in NC_001146 between 164130 and 165129 with 100% identity.
2733_g_at 1338.5 P
Saccharomyces cerevisiae chromosome XIV, complete chromosome sequence. Found forward in NC_001146 between 164130 and 165129 with 100% identity.
2734_s_at 1090.0 P
Saccharomyces cerevisiae chromosome XIV, complete chromosome sequence. Found forward in NC_001146 between 165130 and 166129 with 100% identity.
2735_s_at 3116.5 P
Saccharomyces cerevisiae chromosome XIV, complete chromosome sequence. Found forward in NC_001146 between 166130 and 166596 with 100% identity.
2736_at -131.7 A
Saccharomyces cerevisiae chromosome XIV, complete chromosome sequence. Found forward in NC_001146 between 173087 and 174086 with 100% identity.
2737_at 116.0 P
Saccharomyces cerevisiae chromosome XIV, complete chromosome sequence. Found forward in NC_001146 between 174087 and 175086 with 100% identity.
2738_at -947.6 P
Saccharomyces cerevisiae chromosome XIV, complete chromosome sequence. Found forward in NC_001146 between 175087 and 176086 with 100% identity.
2739_g_at 208.0 P
Saccharomyces cerevisiae chromosome XIV, complete chromosome sequence. Found forward in NC_001146 between 175087 and 176086 with 100% identity.
2740_s_at 192.2 P
Saccharomyces cerevisiae chromosome XIV, complete chromosome sequence. Found forward in NC_001146 between 176087 and 177086 with 100% identity.
2741_s_at 130.6 P
Saccharomyces cerevisiae chromosome XIV, complete chromosome sequence. Found forward in NC_001146 between 177087 and 178086 with 100% identity.

2742_s_at 349.9 P
Saccharomyces cerevisiae chromosome XIV, complete chromosome sequence. Found forward in NC_001146 between 178087 and 178847 with 100% identity.
2743_at -87.1 A
Saccharomyces cerevisiae chromosome XIV, complete chromosome sequence. Found forward in NC_001146 between 309454 and 310453 with 100% identity.
2744_at 436.8 P
Saccharomyces cerevisiae chromosome XIV, complete chromosome sequence. Found forward in NC_001146 between 310454 and 311453 with 100% identity.
2745_g_at 273.0 P
Saccharomyces cerevisiae chromosome XIV, complete chromosome sequence. Found forward in NC_001146 between 310454 and 311453 with 100% identity.
2660_s_at 230.2 A
Saccharomyces cerevisiae chromosome XIV, complete chromosome sequence. Found forward in NC_001146 between 311454 and 312453 with 100% identity.
2661_s_at 86.5 A
Saccharomyces cerevisiae chromosome XIV, complete chromosome sequence. Found forward in NC_001146 between 312454 and 313453 with 100% identity.
2662_s_at 1040.9 P
Saccharomyces cerevisiae chromosome XIV, complete chromosome sequence. Found forward in NC_001146 between 313454 and 314453 with 100% identity.
2663_s_at 1708.5 P
Saccharomyces cerevisiae chromosome XIV, complete chromosome sequence. Found forward in NC_001146 between 314454 and 315379 with 100% identity.
2664_at 2297.4 A
Saccharomyces cerevisiae chromosome XIV, complete chromosome sequence. Found forward in NC_001146 between 524084 and 525083 with 100% identity.
2665_at 146.5 P
Saccharomyces cerevisiae chromosome XIV, complete chromosome sequence. Found forward in NC_001146 between 525084 and 526083 with 100% identity.
2666_s_at -810.1 A
Saccharomyces cerevisiae chromosome XIV, complete chromosome sequence. Found forward in NC_001146 between 526084 and 527083 with 100% identity.
2667_s_at 783.0 P
Saccharomyces cerevisiae chromosome XIV, complete chromosome sequence. Found forward in NC_001146 between 527084 and 528083 with 100% identity.
2668_s_at 1251.8 P
Saccharomyces cerevisiae chromosome XIV, complete chromosome sequence. Found forward in NC_001146 between 528084 and 529079 with 100% identity.
2669_at 3656.6 P
Saccharomyces cerevisiae chromosome XIV, complete chromosome sequence. Found forward in NC_001146 between 655170 and 656169 with 100% identity.
2670_at 318.8 P
Saccharomyces cerevisiae chromosome XIV, complete chromosome sequence. Found forward in NC_001146 between 656170 and 657169 with 100% identity.
2671_at -339.5 A
Saccharomyces cerevisiae chromosome XIV, complete chromosome sequence. Found forward in NC_001146 between 657170 and 658169 with 100% identity.
2672_at 209.8 A
Saccharomyces cerevisiae chromosome XIV, complete chromosome sequence. Found forward in NC_001146 between 658170 and 659169 with 100% identity.
2673_at 156.7 A
Saccharomyces cerevisiae chromosome XIV, complete chromosome sequence. Found forward in NC_001146 between 659170 and 660169 with 100% identity.
2674_at -137.3 A
Saccharomyces cerevisiae chromosome XIV, complete chromosome sequence. Found forward in

NC_001146 between 660170 and 661169 with 100% identity.
2675_at 752.4 P
Saccharomyces cerevisiae chromosome XIV, complete chromosome sequence. Found forward in NC_001146 between 661170 and 661997 with 100% identity.
2676_at 19.0 A
Saccharomyces cerevisiae chromosome XIV, complete chromosome sequence. Found forward in NC_001146 between 681191 and 682190 with 100% identity.
2677_at 55.7 A
Saccharomyces cerevisiae chromosome XIV, complete chromosome sequence. Found forward in NC_001146 between 682191 and 683190 with 100% identity.
2678_at -2089.4 A
Saccharomyces cerevisiae chromosome XIV, complete chromosome sequence. Found forward in NC_001146 between 683191 and 684190 with 100% identity.
2679_at 699.5 A
Saccharomyces cerevisiae chromosome XIV, complete chromosome sequence. Found forward in NC_001146 between 684191 and 685190 with 100% identity.
2680_at -29.9 A
Saccharomyces cerevisiae chromosome XIV, complete chromosome sequence. Found forward in NC_001146 between 685191 and 686190 with 100% identity.
2681_g_at 2554.3 P
Saccharomyces cerevisiae chromosome XIV, complete chromosome sequence. Found forward in NC_001146 between 685191 and 686190 with 100% identity.
2682_s_at 1938.2 A
Saccharomyces cerevisiae chromosome XIV, complete chromosome sequence. Found forward in NC_001146 between 686191 and 686613 with 100% identity.
2683_at -813.9 A
Saccharomyces cerevisiae chromosome XIV, complete chromosome sequence. Found forward in NC_001146 between 761618 and 762617 with 100% identity.
2684_at -181.0 P
Saccharomyces cerevisiae chromosome XIV, complete chromosome sequence. Found forward in NC_001146 between 762618 and 763617 with 100% identity.
2685_at 1439.9 P
Saccharomyces cerevisiae chromosome XIV, complete chromosome sequence. Found forward in NC_001146 between 763618 and 764617 with 100% identity.
2686_at 1227.4 M
Saccharomyces cerevisiae chromosome XIV, complete chromosome sequence. Found forward in NC_001146 between 764618 and 765617 with 100% identity.
2687_g_at 39.7 A
Saccharomyces cerevisiae chromosome XIV, complete chromosome sequence. Found forward in NC_001146 between 764618 and 765617 with 100% identity.
2688_s_at 688.6 P
Saccharomyces cerevisiae chromosome XIV, complete chromosome sequence. Found forward in NC_001146 between 765618 and 766617 with 100% identity.
2689_s_at -651.9 A
Saccharomyces cerevisiae chromosome XIV, complete chromosome sequence. Found forward in NC_001146 between 766618 and 767617 with 100% identity.
2690_s_at 773.6 A
Saccharomyces cerevisiae chromosome XIV, complete chromosome sequence. Found forward in NC_001146 between 767618 and 768617 with 100% identity.
2691_s_at -45.9 A
Saccharomyces cerevisiae chromosome XIV, complete chromosome sequence. Found forward in NC_001146 between 768618 and 768871 with 100% identity.
2692_at 65.8 A
Saccharomyces cerevisiae chromosome XV, complete chromosome sequence. Found forward in NC_001147 between 2078 and 3077 with 100% identity.
2693_at 291.1 P

Saccharomyces cerevisiae chromosome XV, complete chromosome sequence. Found forward in NC_001147 between 3078 and 4077 with 100% identity.
2694_at 1625.7 A
Saccharomyces cerevisiae chromosome XV, complete chromosome sequence. Found forward in NC_001147 between 4078 and 5077 with 100% identity.
2695_at -531.5 A
Saccharomyces cerevisiae chromosome XV, complete chromosome sequence. Found forward in NC_001147 between 5078 and 6077 with 100% identity.
2696_at 601.8 P
Saccharomyces cerevisiae chromosome XV, complete chromosome sequence. Found forward in NC_001147 between 6078 and 7077 with 100% identity.
2697_g_at 165.9 A
Saccharomyces cerevisiae chromosome XV, complete chromosome sequence. Found forward in NC_001147 between 6078 and 7077 with 100% identity.
2698_s_at 672.5 P
Saccharomyces cerevisiae chromosome XV, complete chromosome sequence. Found forward in NC_001147 between 7078 and 7615 with 100% identity.
2699_at 685.0 A
Saccharomyces cerevisiae chromosome XV, complete chromosome sequence. Found forward in NC_001147 between 169973 and 170972 with 100% identity.
2700_at 35.8 A
Saccharomyces cerevisiae chromosome XV, complete chromosome sequence. Found forward in NC_001147 between 170973 and 171972 with 100% identity.
2701_g_at 361.0 P
Saccharomyces cerevisiae chromosome XV, complete chromosome sequence. Found forward in NC_001147 between 170973 and 171972 with 100% identity.
2702_s_at 1591.6 M
Saccharomyces cerevisiae chromosome XV, complete chromosome sequence. Found forward in NC_001147 between 171973 and 172972 with 100% identity.
2618_s_at 424.3 A
Saccharomyces cerevisiae chromosome XV, complete chromosome sequence. Found forward in NC_001147 between 172973 and 173972 with 100% identity.
2619_s_at 79.5 P
Saccharomyces cerevisiae chromosome XV, complete chromosome sequence. Found forward in NC_001147 between 173973 and 174972 with 100% identity.
2620_s_at 294.6 P
Saccharomyces cerevisiae chromosome XV, complete chromosome sequence. Found forward in NC_001147 between 174973 and 175972 with 100% identity.
2621_s_at 911.5 P
Saccharomyces cerevisiae chromosome XV, complete chromosome sequence. Found forward in NC_001147 between 175973 and 176972 with 100% identity.
2622_s_at 2296.5 P
Saccharomyces cerevisiae chromosome XV, complete chromosome sequence. Found forward in NC_001147 between 176973 and 177972 with 100% identity.
2623_s_at 3.1 P
Saccharomyces cerevisiae chromosome XV, complete chromosome sequence. Found forward in NC_001147 between 177973 and 178972 with 100% identity.
2624_s_at 1819.5 P
Saccharomyces cerevisiae chromosome XV, complete chromosome sequence. Found forward in NC_001147 between 178973 and 179808 with 100% identity.
2625_at 854.3 P
Saccharomyces cerevisiae chromosome XV, complete chromosome sequence. Found forward in NC_001147 between 346694 and 347693 with 100% identity.
2626_at 1889.2 A
Saccharomyces cerevisiae chromosome XV, complete chromosome sequence. Found forward in NC_001147 between 347694 and 348693 with 100% identity.

2627_at 1624.6 P
Saccharomyces cerevisiae chromosome XV, complete chromosome sequence. Found forward in NC_001147 between 348694 and 349693 with 100% identity.
2628_s_at 777.7 A
Saccharomyces cerevisiae chromosome XV, complete chromosome sequence. Found forward in NC_001147 between 349694 and 350693 with 100% identity.
2629_s_at 1448.1 P
Saccharomyces cerevisiae chromosome XV, complete chromosome sequence. Found forward in NC_001147 between 350694 and 351693 with 100% identity.
2630_s_at 888.4 P
Saccharomyces cerevisiae chromosome XV, complete chromosome sequence. Found forward in NC_001147 between 351694 and 352693 with 100% identity.
2631_s_at 1348.0 P
Saccharomyces cerevisiae chromosome XV, complete chromosome sequence. Found forward in NC_001147 between 352694 and 353362 with 100% identity.
2632_at 495.2 P
Saccharomyces cerevisiae chromosome XV, complete chromosome sequence. Found forward in NC_001147 between 540261 and 541260 with 100% identity.
2633_at 516.6 P
Saccharomyces cerevisiae chromosome XV, complete chromosome sequence. Found forward in NC_001147 between 541261 and 542260 with 100% identity.
2634_at 294.7 P
Saccharomyces cerevisiae chromosome XV, complete chromosome sequence. Found forward in NC_001147 between 542261 and 543260 with 100% identity.
2635_at 57.1 A
Saccharomyces cerevisiae chromosome XV, complete chromosome sequence. Found forward in NC_001147 between 543261 and 544260 with 100% identity.
2636_at 134.8 P
Saccharomyces cerevisiae chromosome XV, complete chromosome sequence. Found forward in NC_001147 between 544261 and 545260 with 100% identity.
2637_g_at 3948.9 P
Saccharomyces cerevisiae chromosome XV, complete chromosome sequence. Found forward in NC_001147 between 544261 and 545260 with 100% identity.
2638_s_at 7345.7 P
Saccharomyces cerevisiae chromosome XV, complete chromosome sequence. Found forward in NC_001147 between 545261 and 545831 with 100% identity.
2639_at -304.4 A
Saccharomyces cerevisiae chromosome XV, complete chromosome sequence. Found forward in NC_001147 between 618016 and 619015 with 100% identity.
2640_at 1111.9 P
Saccharomyces cerevisiae chromosome XV, complete chromosome sequence. Found forward in NC_001147 between 619016 and 620015 with 100% identity.
2641_g_at 6642.0 P
Saccharomyces cerevisiae chromosome XV, complete chromosome sequence. Found forward in NC_001147 between 619016 and 620015 with 100% identity.
2642_s_at 8141.5 P
Saccharomyces cerevisiae chromosome XV, complete chromosome sequence. Found forward in NC_001147 between 620016 and 621015 with 100% identity.
2643_s_at 9406.4 P
Saccharomyces cerevisiae chromosome XV, complete chromosome sequence. Found forward in NC_001147 between 621016 and 622015 with 100% identity.
2644_s_at 12897.9 P
Saccharomyces cerevisiae chromosome XV, complete chromosome sequence. Found forward in NC_001147 between 622016 and 623015 with 100% identity.
2645_s_at 11104.7 P
Saccharomyces cerevisiae chromosome XV, complete chromosome sequence. Found forward in

NC_001147 between 623016 and 623873 with 100% identity.

2646_at -1273.9 A

Saccharomyces cerevisiae chromosome XV, complete chromosome sequence. Found forward in NC_001147 between 730506 and 731505 with 100% identity.

2647_at -581.6 A

Saccharomyces cerevisiae chromosome XV, complete chromosome sequence. Found forward in NC_001147 between 731506 and 732505 with 100% identity.

2648_at 438.9 A

Saccharomyces cerevisiae chromosome XV, complete chromosome sequence. Found forward in NC_001147 between 732506 and 733505 with 100% identity.

2649_at -907.7 A

Saccharomyces cerevisiae chromosome XV, complete chromosome sequence. Found forward in NC_001147 between 733506 and 734505 with 100% identity.

2650_g_at 956.0 P

Saccharomyces cerevisiae chromosome XV, complete chromosome sequence. Found forward in NC_001147 between 733506 and 734505 with 100% identity.

2651_s_at 1352.0 P

Saccharomyces cerevisiae chromosome XV, complete chromosome sequence. Found forward in NC_001147 between 734506 and 735505 with 100% identity.

2652_s_at 2515.6 P

Saccharomyces cerevisiae chromosome XV, complete chromosome sequence. Found forward in NC_001147 between 735506 and 735675 with 100% identity.

2653_at 483.2 A

Saccharomyces cerevisiae chromosome XV, complete chromosome sequence. Found forward in NC_001147 between 855642 and 856641 with 100% identity.

2654_at 218.9 A

Saccharomyces cerevisiae chromosome XV, complete chromosome sequence. Found forward in NC_001147 between 856642 and 857641 with 100% identity.

2655_at 1705.2 A

Saccharomyces cerevisiae chromosome XV, complete chromosome sequence. Found forward in NC_001147 between 857642 and 858641 with 100% identity.

2656_at 1227.6 A

Saccharomyces cerevisiae chromosome XV, complete chromosome sequence. Found forward in NC_001147 between 858642 and 859641 with 100% identity.

2657_at 74.3 M

Saccharomyces cerevisiae chromosome XV, complete chromosome sequence. Found forward in NC_001147 between 859642 and 860641 with 100% identity.

2658_at 107.6 A

Saccharomyces cerevisiae chromosome XV, complete chromosome sequence. Found forward in NC_001147 between 860642 and 861641 with 100% identity.

2659_g_at 346.9 P

Saccharomyces cerevisiae chromosome XV, complete chromosome sequence. Found forward in NC_001147 between 860642 and 861641 with 100% identity.

2575_s_at 1836.5 P

Saccharomyces cerevisiae chromosome XV, complete chromosome sequence. Found forward in NC_001147 between 861642 and 862641 with 100% identity.

2576_s_at 1242.0 P

Saccharomyces cerevisiae chromosome XV, complete chromosome sequence. Found forward in NC_001147 between 862642 and 863641 with 100% identity.

2577_s_at 1429.3 P

Saccharomyces cerevisiae chromosome XV, complete chromosome sequence. Found forward in NC_001147 between 863642 and 864641 with 100% identity.

2578_s_at 3055.5 P

Saccharomyces cerevisiae chromosome XV, complete chromosome sequence. Found forward in NC_001147 between 864642 and 865088 with 100% identity.

2579_at 1392.9 A

Saccharomyces cerevisiae chromosome XV, complete chromosome sequence. Found forward in NC_001147 between 946724 and 947723 with 100% identity.
2580_at 235.5 P
Saccharomyces cerevisiae chromosome XV, complete chromosome sequence. Found forward in NC_001147 between 947724 and 948723 with 100% identity.
2581_at 250.6 A
Saccharomyces cerevisiae chromosome XV, complete chromosome sequence. Found forward in NC_001147 between 948724 and 949723 with 100% identity.
2582_at -1538.1 A
Saccharomyces cerevisiae chromosome XV, complete chromosome sequence. Found forward in NC_001147 between 949724 and 950723 with 100% identity.
2583_g_at 1529.1 P
Saccharomyces cerevisiae chromosome XV, complete chromosome sequence. Found forward in NC_001147 between 949724 and 950723 with 100% identity.
2584_s_at 1748.8 P
Saccharomyces cerevisiae chromosome XV, complete chromosome sequence. Found forward in NC_001147 between 950724 and 951723 with 100% identity.
2585_s_at 4599.1 P
Saccharomyces cerevisiae chromosome XV, complete chromosome sequence. Found forward in NC_001147 between 951724 and 952723 with 100% identity.
2586_s_at 2765.4 P
Saccharomyces cerevisiae chromosome XV, complete chromosome sequence. Found forward in NC_001147 between 952724 and 953361 with 100% identity.
2587_at 819.7 A
Saccharomyces cerevisiae chromosome XV, complete chromosome sequence. Found forward in NC_001147 between 959693 and 960692 with 100% identity.
2588_at 1241.0 P
Saccharomyces cerevisiae chromosome XV, complete chromosome sequence. Found forward in NC_001147 between 960693 and 961692 with 100% identity.
2589_g_at 2958.0 P
Saccharomyces cerevisiae chromosome XV, complete chromosome sequence. Found forward in NC_001147 between 960693 and 961692 with 100% identity.
2590_s_at 5064.7 P
Saccharomyces cerevisiae chromosome XV, complete chromosome sequence. Found forward in NC_001147 between 961693 and 962692 with 100% identity.
2591_s_at 2858.3 P
Saccharomyces cerevisiae chromosome XV, complete chromosome sequence. Found forward in NC_001147 between 962693 and 963692 with 100% identity.
2592_s_at 6788.8 P
Saccharomyces cerevisiae chromosome XV, complete chromosome sequence. Found forward in NC_001147 between 963693 and 964692 with 100% identity.
2593_s_at 9431.3 P
Saccharomyces cerevisiae chromosome XV, complete chromosome sequence. Found forward in NC_001147 between 964693 and 965472 with 100% identity.
2594_at 480.6 A
Saccharomyces cerevisiae chromosome XVI, complete chromosome sequence. Found forward in NC_001148 between 19079 and 20078 with 100% identity.
2595_at 120.7 P
Saccharomyces cerevisiae chromosome XVI, complete chromosome sequence. Found forward in NC_001148 between 20079 and 21078 with 100% identity.
2596_at -1889.2 A
Saccharomyces cerevisiae chromosome XVI, complete chromosome sequence. Found forward in NC_001148 between 21079 and 22078 with 100% identity.
2597_at 97.5 A
Saccharomyces cerevisiae chromosome XVI, complete chromosome sequence. Found forward in NC_001148 between 22079 and 23078 with 100% identity.

2598_g_at -1117.9 A
Saccharomyces cerevisiae chromosome XVI, complete chromosome sequence. Found forward in NC_001148 between 22079 and 23078 with 100% identity.
2599_s_at 1831.6 A
Saccharomyces cerevisiae chromosome XVI, complete chromosome sequence. Found forward in NC_001148 between 23079 and 24078 with 100% identity.
2600_s_at 25.0 P
Saccharomyces cerevisiae chromosome XVI, complete chromosome sequence. Found forward in NC_001148 between 24079 and 24201 with 100% identity.
2601_at 570.3 P
Saccharomyces cerevisiae chromosome XVI, complete chromosome sequence. Found forward in NC_001148 between 108147 and 109146 with 100% identity.
2602_g_at 4757.3 P
Saccharomyces cerevisiae chromosome XVI, complete chromosome sequence. Found forward in NC_001148 between 108147 and 109146 with 100% identity.
2603_s_at 4368.8 P
Saccharomyces cerevisiae chromosome XVI, complete chromosome sequence. Found forward in NC_001148 between 109147 and 110146 with 100% identity.
2604_s_at 8995.9 P
Saccharomyces cerevisiae chromosome XVI, complete chromosome sequence. Found forward in NC_001148 between 110147 and 111146 with 100% identity.
2605_s_at 12207.4 P
Saccharomyces cerevisiae chromosome XVI, complete chromosome sequence. Found forward in NC_001148 between 111147 and 112146 with 100% identity.
2606_s_at 10723.7 P
Saccharomyces cerevisiae chromosome XVI, complete chromosome sequence. Found forward in NC_001148 between 112147 and 113146 with 100% identity.
2607_s_at 12079.0 P
Saccharomyces cerevisiae chromosome XVI, complete chromosome sequence. Found forward in NC_001148 between 113147 and 113815 with 100% identity.
2608_at 589.5 P
Saccharomyces cerevisiae chromosome XVI, complete chromosome sequence. Found forward in NC_001148 between 140119 and 141118 with 100% identity.
2609_at 1700.7 P
Saccharomyces cerevisiae chromosome XVI, complete chromosome sequence. Found forward in NC_001148 between 141119 and 142118 with 100% identity.
2610_at 110.2 A
Saccharomyces cerevisiae chromosome XVI, complete chromosome sequence. Found forward in NC_001148 between 142119 and 143118 with 100% identity.
2611_at 153.3 P
Saccharomyces cerevisiae chromosome XVI, complete chromosome sequence. Found forward in NC_001148 between 143119 and 144118 with 100% identity.
2612_g_at 1017.9 A
Saccharomyces cerevisiae chromosome XVI, complete chromosome sequence. Found forward in NC_001148 between 143119 and 144118 with 100% identity.
2613_s_at 481.6 A
Saccharomyces cerevisiae chromosome XVI, complete chromosome sequence. Found forward in NC_001148 between 144119 and 145118 with 100% identity.
2614_s_at 525.1 P
Saccharomyces cerevisiae chromosome XVI, complete chromosome sequence. Found forward in NC_001148 between 145119 and 146118 with 100% identity.
2615_s_at 318.9 P
Saccharomyces cerevisiae chromosome XVI, complete chromosome sequence. Found forward in NC_001148 between 146119 and 146628 with 100% identity.
2616_at 10.1 A
Saccharomyces cerevisiae chromosome XVI, complete chromosome sequence. Found forward in

NC_001148 between 385268 and 386267 with 100% identity.
2617_at 564.9 A
Saccharomyces cerevisiae chromosome XVI, complete chromosome sequence. Found forward in NC_001148 between 386268 and 387267 with 100% identity.
2532_g_at 166.4 P
Saccharomyces cerevisiae chromosome XVI, complete chromosome sequence. Found forward in NC_001148 between 386268 and 387267 with 100% identity.
2533_s_at 347.3 P
Saccharomyces cerevisiae chromosome XVI, complete chromosome sequence. Found forward in NC_001148 between 387268 and 388267 with 100% identity.
2534_s_at 1590.0 A
Saccharomyces cerevisiae chromosome XVI, complete chromosome sequence. Found forward in NC_001148 between 388268 and 389267 with 100% identity.
2535_s_at 1811.3 P
Saccharomyces cerevisiae chromosome XVI, complete chromosome sequence. Found forward in NC_001148 between 389268 and 390267 with 100% identity.
2536_s_at 1563.6 P
Saccharomyces cerevisiae chromosome XVI, complete chromosome sequence. Found forward in NC_001148 between 390268 and 391267 with 100% identity.
2537_s_at 4882.1 P
Saccharomyces cerevisiae chromosome XVI, complete chromosome sequence. Found forward in NC_001148 between 391268 and 392267 with 100% identity.
2538_s_at 4285.7 P
Saccharomyces cerevisiae chromosome XVI, complete chromosome sequence. Found forward in NC_001148 between 392268 and 393149 with 100% identity.
2539_at 689.5 P
Saccharomyces cerevisiae chromosome XVI, complete chromosome sequence. Found forward in NC_001148 between 398975 and 399974 with 100% identity.
2540_at 206.6 A
Saccharomyces cerevisiae chromosome XVI, complete chromosome sequence. Found forward in NC_001148 between 399975 and 400974 with 100% identity.
2541_at 108.5 A
Saccharomyces cerevisiae chromosome XVI, complete chromosome sequence. Found forward in NC_001148 between 400975 and 401974 with 100% identity.
2542_at -157.6 A
Saccharomyces cerevisiae chromosome XVI, complete chromosome sequence. Found forward in NC_001148 between 401975 and 402974 with 100% identity.
2543_at -1128.5 A
Saccharomyces cerevisiae chromosome XVI, complete chromosome sequence. Found forward in NC_001148 between 402975 and 403974 with 100% identity.
2544_at -5.4 A
Saccharomyces cerevisiae chromosome XVI, complete chromosome sequence. Found forward in NC_001148 between 403975 and 404451 with 100% identity.
2545_at 211.7 A
Saccharomyces cerevisiae chromosome XVI, complete chromosome sequence. Found forward in NC_001148 between 435759 and 436758 with 100% identity.
2546_at 167.4 P
Saccharomyces cerevisiae chromosome XVI, complete chromosome sequence. Found forward in NC_001148 between 436759 and 437758 with 100% identity.
2547_at 332.9 A
Saccharomyces cerevisiae chromosome XVI, complete chromosome sequence. Found forward in NC_001148 between 437759 and 438758 with 100% identity.
2548_at 226.5 P
Saccharomyces cerevisiae chromosome XVI, complete chromosome sequence. Found forward in NC_001148 between 438759 and 439758 with 100% identity.
2549_at 2.8 P

Saccharomyces cerevisiae chromosome XVI, complete chromosome sequence. Found forward in NC_001148 between 439759 and 440758 with 100% identity.
2550_at	-31.5	A
Saccharomyces cerevisiae chromosome XVI, complete chromosome sequence. Found forward in NC_001148 between 440759 and 441758 with 100% identity.
2551_at	-233.8	A
Saccharomyces cerevisiae chromosome XVI, complete chromosome sequence. Found forward in NC_001148 between 441759 and 442758 with 100% identity.
2552_at	-199.1	A
Saccharomyces cerevisiae chromosome XVI, complete chromosome sequence. Found forward in NC_001148 between 442759 and 443758 with 100% identity.
2553_at	486.8	P
Saccharomyces cerevisiae chromosome XVI, complete chromosome sequence. Found forward in NC_001148 between 443759 and 444574 with 100% identity.
2554_at	488.4	A
Saccharomyces cerevisiae chromosome XVI, complete chromosome sequence. Found forward in NC_001148 between 446337 and 447336 with 100% identity.
2555_at	2441.8	P
Saccharomyces cerevisiae chromosome XVI, complete chromosome sequence. Found forward in NC_001148 between 447337 and 448336 with 100% identity.
2556_at	-271.5	A
Saccharomyces cerevisiae chromosome XVI, complete chromosome sequence. Found forward in NC_001148 between 448337 and 449336 with 100% identity.
2557_at	373.5	P
Saccharomyces cerevisiae chromosome XVI, complete chromosome sequence. Found forward in NC_001148 between 449337 and 450336 with 100% identity.
2558_at	177.4	A
Saccharomyces cerevisiae chromosome XVI, complete chromosome sequence. Found forward in NC_001148 between 450337 and 451336 with 100% identity.
2559_at	670.9	P
Saccharomyces cerevisiae chromosome XVI, complete chromosome sequence. Found forward in NC_001148 between 451337 and 451904 with 100% identity.
2560_at	578.3	A
Saccharomyces cerevisiae chromosome XVI, complete chromosome sequence. Found forward in NC_001148 between 519230 and 520229 with 100% identity.
2561_at	1241.7	P
Saccharomyces cerevisiae chromosome XVI, complete chromosome sequence. Found forward in NC_001148 between 520230 and 521229 with 100% identity.
2562_g_at	25.8	A
Saccharomyces cerevisiae chromosome XVI, complete chromosome sequence. Found forward in NC_001148 between 520230 and 521229 with 100% identity.
2563_s_at	1935.3	P
Saccharomyces cerevisiae chromosome XVI, complete chromosome sequence. Found forward in NC_001148 between 521230 and 522229 with 100% identity.
2564_s_at	3227.0	P
Saccharomyces cerevisiae chromosome XVI, complete chromosome sequence. Found forward in NC_001148 between 522230 and 523229 with 100% identity.
2565_s_at	1209.8	P
Saccharomyces cerevisiae chromosome XVI, complete chromosome sequence. Found forward in NC_001148 between 523230 and 524229 with 100% identity.
2566_s_at	-836.2	P
Saccharomyces cerevisiae chromosome XVI, complete chromosome sequence. Found forward in NC_001148 between 524230 and 524453 with 100% identity.
2567_at	686.4	P
Saccharomyces cerevisiae chromosome XVI, complete chromosome sequence. Found forward in NC_001148 between 536315 and 537314 with 100% identity.

2568_at	17.9	P	Saccharomyces cerevisiae chromosome XVI, complete chromosome sequence. Found forward in NC_001148 between 537315 and 538314 with 100% identity.
2569_at	-892.8	A	Saccharomyces cerevisiae chromosome XVI, complete chromosome sequence. Found forward in NC_001148 between 538315 and 539314 with 100% identity.
2570_at	402.2	P	Saccharomyces cerevisiae chromosome XVI, complete chromosome sequence. Found forward in NC_001148 between 539315 and 540314 with 100% identity.
2571_s_at	1036.4	P	Saccharomyces cerevisiae chromosome XVI, complete chromosome sequence. Found forward in NC_001148 between 540315 and 541314 with 100% identity.
2572_s_at	728.6	P	Saccharomyces cerevisiae chromosome XVI, complete chromosome sequence. Found forward in NC_001148 between 541315 and 541465 with 100% identity.
2573_at	157.1	A	Saccharomyces cerevisiae chromosome XVI, complete chromosome sequence. Found forward in NC_001148 between 542577 and 543576 with 100% identity.
2574_at	1103.2	P	Saccharomyces cerevisiae chromosome XVI, complete chromosome sequence. Found forward in NC_001148 between 543577 and 544576 with 100% identity.
2489_at	153.3	P	Saccharomyces cerevisiae chromosome XVI, complete chromosome sequence. Found forward in NC_001148 between 544577 and 545576 with 100% identity.
2490_s_at	3272.2	P	Saccharomyces cerevisiae chromosome XVI, complete chromosome sequence. Found forward in NC_001148 between 545577 and 546576 with 100% identity.
2491_s_at	3319.9	P	Saccharomyces cerevisiae chromosome XVI, complete chromosome sequence. Found forward in NC_001148 between 546577 and 547576 with 100% identity.
2492_f_at	924.5	P	Saccharomyces cerevisiae chromosome XVI, complete chromosome sequence. Found forward in NC_001148 between 547577 and 547638 with 100% identity.
2493_at	-122.1	A	Saccharomyces cerevisiae chromosome XVI, complete chromosome sequence. Found forward in NC_001148 between 624964 and 625963 with 100% identity.
2494_at	702.9	P	Saccharomyces cerevisiae chromosome XVI, complete chromosome sequence. Found forward in NC_001148 between 625964 and 626963 with 100% identity.
2495_at	104.1	A	Saccharomyces cerevisiae chromosome XVI, complete chromosome sequence. Found forward in NC_001148 between 626964 and 627963 with 100% identity.
2496_g_at	-934.7	A	Saccharomyces cerevisiae chromosome XVI, complete chromosome sequence. Found forward in NC_001148 between 626964 and 627963 with 100% identity.
2497_s_at	281.9	A	Saccharomyces cerevisiae chromosome XVI, complete chromosome sequence. Found forward in NC_001148 between 627964 and 628963 with 100% identity.
2498_s_at	739.7	P	Saccharomyces cerevisiae chromosome XVI, complete chromosome sequence. Found forward in NC_001148 between 628964 and 629963 with 100% identity.
2499_s_at	1872.2	P	Saccharomyces cerevisiae chromosome XVI, complete chromosome sequence. Found forward in NC_001148 between 629964 and 630740 with 100% identity.
2500_at	1184.9	P	Saccharomyces cerevisiae chromosome XVI, complete chromosome sequence. Found forward in NC_001148 between 759478 and 760477 with 100% identity.

2501_g_at 1500.1 P
Saccharomyces cerevisiae chromosome XVI, complete chromosome sequence. Found forward in NC_001148 between 759478 and 760477 with 100% identity.
2502_s_at -251.9 P
Saccharomyces cerevisiae chromosome XVI, complete chromosome sequence. Found forward in NC_001148 between 760478 and 761477 with 100% identity.
2503_s_at 149.4 P
Saccharomyces cerevisiae chromosome XVI, complete chromosome sequence. Found forward in NC_001148 between 761478 and 762477 with 100% identity.
2504_s_at 831.2 P
Saccharomyces cerevisiae chromosome XVI, complete chromosome sequence. Found forward in NC_001148 between 762478 and 763477 with 100% identity.
2505_s_at 1100.7 P
Saccharomyces cerevisiae chromosome XVI, complete chromosome sequence. Found forward in NC_001148 between 763478 and 764477 with 100% identity.
2506_s_at 1775.0 P
Saccharomyces cerevisiae chromosome XVI, complete chromosome sequence. Found forward in NC_001148 between 764478 and 765477 with 100% identity.
2507_s_at 732.3 P
Saccharomyces cerevisiae chromosome XVI, complete chromosome sequence. Found forward in NC_001148 between 765478 and 766477 with 100% identity.
2508_s_at 2204.6 P
Saccharomyces cerevisiae chromosome XVI, complete chromosome sequence. Found forward in NC_001148 between 766478 and 766991 with 100% identity.
2509_at 1151.6 P
Saccharomyces cerevisiae chromosome XVI, complete chromosome sequence. Found forward in NC_001148 between 869140 and 870139 with 100% identity.
2510_at 104.6 P
Saccharomyces cerevisiae chromosome XVI, complete chromosome sequence. Found forward in NC_001148 between 870140 and 871139 with 100% identity.
2511_g_at 790.7 P
Saccharomyces cerevisiae chromosome XVI, complete chromosome sequence. Found forward in NC_001148 between 870140 and 871139 with 100% identity.
2512_s_at 87.7 A
Saccharomyces cerevisiae chromosome XVI, complete chromosome sequence. Found forward in NC_001148 between 871140 and 872139 with 100% identity.
2513_s_at 675.0 P
Saccharomyces cerevisiae chromosome XVI, complete chromosome sequence. Found forward in NC_001148 between 872140 and 873139 with 100% identity.
2514_s_at 1010.2 P
Saccharomyces cerevisiae chromosome XVI, complete chromosome sequence. Found forward in NC_001148 between 873140 and 874139 with 100% identity.
2515_s_at 1154.2 A
Saccharomyces cerevisiae chromosome XVI, complete chromosome sequence. Found forward in NC_001148 between 874140 and 874421 with 100% identity.
2516_at 370.5 A
Saccharomyces cerevisiae chromosome II, complete chromosome sequence. Found forward in NC_001134 between 25441 and 26440 with 100% identity.
2517_at 1174.7 P
Saccharomyces cerevisiae chromosome II, complete chromosome sequence. Found forward in NC_001134 between 26441 and 27440 with 100% identity.
2518_at 461.1 A
Saccharomyces cerevisiae chromosome II, complete chromosome sequence. Found forward in NC_001134 between 27441 and 28440 with 100% identity.
2519_at -2486.6 A
Saccharomyces cerevisiae chromosome II, complete chromosome sequence. Found forward in

NC_001134 between 28441 and 29440 with 100% identity.
2520_at -295.1 A
Saccharomyces cerevisiae chromosome II, complete chromosome sequence. Found forward in NC_001134 between 29441 and 30440 with 100% identity.
2521_f_at 295.6 P
Saccharomyces cerevisiae chromosome II, complete chromosome sequence. Found forward in NC_001134 between 35441 and 35606 with 100% identity.
2522_at -428.4 A
Saccharomyces cerevisiae chromosome II, complete chromosome sequence. Found forward in NC_001134 between 51513 and 52512 with 100% identity.
2523_at 345.6 A
Saccharomyces cerevisiae chromosome II, complete chromosome sequence. Found forward in NC_001134 between 52513 and 53512 with 100% identity.
2524_at 78.3 A
Saccharomyces cerevisiae chromosome II, complete chromosome sequence. Found forward in NC_001134 between 53513 and 54512 with 100% identity.
2525_at 349.6 P
Saccharomyces cerevisiae chromosome II, complete chromosome sequence. Found forward in NC_001134 between 54513 and 55512 with 100% identity.
2526_at 118.6 A
Saccharomyces cerevisiae chromosome II, complete chromosome sequence. Found forward in NC_001134 between 55513 and 56512 with 100% identity.
2527_at 216.8 A
Saccharomyces cerevisiae chromosome II, complete chromosome sequence. Found forward in NC_001134 between 56513 and 57512 with 100% identity.
2528_at 534.3 P
Saccharomyces cerevisiae chromosome II, complete chromosome sequence. Found forward in NC_001134 between 57513 and 58512 with 100% identity.
2529_at -1458.0 A
Saccharomyces cerevisiae chromosome II, complete chromosome sequence. Found forward in NC_001134 between 58513 and 59512 with 100% identity.
2530_at 66.2 P
Saccharomyces cerevisiae chromosome II, complete chromosome sequence. Found forward in NC_001134 between 59513 and 59815 with 100% identity.
2531_at 721.4 P
Saccharomyces cerevisiae chromosome II, complete chromosome sequence. Found forward in NC_001134 between 73564 and 74563 with 100% identity.
2446_at -107.5 A
Saccharomyces cerevisiae chromosome II, complete chromosome sequence. Found forward in NC_001134 between 74564 and 75563 with 100% identity.
2447_g_at 259.8 P
Saccharomyces cerevisiae chromosome II, complete chromosome sequence. Found forward in NC_001134 between 74564 and 75563 with 100% identity.
2448_s_at 1165.3 P
Saccharomyces cerevisiae chromosome II, complete chromosome sequence. Found forward in NC_001134 between 75564 and 76563 with 100% identity.
2449_s_at 2203.9 P
Saccharomyces cerevisiae chromosome II, complete chromosome sequence. Found forward in NC_001134 between 76564 and 77563 with 100% identity.
2450_s_at 1709.7 P
Saccharomyces cerevisiae chromosome II, complete chromosome sequence. Found forward in NC_001134 between 77564 and 78563 with 100% identity.
2451_s_at 5465.2 P
Saccharomyces cerevisiae chromosome II, complete chromosome sequence. Found forward in NC_001134 between 78564 and 79261 with 100% identity.
2452_at 432.7 P

Saccharomyces cerevisiae chromosome II, complete chromosome sequence. Found forward in NC_001134 between 187307 and 188306 with 100% identity.
2453_at 168.3 P
Saccharomyces cerevisiae chromosome II, complete chromosome sequence. Found forward in NC_001134 between 188307 and 189306 with 100% identity.
2454_at -83.8 A
Saccharomyces cerevisiae chromosome II, complete chromosome sequence. Found forward in NC_001134 between 189307 and 190306 with 100% identity.
2455_at 1106.3 A
Saccharomyces cerevisiae chromosome II, complete chromosome sequence. Found forward in NC_001134 between 190307 and 191306 with 100% identity.
2456_at 26.3 A
Saccharomyces cerevisiae chromosome II, complete chromosome sequence. Found forward in NC_001134 between 191307 and 192306 with 100% identity.
2457_at 210.5 A
Saccharomyces cerevisiae chromosome II, complete chromosome sequence. Found forward in NC_001134 between 192307 and 192975 with 100% identity.
2458_g_at 5649.4 P
Saccharomyces cerevisiae chromosome II, complete chromosome sequence. Found forward in NC_001134 between 192307 and 192975 with 100% identity.
2459_at 1994.9 P
Saccharomyces cerevisiae chromosome II, complete chromosome sequence. Found forward in NC_001134 between 220363 and 221362 with 100% identity.
2460_at 9.8 A
Saccharomyces cerevisiae chromosome II, complete chromosome sequence. Found forward in NC_001134 between 226363 and 227362 with 100% identity.
2461_at 746.2 P
Saccharomyces cerevisiae chromosome II, complete chromosome sequence. Found forward in NC_001134 between 227363 and 228362 with 100% identity.
2462_g_at 1266.8 P
Saccharomyces cerevisiae chromosome II, complete chromosome sequence. Found forward in NC_001134 between 227363 and 228362 with 100% identity.
2463_s_at 1176.5 P
Saccharomyces cerevisiae chromosome II, complete chromosome sequence. Found forward in NC_001134 between 228363 and 229362 with 100% identity.
2464_s_at 3024.7 P
Saccharomyces cerevisiae chromosome II, complete chromosome sequence. Found forward in NC_001134 between 229363 and 230362 with 100% identity.
2465_s_at 3065.9 P
Saccharomyces cerevisiae chromosome II, complete chromosome sequence. Found forward in NC_001134 between 230363 and 231362 with 100% identity.
2466_s_at 1431.0 P
Saccharomyces cerevisiae chromosome II, complete chromosome sequence. Found forward in NC_001134 between 231363 and 232362 with 100% identity.
2467_s_at 2907.2 P
Saccharomyces cerevisiae chromosome II, complete chromosome sequence. Found forward in NC_001134 between 232363 and 233362 with 100% identity.
2468_s_at 3670.9 P
Saccharomyces cerevisiae chromosome II, complete chromosome sequence. Found forward in NC_001134 between 233363 and 234362 with 100% identity.
2469_s_at 4158.4 P
Saccharomyces cerevisiae chromosome II, complete chromosome sequence. Found forward in NC_001134 between 234363 and 234580 with 100% identity.
2470_at 1599.0 P
Saccharomyces cerevisiae chromosome II, complete chromosome sequence. Found forward in NC_001134 between 505265 and 506264 with 100% identity.

2471_g_at -301.2 P
Saccharomyces cerevisiae chromosome II, complete chromosome sequence. Found forward in NC_001134 between 505265 and 506264 with 100% identity.
2472_s_at -322.9 M
Saccharomyces cerevisiae chromosome II, complete chromosome sequence. Found forward in NC_001134 between 506265 and 507264 with 100% identity.
2473_s_at 313.2 A
Saccharomyces cerevisiae chromosome II, complete chromosome sequence. Found forward in NC_001134 between 507265 and 508264 with 100% identity.
2474_s_at 145.8 P
Saccharomyces cerevisiae chromosome II, complete chromosome sequence. Found forward in NC_001134 between 508265 and 509264 with 100% identity.
2475_s_at 425.2 P
Saccharomyces cerevisiae chromosome II, complete chromosome sequence. Found forward in NC_001134 between 509265 and 510264 with 100% identity.
2476_s_at 752.1 P
Saccharomyces cerevisiae chromosome II, complete chromosome sequence. Found forward in NC_001134 between 510265 and 511264 with 100% identity.
2477_s_at 820.3 P
Saccharomyces cerevisiae chromosome II, complete chromosome sequence. Found forward in NC_001134 between 511265 and 512233 with 100% identity.
2478_at -48.3 P
Saccharomyces cerevisiae chromosome II, complete chromosome sequence. Found forward in NC_001134 between 517809 and 518808 with 100% identity.
2479_at -50.3 M
Saccharomyces cerevisiae chromosome II, complete chromosome sequence. Found forward in NC_001134 between 518809 and 519808 with 100% identity.
2480_at 334.2 P
Saccharomyces cerevisiae chromosome II, complete chromosome sequence. Found forward in NC_001134 between 519809 and 520808 with 100% identity.
2481_at -26.4 A
Saccharomyces cerevisiae chromosome II, complete chromosome sequence. Found forward in NC_001134 between 520809 and 521808 with 100% identity.
2482_at 246.2 A
Saccharomyces cerevisiae chromosome II, complete chromosome sequence. Found forward in NC_001134 between 521809 and 522808 with 100% identity.
2483_at -108.6 A
Saccharomyces cerevisiae chromosome II, complete chromosome sequence. Found forward in NC_001134 between 522809 and 523808 with 100% identity.
2484_at -186.2 A
Saccharomyces cerevisiae chromosome II, complete chromosome sequence. Found forward in NC_001134 between 523809 and 524808 with 100% identity.
2485_at -357.8 A
Saccharomyces cerevisiae chromosome II, complete chromosome sequence. Found forward in NC_001134 between 524809 and 525808 with 100% identity.
2486_at 58.0 A
Saccharomyces cerevisiae chromosome II, complete chromosome sequence. Found forward in NC_001134 between 525809 and 526808 with 100% identity.
2487_at 467.5 A
Saccharomyces cerevisiae chromosome II, complete chromosome sequence. Found forward in NC_001134 between 526809 and 526984 with 100% identity.
2488_at 328.2 A
Saccharomyces cerevisiae chromosome II, complete chromosome sequence. Found forward in NC_001134 between 637162 and 638161 with 100% identity.
2421_at 68.4 A
Saccharomyces cerevisiae chromosome II, complete chromosome sequence. Found forward in

NC_001134 between 638162 and 639161 with 100% identity.
2422_at 196.7 A
Saccharomyces cerevisiae chromosome II, complete chromosome sequence. Found forward in NC_001134 between 639162 and 640161 with 100% identity.
2423_at 78.8 P
Saccharomyces cerevisiae chromosome II, complete chromosome sequence. Found forward in NC_001134 between 640162 and 641161 with 100% identity.
2424_at 120.1 A
Saccharomyces cerevisiae chromosome II, complete chromosome sequence. Found forward in NC_001134 between 641162 and 642161 with 100% identity.
2425_at 397.4 A
Saccharomyces cerevisiae chromosome II, complete chromosome sequence. Found forward in NC_001134 between 642162 and 642542 with 100% identity.
2426_at 650.1 P
Saccharomyces cerevisiae chromosome II, complete chromosome sequence. Found forward in NC_001134 between 751813 and 752812 with 100% identity.
2427_at 520.7 P
Saccharomyces cerevisiae chromosome II, complete chromosome sequence. Found forward in NC_001134 between 752813 and 753812 with 100% identity.
2428_at -218.8 A
Saccharomyces cerevisiae chromosome II, complete chromosome sequence. Found forward in NC_001134 between 753813 and 754812 with 100% identity.
2429_at -776.3 A
Saccharomyces cerevisiae chromosome II, complete chromosome sequence. Found forward in NC_001134 between 754813 and 755812 with 100% identity.
2430_at 557.9 A
Saccharomyces cerevisiae chromosome II, complete chromosome sequence. Found forward in NC_001134 between 755813 and 756812 with 100% identity.
2431_at 6.7 A
Saccharomyces cerevisiae chromosome II, complete chromosome sequence. Found forward in NC_001134 between 756813 and 757578 with 100% identity.
2432_at 5613.7 P
Saccharomyces cerevisiae chromosome III, complete chromosome sequence. Found forward in NC_001135 between 82220 and 83219 with 100% identity.
2433_at 3755.3 P
Saccharomyces cerevisiae chromosome III, complete chromosome sequence. Found forward in NC_001135 between 83220 and 84219 with 100% identity.
2434_at 1822.1 P
Saccharomyces cerevisiae chromosome III, complete chromosome sequence. Found forward in NC_001135 between 84220 and 85219 with 100% identity.
2435_at 265.1 A
Saccharomyces cerevisiae chromosome III, complete chromosome sequence. Found forward in NC_001135 between 90220 and 91219 with 100% identity.
2436_g_at 1358.8 A
Saccharomyces cerevisiae chromosome III, complete chromosome sequence. Found forward in NC_001135 between 90220 and 91219 with 100% identity.
2437_s_at 4580.8 P
Saccharomyces cerevisiae chromosome III, complete chromosome sequence. Found forward in NC_001135 between 91220 and 91533 with 100% identity.
2438_at -216.2 A
Saccharomyces cerevisiae chromosome III, complete chromosome sequence. Found forward in NC_001135 between 177526 and 178525 with 100% identity.
2439_g_at 199.9 P
Saccharomyces cerevisiae chromosome III, complete chromosome sequence. Found forward in NC_001135 between 177526 and 178525 with 100% identity.
2440_s_at 315.9 M

Saccharomyces cerevisiae chromosome III, complete chromosome sequence. Found forward in NC_001135 between 178526 and 179525 with 100% identity.
2441_s_at 248.4 P
Saccharomyces cerevisiae chromosome III, complete chromosome sequence. Found forward in NC_001135 between 179526 and 180525 with 100% identity.
2442_s_at 1633.4 P
Saccharomyces cerevisiae chromosome III, complete chromosome sequence. Found forward in NC_001135 between 180526 and 181525 with 100% identity.
2443_s_at 747.7 P
Saccharomyces cerevisiae chromosome III, complete chromosome sequence. Found forward in NC_001135 between 181526 and 182525 with 100% identity.
2444_s_at -986.8 A
Saccharomyces cerevisiae chromosome III, complete chromosome sequence. Found forward in NC_001135 between 182526 and 183525 with 100% identity.
2445_s_at 1573.0 P
Saccharomyces cerevisiae chromosome III, complete chromosome sequence. Found forward in NC_001135 between 183526 and 184252 with 100% identity.
2395_at 413.0 A
Saccharomyces cerevisiae chromosome III, complete chromosome sequence. Found forward in NC_001135 between 275986 and 276985 with 100% identity.
2396_at 146.1 P
Saccharomyces cerevisiae chromosome III, complete chromosome sequence. Found forward in NC_001135 between 276986 and 277985 with 100% identity.
2397_at -694.5 A
Saccharomyces cerevisiae chromosome III, complete chromosome sequence. Found forward in NC_001135 between 277986 and 278985 with 100% identity.
2398_g_at 1248.6 P
Saccharomyces cerevisiae chromosome III, complete chromosome sequence. Found forward in NC_001135 between 277986 and 278985 with 100% identity.
2399_s_at 680.2 P
Saccharomyces cerevisiae chromosome III, complete chromosome sequence. Found forward in NC_001135 between 278986 and 279985 with 100% identity.
2400_s_at 1593.9 P
Saccharomyces cerevisiae chromosome III, complete chromosome sequence. Found forward in NC_001135 between 279986 and 280985 with 100% identity.
2401_s_at 1305.9 P
Saccharomyces cerevisiae chromosome III, complete chromosome sequence. Found forward in NC_001135 between 280986 and 281985 with 100% identity.
2402_s_at 1937.4 P
Saccharomyces cerevisiae chromosome III, complete chromosome sequence. Found forward in NC_001135 between 281986 and 282985 with 100% identity.
2403_s_at 5348.9 P
Saccharomyces cerevisiae chromosome III, complete chromosome sequence. Found forward in NC_001135 between 282986 and 283985 with 100% identity.
2404_s_at 3833.8 P
Saccharomyces cerevisiae chromosome III, complete chromosome sequence. Found forward in NC_001135 between 283986 and 284665 with 100% identity.
2405_at 1082.2 A
Saccharomyces cerevisiae chromosome IV, complete chromosome sequence. Found forward in NC_001136 between 79795 and 80794 with 100% identity.
2406_at 119.5 P
Saccharomyces cerevisiae chromosome IV, complete chromosome sequence. Found forward in NC_001136 between 80795 and 81794 with 100% identity.
2407_at 1159.0 P
Saccharomyces cerevisiae chromosome IV, complete chromosome sequence. Found forward in NC_001136 between 81795 and 82794 with 100% identity.

2408_at 492.9 P
Saccharomyces cerevisiae chromosome IV, complete chromosome sequence. Found forward in NC_001136 between 82795 and 83794 with 100% identity.
2409_at 96.2 P
Saccharomyces cerevisiae chromosome IV, complete chromosome sequence. Found forward in NC_001136 between 83795 and 84794 with 100% identity.
2410_g_at 586.5 A
Saccharomyces cerevisiae chromosome IV, complete chromosome sequence. Found forward in NC_001136 between 83795 and 84794 with 100% identity.
2411_s_at 639.5 P
Saccharomyces cerevisiae chromosome IV, complete chromosome sequence. Found forward in NC_001136 between 84795 and 85486 with 100% identity.
2412_at 488.5 A
Saccharomyces cerevisiae chromosome IV, complete chromosome sequence. Found forward in NC_001136 between 149704 and 150703 with 100% identity.
2413_at 231.3 A
Saccharomyces cerevisiae chromosome IV, complete chromosome sequence. Found forward in NC_001136 between 150704 and 151703 with 100% identity.
2414_at 205.0 A
Saccharomyces cerevisiae chromosome IV, complete chromosome sequence. Found forward in NC_001136 between 151704 and 152703 with 100% identity.
2415_at -123.3 A
Saccharomyces cerevisiae chromosome IV, complete chromosome sequence. Found forward in NC_001136 between 152704 and 153703 with 100% identity.
2416_at 230.9 P
Saccharomyces cerevisiae chromosome IV, complete chromosome sequence. Found forward in NC_001136 between 153704 and 154703 with 100% identity.
2417_at 270.8 A
Saccharomyces cerevisiae chromosome IV, complete chromosome sequence. Found forward in NC_001136 between 154704 and 155703 with 100% identity.
2418_at 29.7 A
Saccharomyces cerevisiae chromosome IV, complete chromosome sequence. Found forward in NC_001136 between 155704 and 156703 with 100% identity.
2419_g_at 1119.7 P
Saccharomyces cerevisiae chromosome IV, complete chromosome sequence. Found forward in NC_001136 between 155704 and 156703 with 100% identity.
2420_s_at 1415.6 P
Saccharomyces cerevisiae chromosome IV, complete chromosome sequence. Found forward in NC_001136 between 156704 and 157405 with 100% identity.
2352_at 442.1 A
Saccharomyces cerevisiae chromosome IV, complete chromosome sequence. Found forward in NC_001136 between 205861 and 206860 with 100% identity.
2353_at 867.8 A
Saccharomyces cerevisiae chromosome IV, complete chromosome sequence. Found forward in NC_001136 between 206861 and 207860 with 100% identity.
2354_at -440.6 A
Saccharomyces cerevisiae chromosome IV, complete chromosome sequence. Found forward in NC_001136 between 207861 and 208860 with 100% identity.
2355_at -142.4 A
Saccharomyces cerevisiae chromosome IV, complete chromosome sequence. Found forward in NC_001136 between 208861 and 209860 with 100% identity.
2356_at 466.2 P
Saccharomyces cerevisiae chromosome IV, complete chromosome sequence. Found forward in NC_001136 between 209861 and 210860 with 100% identity.
2357_at 726.6 P
Saccharomyces cerevisiae chromosome IV, complete chromosome sequence. Found forward in

NC_001136 between 210861 and 211376 with 100% identity.
2358_at 70.9 A
Saccharomyces cerevisiae chromosome IV, complete chromosome sequence. Found forward in NC_001136 between 257132 and 258131 with 100% identity.
2359_at -21.5 A
Saccharomyces cerevisiae chromosome IV, complete chromosome sequence. Found forward in NC_001136 between 258132 and 259131 with 100% identity.
2360_g_at 1342.5 P
Saccharomyces cerevisiae chromosome IV, complete chromosome sequence. Found forward in NC_001136 between 258132 and 259131 with 100% identity.
2361_s_at 2872.8 P
Saccharomyces cerevisiae chromosome IV, complete chromosome sequence. Found forward in NC_001136 between 259132 and 260131 with 100% identity.
2362_s_at 2609.6 P
Saccharomyces cerevisiae chromosome IV, complete chromosome sequence. Found forward in NC_001136 between 260132 and 261131 with 100% identity.
2363_s_at 2293.6 P
Saccharomyces cerevisiae chromosome IV, complete chromosome sequence. Found forward in NC_001136 between 261132 and 262131 with 100% identity.
2364_s_at 2534.8 P
Saccharomyces cerevisiae chromosome IV, complete chromosome sequence. Found forward in NC_001136 between 262132 and 262724 with 100% identity.
2365_at 300.6 A
Saccharomyces cerevisiae chromosome IV, complete chromosome sequence. Found forward in NC_001136 between 344736 and 345735 with 100% identity.
2366_s_at -333.7 P
Saccharomyces cerevisiae chromosome IV, complete chromosome sequence. Found forward in NC_001136 between 345736 and 346735 with 100% identity.
2367_s_at 2958.7 P
Saccharomyces cerevisiae chromosome IV, complete chromosome sequence. Found forward in NC_001136 between 346736 and 347735 with 100% identity.
2368_s_at 497.8 P
Saccharomyces cerevisiae chromosome IV, complete chromosome sequence. Found forward in NC_001136 between 347736 and 348735 with 100% identity.
2369_s_at 441.4 P
Saccharomyces cerevisiae chromosome IV, complete chromosome sequence. Found forward in NC_001136 between 348736 and 349735 with 100% identity.
2370_s_at 1052.4 P
Saccharomyces cerevisiae chromosome IV, complete chromosome sequence. Found forward in NC_001136 between 349736 and 350536 with 100% identity.
2371_at 3.0 A
Saccharomyces cerevisiae chromosome IV, complete chromosome sequence. Found forward in NC_001136 between 618990 and 619989 with 100% identity.
2372_at 1214.6 P
Saccharomyces cerevisiae chromosome IV, complete chromosome sequence. Found forward in NC_001136 between 619990 and 620989 with 100% identity.
2373_at -1228.1 A
Saccharomyces cerevisiae chromosome IV, complete chromosome sequence. Found forward in NC_001136 between 620990 and 621989 with 100% identity.
2374_at 1710.2 P
Saccharomyces cerevisiae chromosome IV, complete chromosome sequence. Found forward in NC_001136 between 621990 and 622989 with 100% identity.
2375_s_at 455.3 P
Saccharomyces cerevisiae chromosome IV, complete chromosome sequence. Found forward in NC_001136 between 622990 and 623989 with 100% identity.
2376_s_at 1900.3 P

Saccharomyces cerevisiae chromosome IV, complete chromosome sequence. Found forward in NC_001136 between 623990 and 624214 with 100% identity.

2377_at 1279.8 P

Saccharomyces cerevisiae chromosome IV, complete chromosome sequence. Found forward in NC_001136 between 630598 and 631597 with 100% identity.

2378_g_at 3991.7 P

Saccharomyces cerevisiae chromosome IV, complete chromosome sequence. Found forward in NC_001136 between 630598 and 631597 with 100% identity.

2379_s_at 1963.6 P

Saccharomyces cerevisiae chromosome IV, complete chromosome sequence. Found forward in NC_001136 between 631598 and 632597 with 100% identity.

2380_s_at 3357.3 P

Saccharomyces cerevisiae chromosome IV, complete chromosome sequence. Found forward in NC_001136 between 632598 and 633597 with 100% identity.

2381_s_at 3495.4 P

Saccharomyces cerevisiae chromosome IV, complete chromosome sequence. Found forward in NC_001136 between 633598 and 634597 with 100% identity.

2382_s_at 4811.3 P

Saccharomyces cerevisiae chromosome IV, complete chromosome sequence. Found forward in NC_001136 between 634598 and 635597 with 100% identity.

2383_at 683.2 A

Saccharomyces cerevisiae chromosome IV, complete chromosome sequence. Found forward in NC_001136 between 735394 and 736393 with 100% identity.

2384_at 588.9 P

Saccharomyces cerevisiae chromosome IV, complete chromosome sequence. Found forward in NC_001136 between 736394 and 737393 with 100% identity.

2385_at -266.8 A

Saccharomyces cerevisiae chromosome IV, complete chromosome sequence. Found forward in NC_001136 between 737394 and 738393 with 100% identity.

2386_at 267.1 A

Saccharomyces cerevisiae chromosome IV, complete chromosome sequence. Found forward in NC_001136 between 738394 and 739393 with 100% identity.

2387_at -39.4 A

Saccharomyces cerevisiae chromosome IV, complete chromosome sequence. Found forward in NC_001136 between 739394 and 740393 with 100% identity.

2388_s_at 191.3 P

Saccharomyces cerevisiae chromosome IV, complete chromosome sequence. Found forward in NC_001136 between 756048 and 757047 with 100% identity.

2389_s_at 19.8 A

Saccharomyces cerevisiae chromosome IV, complete chromosome sequence. Found forward in NC_001136 between 757048 and 758047 with 100% identity.

2390_s_at 169.2 P

Saccharomyces cerevisiae chromosome IV, complete chromosome sequence. Found forward in NC_001136 between 759048 and 760047 with 100% identity.

2391_s_at 91.8 P

Saccharomyces cerevisiae chromosome IV, complete chromosome sequence. Found forward in NC_001136 between 760048 and 761047 with 100% identity.

2392_s_at 867.6 P

Saccharomyces cerevisiae chromosome IV, complete chromosome sequence. Found forward in NC_001136 between 761048 and 762047 with 100% identity.

2393_s_at 2062.3 P

Saccharomyces cerevisiae chromosome IV, complete chromosome sequence. Found forward in NC_001136 between 762048 and 763047 with 100% identity.

2394_s_at 1623.9 P

Saccharomyces cerevisiae chromosome IV, complete chromosome sequence. Found forward in NC_001136 between 763048 and 763367 with 100% identity.

2309_at 430.6 A
Saccharomyces cerevisiae chromosome IV, complete chromosome sequence. Found forward in NC_001136 between 796686 and 797685 with 100% identity.
2310_at -196.0 P
Saccharomyces cerevisiae chromosome IV, complete chromosome sequence. Found forward in NC_001136 between 797686 and 798685 with 100% identity.
2311_at 1030.3 P
Saccharomyces cerevisiae chromosome IV, complete chromosome sequence. Found forward in NC_001136 between 798686 and 799685 with 100% identity.
2312_at 729.9 A
Saccharomyces cerevisiae chromosome IV, complete chromosome sequence. Found forward in NC_001136 between 799686 and 800685 with 100% identity.
2313_at 795.7 P
Saccharomyces cerevisiae chromosome IV, complete chromosome sequence. Found forward in NC_001136 between 800686 and 801685 with 100% identity.
2314_at 927.9 P
Saccharomyces cerevisiae chromosome IV, complete chromosome sequence. Found forward in NC_001136 between 801686 and 802685 with 100% identity.
2315_at 810.9 P
Saccharomyces cerevisiae chromosome IV, complete chromosome sequence. Found forward in NC_001136 between 802686 and 803685 with 100% identity.
2316_at 203.2 A
Saccharomyces cerevisiae chromosome IV, complete chromosome sequence. Found forward in NC_001136 between 877250 and 878249 with 100% identity.
2317_at 300.8 P
Saccharomyces cerevisiae chromosome IV, complete chromosome sequence. Found forward in NC_001136 between 878250 and 879249 with 100% identity.
2319_f_at -250.2 A
Saccharomyces cerevisiae chromosome IV, complete chromosome sequence. Found forward in NC_001136 between 647450 and 647656 with 100% identity.
2320_at -99.4 A
Saccharomyces cerevisiae chromosome IV, complete chromosome sequence. Found forward in NC_001136 between 1133751 and 1134750 with 100% identity.
2321_at 386.1 P
Saccharomyces cerevisiae chromosome IV, complete chromosome sequence. Found forward in NC_001136 between 1134751 and 1135750 with 100% identity.
2322_at 959.5 P
Saccharomyces cerevisiae chromosome IV, complete chromosome sequence. Found forward in NC_001136 between 1135751 and 1136750 with 100% identity.
2323_g_at 767.0 P
Saccharomyces cerevisiae chromosome IV, complete chromosome sequence. Found forward in NC_001136 between 1135751 and 1136750 with 100% identity.
2324_s_at 10.0 P
Saccharomyces cerevisiae chromosome IV, complete chromosome sequence. Found forward in NC_001136 between 1136751 and 1137750 with 100% identity.
2325_s_at 1178.8 P
Saccharomyces cerevisiae chromosome IV, complete chromosome sequence. Found forward in NC_001136 between 1137751 and 1138750 with 100% identity.
2326_s_at 1151.5 P
Saccharomyces cerevisiae chromosome IV, complete chromosome sequence. Found forward in NC_001136 between 1138751 and 1139750 with 100% identity.
2327_s_at 853.4 P
Saccharomyces cerevisiae chromosome IV, complete chromosome sequence. Found forward in NC_001136 between 1139751 and 1139967 with 100% identity.
2328_at 94.7 P
Saccharomyces cerevisiae chromosome IV, complete chromosome sequence. Found forward in

NC_001136 between 1305061 and 1306060 with 100% identity.
2329_at 539.4 P
Saccharomyces cerevisiae chromosome IV, complete chromosome sequence. Found forward in NC_001136 between 1306061 and 1307060 with 100% identity.
2330_g_at 324.9 P
Saccharomyces cerevisiae chromosome IV, complete chromosome sequence. Found forward in NC_001136 between 1306061 and 1307060 with 100% identity.
2331_s_at 1319.1 P
Saccharomyces cerevisiae chromosome IV, complete chromosome sequence. Found forward in NC_001136 between 1307061 and 1308060 with 100% identity.
2332_s_at 2868.3 P
Saccharomyces cerevisiae chromosome IV, complete chromosome sequence. Found forward in NC_001136 between 1308061 and 1309060 with 100% identity.
2333_s_at 1915.5 P
Saccharomyces cerevisiae chromosome IV, complete chromosome sequence. Found forward in NC_001136 between 1309061 and 1310060 with 100% identity.
2334_s_at 1199.8 P
Saccharomyces cerevisiae chromosome IV, complete chromosome sequence. Found forward in NC_001136 between 1310061 and 1311060 with 100% identity.
2335_s_at 1456.4 P
Saccharomyces cerevisiae chromosome IV, complete chromosome sequence. Found forward in NC_001136 between 1311061 and 1311164 with 100% identity.
2336_at 1545.0 P
Saccharomyces cerevisiae chromosome IV, complete chromosome sequence. Found forward in NC_001136 between 1346165 and 1347164 with 100% identity.
2337_at -275.7 A
Saccharomyces cerevisiae chromosome IV, complete chromosome sequence. Found forward in NC_001136 between 1347165 and 1348164 with 100% identity.
2338_at -293.5 A
Saccharomyces cerevisiae chromosome IV, complete chromosome sequence. Found forward in NC_001136 between 1348165 and 1349164 with 100% identity.
2339_at 606.0 A
Saccharomyces cerevisiae chromosome IV, complete chromosome sequence. Found forward in NC_001136 between 1349165 and 1350164 with 100% identity.
2340_at 264.8 P
Saccharomyces cerevisiae chromosome IV, complete chromosome sequence. Found forward in NC_001136 between 1350165 and 1351164 with 100% identity.
2341_g_at 1150.0 P
Saccharomyces cerevisiae chromosome IV, complete chromosome sequence. Found forward in NC_001136 between 1350165 and 1351164 with 100% identity.
2342_s_at 1062.9 A
Saccharomyces cerevisiae chromosome IV, complete chromosome sequence. Found forward in NC_001136 between 1351165 and 1351842 with 100% identity.
2343_at 2041.8 P
Saccharomyces cerevisiae chromosome IV, complete chromosome sequence. Found forward in NC_001136 between 1369375 and 1370374 with 100% identity.
2344_g_at 3711.6 P
Saccharomyces cerevisiae chromosome IV, complete chromosome sequence. Found forward in NC_001136 between 1369375 and 1370374 with 100% identity.
2345_s_at 686.3 P
Saccharomyces cerevisiae chromosome IV, complete chromosome sequence. Found forward in NC_001136 between 1370375 and 1371374 with 100% identity.
2346_s_at 159.2 A
Saccharomyces cerevisiae chromosome IV, complete chromosome sequence. Found forward in NC_001136 between 1371375 and 1372374 with 100% identity.
2347_s_at 15.5 A

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

2348_s_at 1879.9 P

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

2349_s_at 229.4 P

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

2350_s_at 2426.8 P

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

2351_s_at 1296.4 P

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

2266_s_at 4635.3 P

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

2267_s_at 2892.1 P

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

2268_at 284.8 P

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

2269_at 302.3 A

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

2270_at 270.1 P

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

2271_at -372.0 A

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

2272_at 416.6 P

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

2273_at -171.2 A

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

2274_at 66.2 A

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

2275_g_at -1287.9 A

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

2276_at 366.5 A

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

2277_at 57.9 P

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

2278_at 443.8 P

Saccharomyces cerevisiae chromosome V, complete chromosome sequence. Found forward in NC_001137 between 111004 and 112003 with 100% identity.

2279_g_at 1845.5 P

Saccharomyces cerevisiae chromosome V, complete chromosome sequence. Found forward in NC_001137 between 111004 and 112003 with 100% identity.

2280_s_at 2050.9 P
Saccharomyces cerevisiae chromosome V, complete chromosome sequence. Found forward in NC_001137 between 112004 and 113003 with 100% identity.
2281_s_at 1970.7 P
Saccharomyces cerevisiae chromosome V, complete chromosome sequence. Found forward in NC_001137 between 113004 and 114003 with 100% identity.
2282_s_at 5159.4 P
Saccharomyces cerevisiae chromosome V, complete chromosome sequence. Found forward in NC_001137 between 114004 and 115003 with 100% identity.
2283_s_at 3309.1 P
Saccharomyces cerevisiae chromosome V, complete chromosome sequence. Found forward in NC_001137 between 115004 and 115300 with 100% identity.
2284_at 109.5 P
Saccharomyces cerevisiae chromosome V, complete chromosome sequence. Found forward in NC_001137 between 425685 and 426684 with 100% identity.
2285_at -216.4 A
Saccharomyces cerevisiae chromosome V, complete chromosome sequence. Found forward in NC_001137 between 426685 and 427684 with 100% identity.
2286_at 928.8 A
Saccharomyces cerevisiae chromosome V, complete chromosome sequence. Found forward in NC_001137 between 427685 and 428684 with 100% identity.
2287_at 245.4 A
Saccharomyces cerevisiae chromosome V, complete chromosome sequence. Found forward in NC_001137 between 428685 and 429684 with 100% identity.
2288_at 1912.1 A
Saccharomyces cerevisiae chromosome V, complete chromosome sequence. Found forward in NC_001137 between 429685 and 430684 with 100% identity.
2289_at -537.6 A
Saccharomyces cerevisiae chromosome V, complete chromosome sequence. Found forward in NC_001137 between 430685 and 431126 with 100% identity.
2290_at 793.4 P
Saccharomyces cerevisiae chromosome V, complete chromosome sequence. Found forward in NC_001137 between 442412 and 443411 with 100% identity.
2291_g_at 2432.3 P
Saccharomyces cerevisiae chromosome V, complete chromosome sequence. Found forward in NC_001137 between 442412 and 443411 with 100% identity.
2294_f_at 3206.7 P
Saccharomyces cerevisiae chromosome V, complete chromosome sequence. Found forward in NC_001137 between 446412 and 447411 with 100% identity.
2295_at 697.4 P
Saccharomyces cerevisiae chromosome V, complete chromosome sequence. Found forward in NC_001137 between 476841 and 477840 with 100% identity.
2296_at 1243.6 P
Saccharomyces cerevisiae chromosome V, complete chromosome sequence. Found forward in NC_001137 between 477841 and 478840 with 100% identity.
2297_at 88.9 A
Saccharomyces cerevisiae chromosome V, complete chromosome sequence. Found forward in NC_001137 between 478841 and 479840 with 100% identity.
2298_at -10.0 A
Saccharomyces cerevisiae chromosome V, complete chromosome sequence. Found forward in NC_001137 between 479841 and 480840 with 100% identity.
2299_at -58.9 P
Saccharomyces cerevisiae chromosome V, complete chromosome sequence. Found forward in NC_001137 between 480841 and 481840 with 100% identity.
2300_at 976.1 A
Saccharomyces cerevisiae chromosome V, complete chromosome sequence. Found forward in

NC_001137 between 481841 and 482840 with 100% identity.

2301_at 75.9 A

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

2302_at 310.9 A

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

2303_f_at 1177.1 A

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

2306_at 787.5 P

Saccharomyces cerevisiae chromosome V, complete chromosome sequence. Found forward in NC_001137 between 497954 and 498953 with 100% identity.

2307_at 157.8 P

Saccharomyces cerevisiae chromosome V, complete chromosome sequence. Found forward in NC_001137 between 498954 and 499172 with 100% identity.

2308_at -647.6 A

Saccharomyces cerevisiae chromosome V, complete chromosome sequence. Found forward in NC_001137 between 530026 and 531025 with 100% identity.

2223_at 74.0 A

Saccharomyces cerevisiae chromosome V, complete chromosome sequence. Found forward in NC_001137 between 531026 and 532025 with 100% identity.

2224_at 345.8 A

Saccharomyces cerevisiae chromosome V, complete chromosome sequence. Found forward in NC_001137 between 532026 and 533025 with 100% identity.

2225_at 377.4 P

Saccharomyces cerevisiae chromosome V, complete chromosome sequence. Found forward in NC_001137 between 533026 and 534025 with 100% identity.

2226_at 1099.8 P

Saccharomyces cerevisiae chromosome V, complete chromosome sequence. Found forward in NC_001137 between 534026 and 535025 with 100% identity.

2227_at -110.9 A

Saccharomyces cerevisiae chromosome V, complete chromosome sequence. Found forward in NC_001137 between 535026 and 536025 with 100% identity.

2228_at 94.7 A

Saccharomyces cerevisiae chromosome V, complete chromosome sequence. Found forward in NC_001137 between 536026 and 536271 with 100% identity.

2229_at 153.5 A

Saccharomyces cerevisiae chromosome VI, complete chromosome sequence. Found forward in NC_001138 between 69614 and 70613 with 100% identity.

2230_at 599.8 P

Saccharomyces cerevisiae chromosome VI, complete chromosome sequence. Found forward in NC_001138 between 70614 and 71613 with 100% identity.

2231_at -220.7 M

Saccharomyces cerevisiae chromosome VI, complete chromosome sequence. Found forward in NC_001138 between 71614 and 72613 with 100% identity.

2232_at 265.7 A

Saccharomyces cerevisiae chromosome VI, complete chromosome sequence. Found forward in NC_001138 between 72614 and 73613 with 100% identity.

2233_at 534.0 P

Saccharomyces cerevisiae chromosome VI, complete chromosome sequence. Found forward in NC_001138 between 73614 and 74613 with 100% identity.

2234_at 220.8 A

Saccharomyces cerevisiae chromosome VI, complete chromosome sequence. Found forward in NC_001138 between 74614 and 74871 with 100% identity.

2235_at 1090.1 P

Saccharomyces cerevisiae chromosome VI, complete chromosome sequence. Found forward in NC_001138 between 136029 and 137028 with 100% identity.

2236_at -220.6 A

Saccharomyces cerevisiae chromosome VI, complete chromosome sequence. Found forward in NC_001138 between 137029 and 138028 with 100% identity.

2237_at 36.0 A

Saccharomyces cerevisiae chromosome VI, complete chromosome sequence. Found forward in NC_001138 between 143029 and 144028 with 100% identity.

2238_at -212.1 A

Saccharomyces cerevisiae chromosome VI, complete chromosome sequence. Found forward in NC_001138 between 144029 and 145028 with 100% identity.

2239_at 1301.0 P

Saccharomyces cerevisiae chromosome VI, complete chromosome sequence. Found forward in NC_001138 between 145029 and 145108 with 100% identity.

2240_at -643.8 A

Saccharomyces cerevisiae chromosome VI, complete chromosome sequence. Found forward in NC_001138 between 184470 and 185469 with 100% identity.

2241_s_at 590.5 P

Saccharomyces cerevisiae chromosome VI, complete chromosome sequence. Found forward in NC_001138 between 185470 and 186469 with 100% identity.

2242_s_at 537.4 A

Saccharomyces cerevisiae chromosome VI, complete chromosome sequence. Found forward in NC_001138 between 186470 and 187469 with 100% identity.

2243_s_at 535.2 P

Saccharomyces cerevisiae chromosome VI, complete chromosome sequence. Found forward in NC_001138 between 187470 and 188469 with 100% identity.

2244_s_at 840.4 P

Saccharomyces cerevisiae chromosome VI, complete chromosome sequence. Found forward in NC_001138 between 188470 and 189469 with 100% identity.

2245_s_at 1581.9 A

Saccharomyces cerevisiae chromosome VI, complete chromosome sequence. Found forward in NC_001138 between 189470 and 190469 with 100% identity.

2246_s_at 2208.7 P

Saccharomyces cerevisiae chromosome VI, complete chromosome sequence. Found forward in NC_001138 between 190470 and 190825 with 100% identity.

2247_at 1185.6 P

Saccharomyces cerevisiae chromosome VII, complete chromosome sequence. Found forward in NC_001139 between 16307 and 17306 with 100% identity.

2248_at 229.1 A

Saccharomyces cerevisiae chromosome VII, complete chromosome sequence. Found forward in NC_001139 between 17307 and 18306 with 100% identity.

2249_at -68.6 A

Saccharomyces cerevisiae chromosome VII, complete chromosome sequence. Found forward in NC_001139 between 18307 and 19306 with 100% identity.

2250_at 2971.9 P

Saccharomyces cerevisiae chromosome VII, complete chromosome sequence. Found forward in NC_001139 between 19307 and 20306 with 100% identity.

2251_at 419.9 P

Saccharomyces cerevisiae chromosome VII, complete chromosome sequence. Found forward in NC_001139 between 20307 and 21306 with 100% identity.

2252_g_at 1355.7 P

Saccharomyces cerevisiae chromosome VII, complete chromosome sequence. Found forward in NC_001139 between 20307 and 21306 with 100% identity.

2253_s_at -139.6 P

Saccharomyces cerevisiae chromosome VII, complete chromosome sequence. Found forward in NC_001139 between 21307 and 21608 with 100% identity.

2254_at 218.9 A
Saccharomyces cerevisiae chromosome VII, complete chromosome sequence. Found forward in NC_001139 between 103045 and 104044 with 100% identity.
2255_at 294.3 P
Saccharomyces cerevisiae chromosome VII, complete chromosome sequence. Found forward in NC_001139 between 104045 and 105044 with 100% identity.
2256_at -219.0 A
Saccharomyces cerevisiae chromosome VII, complete chromosome sequence. Found forward in NC_001139 between 105045 and 106044 with 100% identity.
2257_at 1328.5 P
Saccharomyces cerevisiae chromosome VII, complete chromosome sequence. Found forward in NC_001139 between 106045 and 107044 with 100% identity.
2258_at 243.4 P
Saccharomyces cerevisiae chromosome VII, complete chromosome sequence. Found forward in NC_001139 between 107045 and 108044 with 100% identity.
2259_at 610.2 P
Saccharomyces cerevisiae chromosome VII, complete chromosome sequence. Found forward in NC_001139 between 108045 and 109044 with 100% identity.
2260_g_at 312.1 P
Saccharomyces cerevisiae chromosome VII, complete chromosome sequence. Found forward in NC_001139 between 108045 and 109044 with 100% identity.
2261_s_at 924.9 M
Saccharomyces cerevisiae chromosome VII, complete chromosome sequence. Found forward in NC_001139 between 109045 and 109906 with 100% identity.
2262_at 1623.2 P
Saccharomyces cerevisiae chromosome VII, complete chromosome sequence. Found forward in NC_001139 between 131050 and 132049 with 100% identity.
2263_g_at 1725.8 P
Saccharomyces cerevisiae chromosome VII, complete chromosome sequence. Found forward in NC_001139 between 131050 and 132049 with 100% identity.
2264_s_at 2298.4 P
Saccharomyces cerevisiae chromosome VII, complete chromosome sequence. Found forward in NC_001139 between 132050 and 133049 with 100% identity.
2265_s_at 1482.4 P
Saccharomyces cerevisiae chromosome VII, complete chromosome sequence. Found forward in NC_001139 between 133050 and 134049 with 100% identity.
2180_s_at 2622.9 P
Saccharomyces cerevisiae chromosome VII, complete chromosome sequence. Found forward in NC_001139 between 134050 and 135049 with 100% identity.
2181_s_at 2989.5 P
Saccharomyces cerevisiae chromosome VII, complete chromosome sequence. Found forward in NC_001139 between 135050 and 136049 with 100% identity.
2182_s_at 6604.5 P
Saccharomyces cerevisiae chromosome VII, complete chromosome sequence. Found forward in NC_001139 between 136050 and 137049 with 100% identity.
2183_s_at 10632.8 P
Saccharomyces cerevisiae chromosome VII, complete chromosome sequence. Found forward in NC_001139 between 137050 and 138049 with 100% identity.
2184_s_at 7060.5 P
Saccharomyces cerevisiae chromosome VII, complete chromosome sequence. Found forward in NC_001139 between 138050 and 139047 with 100% identity.
2185_at 987.4 P
Saccharomyces cerevisiae chromosome VII, complete chromosome sequence. Found forward in NC_001139 between 176031 and 177030 with 100% identity.
2186_at 1035.5 P
Saccharomyces cerevisiae chromosome VII, complete chromosome sequence. Found forward in

NC_001139 between 177031 and 178030 with 100% identity.
2187_at 641.2 P
Saccharomyces cerevisiae chromosome VII, complete chromosome sequence. Found forward in NC_001139 between 178031 and 179030 with 100% identity.
2188_at 235.3 P
Saccharomyces cerevisiae chromosome VII, complete chromosome sequence. Found forward in NC_001139 between 179031 and 180030 with 100% identity.
2189_at 338.3 P
Saccharomyces cerevisiae chromosome VII, complete chromosome sequence. Found forward in NC_001139 between 180031 and 181030 with 100% identity.
2190_g_at 2209.5 P
Saccharomyces cerevisiae chromosome VII, complete chromosome sequence. Found forward in NC_001139 between 180031 and 181030 with 100% identity.
2191_s_at 2618.9 P
Saccharomyces cerevisiae chromosome VII, complete chromosome sequence. Found forward in NC_001139 between 181031 and 181622 with 100% identity.
2192_at -308.8 A
Saccharomyces cerevisiae chromosome VII, complete chromosome sequence. Found forward in NC_001139 between 241856 and 242855 with 100% identity.
2193_at 212.7 M
Saccharomyces cerevisiae chromosome VII, complete chromosome sequence. Found forward in NC_001139 between 242856 and 243855 with 100% identity.
2194_at 3514.2 A
Saccharomyces cerevisiae chromosome VII, complete chromosome sequence. Found forward in NC_001139 between 243856 and 244855 with 100% identity.
2195_at 800.1 M
Saccharomyces cerevisiae chromosome VII, complete chromosome sequence. Found forward in NC_001139 between 244856 and 245855 with 100% identity.
2196_s_at 1997.7 P
Saccharomyces cerevisiae chromosome VII, complete chromosome sequence. Found forward in NC_001139 between 245856 and 246855 with 100% identity.
2197_s_at 3167.4 P
Saccharomyces cerevisiae chromosome VII, complete chromosome sequence. Found forward in NC_001139 between 246856 and 247627 with 100% identity.
2198_at 309.1 P
Saccharomyces cerevisiae chromosome VII, complete chromosome sequence. Found forward in NC_001139 between 331616 and 332615 with 100% identity.
2199_at -32.3 A
Saccharomyces cerevisiae chromosome VII, complete chromosome sequence. Found forward in NC_001139 between 332616 and 333615 with 100% identity.
2200_at -215.5 A
Saccharomyces cerevisiae chromosome VII, complete chromosome sequence. Found forward in NC_001139 between 333616 and 334615 with 100% identity.
2201_at -2783.4 A
Saccharomyces cerevisiae chromosome VII, complete chromosome sequence. Found forward in NC_001139 between 334616 and 335615 with 100% identity.
2202_g_at 713.6 P
Saccharomyces cerevisiae chromosome VII, complete chromosome sequence. Found forward in NC_001139 between 334616 and 335615 with 100% identity.
2203_s_at 1699.4 P
Saccharomyces cerevisiae chromosome VII, complete chromosome sequence. Found forward in NC_001139 between 335616 and 336615 with 100% identity.
2204_s_at 2590.7 P
Saccharomyces cerevisiae chromosome VII, complete chromosome sequence. Found forward in NC_001139 between 336616 and 337137 with 100% identity.
2205_at 2515.2 P

Saccharomyces cerevisiae chromosome VII, complete chromosome sequence. Found forward in NC_001139 between 547463 and 548462 with 100% identity.
2206_g_at 739.7 P
Saccharomyces cerevisiae chromosome VII, complete chromosome sequence. Found forward in NC_001139 between 547463 and 548462 with 100% identity.
2207_s_at 1200.9 P
Saccharomyces cerevisiae chromosome VII, complete chromosome sequence. Found forward in NC_001139 between 548463 and 549462 with 100% identity.
2208_s_at 1423.5 P
Saccharomyces cerevisiae chromosome VII, complete chromosome sequence. Found forward in NC_001139 between 549463 and 550462 with 100% identity.
2209_s_at 2139.0 P
Saccharomyces cerevisiae chromosome VII, complete chromosome sequence. Found forward in NC_001139 between 550463 and 551462 with 100% identity.
2210_s_at 4923.7 P
Saccharomyces cerevisiae chromosome VII, complete chromosome sequence. Found forward in NC_001139 between 551463 and 552462 with 100% identity.
2211_s_at 4593.9 P
Saccharomyces cerevisiae chromosome VII, complete chromosome sequence. Found forward in NC_001139 between 552463 and 553445 with 100% identity.
2212_at 960.2 P
Saccharomyces cerevisiae chromosome VII, complete chromosome sequence. Found forward in NC_001139 between 659764 and 660763 with 100% identity.
2213_at -1419.0 A
Saccharomyces cerevisiae chromosome VII, complete chromosome sequence. Found forward in NC_001139 between 660764 and 661763 with 100% identity.
2214_at -973.4 P
Saccharomyces cerevisiae chromosome VII, complete chromosome sequence. Found forward in NC_001139 between 661764 and 662763 with 100% identity.
2215_g_at 3887.5 P
Saccharomyces cerevisiae chromosome VII, complete chromosome sequence. Found forward in NC_001139 between 661764 and 662763 with 100% identity.
2216_s_at 4334.0 P
Saccharomyces cerevisiae chromosome VII, complete chromosome sequence. Found forward in NC_001139 between 662764 and 663763 with 100% identity.
2217_s_at 3870.2 P
Saccharomyces cerevisiae chromosome VII, complete chromosome sequence. Found forward in NC_001139 between 663764 and 664763 with 100% identity.
2218_s_at 4024.6 P
Saccharomyces cerevisiae chromosome VII, complete chromosome sequence. Found forward in NC_001139 between 664764 and 665565 with 100% identity.
2219_at -396.1 A
Saccharomyces cerevisiae chromosome VII, complete chromosome sequence. Found forward in NC_001139 between 683060 and 684059 with 100% identity.
2220_at -79.0 A
Saccharomyces cerevisiae chromosome VII, complete chromosome sequence. Found forward in NC_001139 between 684060 and 685059 with 100% identity.
2221_at -202.5 A
Saccharomyces cerevisiae chromosome VII, complete chromosome sequence. Found forward in NC_001139 between 685060 and 686059 with 100% identity.
2222_at 353.1 A
Saccharomyces cerevisiae chromosome VII, complete chromosome sequence. Found forward in NC_001139 between 686060 and 687059 with 100% identity.
2138_at 319.9 P
Saccharomyces cerevisiae chromosome VII, complete chromosome sequence. Found forward in NC_001139 between 687060 and 688059 with 100% identity.

2139_g_at	684.4	A
Saccharomyces cerevisiae chromosome VII, complete chromosome sequence. Found forward in NC_001139 between 687060 and 688059 with 100% identity.
2140_s_at	448.7	P
Saccharomyces cerevisiae chromosome VII, complete chromosome sequence. Found forward in NC_001139 between 688060 and 689059 with 100% identity.
2141_s_at	2016.3	P
Saccharomyces cerevisiae chromosome VII, complete chromosome sequence. Found forward in NC_001139 between 689060 and 689459 with 100% identity.
2142_at	1493.3	P
Saccharomyces cerevisiae chromosome VII, complete chromosome sequence. Found forward in NC_001139 between 860395 and 861394 with 100% identity.
2143_at	114.1	A
Saccharomyces cerevisiae chromosome VII, complete chromosome sequence. Found forward in NC_001139 between 861395 and 862394 with 100% identity.
2144_at	916.5	A
Saccharomyces cerevisiae chromosome VII, complete chromosome sequence. Found forward in NC_001139 between 862395 and 863394 with 100% identity.
2145_at	-125.6	A
Saccharomyces cerevisiae chromosome VII, complete chromosome sequence. Found forward in NC_001139 between 863395 and 864394 with 100% identity.
2146_at	398.0	M
Saccharomyces cerevisiae chromosome VII, complete chromosome sequence. Found forward in NC_001139 between 864395 and 865394 with 100% identity.
2147_at	824.0	A
Saccharomyces cerevisiae chromosome VII, complete chromosome sequence. Found forward in NC_001139 between 865395 and 866330 with 100% identity.
2148_at	158.1	P
Saccharomyces cerevisiae chromosome VII, complete chromosome sequence. Found forward in NC_001139 between 923127 and 924126 with 100% identity.
2149_at	-45.6	A
Saccharomyces cerevisiae chromosome VII, complete chromosome sequence. Found forward in NC_001139 between 924127 and 925126 with 100% identity.
2150_g_at	895.9	A
Saccharomyces cerevisiae chromosome VII, complete chromosome sequence. Found forward in NC_001139 between 924127 and 925126 with 100% identity.
2151_s_at	-122.2	P
Saccharomyces cerevisiae chromosome VII, complete chromosome sequence. Found forward in NC_001139 between 925127 and 926126 with 100% identity.
2152_s_at	462.5	P
Saccharomyces cerevisiae chromosome VII, complete chromosome sequence. Found forward in NC_001139 between 926127 and 927126 with 100% identity.
2153_s_at	1114.4	P
Saccharomyces cerevisiae chromosome VII, complete chromosome sequence. Found forward in NC_001139 between 927127 and 928126 with 100% identity.
2154_s_at	1159.5	P
Saccharomyces cerevisiae chromosome VII, complete chromosome sequence. Found forward in NC_001139 between 928127 and 929126 with 100% identity.
2155_s_at	1273.0	P
Saccharomyces cerevisiae chromosome VII, complete chromosome sequence. Found forward in NC_001139 between 929127 and 930126 with 100% identity.
2156_s_at	1181.9	P
Saccharomyces cerevisiae chromosome VII, complete chromosome sequence. Found forward in NC_001139 between 930127 and 930307 with 100% identity.
2157_at	123.5	M
Saccharomyces cerevisiae chromosome VII, complete chromosome sequence. Found forward in

NC_001139 between 955166 and 956165 with 100% identity.

2158_at 688.3 P

Saccharomyces cerevisiae chromosome VII, complete chromosome sequence. Found forward in NC_001139 between 956166 and 957165 with 100% identity.

2159_at -1062.8 A

Saccharomyces cerevisiae chromosome VII, complete chromosome sequence. Found forward in NC_001139 between 957166 and 958165 with 100% identity.

2160_at 464.5 P

Saccharomyces cerevisiae chromosome VII, complete chromosome sequence. Found forward in NC_001139 between 958166 and 959165 with 100% identity.

2161_at 175.0 P

Saccharomyces cerevisiae chromosome VII, complete chromosome sequence. Found forward in NC_001139 between 959166 and 960165 with 100% identity.

2162_g_at 11297.4 P

Saccharomyces cerevisiae chromosome VII, complete chromosome sequence. Found forward in NC_001139 between 959166 and 960165 with 100% identity.

2163_s_at 12984.1 P

Saccharomyces cerevisiae chromosome VII, complete chromosome sequence. Found forward in NC_001139 between 960166 and 960596 with 100% identity.

2164_at 269.5 P

Saccharomyces cerevisiae chromosome VII, complete chromosome sequence. Found forward in NC_001139 between 1031505 and 1032504 with 100% identity.

2165_g_at 272.1 P

Saccharomyces cerevisiae chromosome VII, complete chromosome sequence. Found forward in NC_001139 between 1031505 and 1032504 with 100% identity.

2166_s_at 585.2 P

Saccharomyces cerevisiae chromosome VII, complete chromosome sequence. Found forward in NC_001139 between 1032505 and 1033504 with 100% identity.

2167_s_at 664.4 P

Saccharomyces cerevisiae chromosome VII, complete chromosome sequence. Found forward in NC_001139 between 1033505 and 1034504 with 100% identity.

2168_s_at 373.9 P

Saccharomyces cerevisiae chromosome VII, complete chromosome sequence. Found forward in NC_001139 between 1034505 and 1035504 with 100% identity.

2169_s_at 2491.1 P

Saccharomyces cerevisiae chromosome VII, complete chromosome sequence. Found forward in NC_001139 between 1035505 and 1036504 with 100% identity.

2170_s_at 1744.5 P

Saccharomyces cerevisiae chromosome VII, complete chromosome sequence. Found forward in NC_001139 between 1036505 and 1037190 with 100% identity.

2171_at 147.6 P

Saccharomyces cerevisiae chromosome VII, complete chromosome sequence. Found forward in NC_001139 between 1051406 and 1052405 with 100% identity.

2172_at 4137.9 P

Saccharomyces cerevisiae chromosome VII, complete chromosome sequence. Found forward in NC_001139 between 1052406 and 1053405 with 100% identity.

2173_g_at 5135.1 P

Saccharomyces cerevisiae chromosome VII, complete chromosome sequence. Found forward in NC_001139 between 1052406 and 1053405 with 100% identity.

2174_s_at 9503.5 P

Saccharomyces cerevisiae chromosome VII, complete chromosome sequence. Found forward in NC_001139 between 1053406 and 1054405 with 100% identity.

2175_s_at 8487.3 P

Saccharomyces cerevisiae chromosome VII, complete chromosome sequence. Found forward in NC_001139 between 1054406 and 1055405 with 100% identity.

2176_s_at 9544.4 P

Saccharomyces cerevisiae chromosome VII, complete chromosome sequence. Found forward in NC_001139 between 1055406 and 1056405 with 100% identity.

2177_s_at 12082.3 P

Saccharomyces cerevisiae chromosome VII, complete chromosome sequence. Found forward in NC_001139 between 1056406 and 1056753 with 100% identity.

2178_at 735.6 P

Saccharomyces cerevisiae chromosome VII, complete chromosome sequence. Found forward in NC_001139 between 1084878 and 1085877 with 100% identity.

2179_at -169.6 A

Saccharomyces cerevisiae chromosome VIII, complete chromosome sequence. Found forward in NC_001140 between 39533 and 40532 with 100% identity.

2100_g_at 2182.7 P

Saccharomyces cerevisiae chromosome VIII, complete chromosome sequence. Found forward in NC_001140 between 39533 and 40532 with 100% identity.

2101_s_at 443.2 P

Saccharomyces cerevisiae chromosome VIII, complete chromosome sequence. Found forward in NC_001140 between 40533 and 41532 with 100% identity.

2102_s_at 1633.9 P

Saccharomyces cerevisiae chromosome VIII, complete chromosome sequence. Found forward in NC_001140 between 41533 and 42532 with 100% identity.

2103_s_at 4179.1 P

Saccharomyces cerevisiae chromosome VIII, complete chromosome sequence. Found forward in NC_001140 between 42533 and 43532 with 100% identity.

2104_s_at 7763.8 P

Saccharomyces cerevisiae chromosome VIII, complete chromosome sequence. Found forward in NC_001140 between 43533 and 44532 with 100% identity.

2105_s_at 3007.1 P

Saccharomyces cerevisiae chromosome VIII, complete chromosome sequence. Found forward in NC_001140 between 44533 and 45188 with 100% identity.

2106_at 1239.7 P

Saccharomyces cerevisiae chromosome VIII, complete chromosome sequence. Found forward in NC_001140 between 84563 and 85562 with 100% identity.

2107_at 106.7 P

Saccharomyces cerevisiae chromosome VIII, complete chromosome sequence. Found forward in NC_001140 between 150066 and 151065 with 100% identity.

2108_at 165.6 A

Saccharomyces cerevisiae chromosome VIII, complete chromosome sequence. Found forward in NC_001140 between 151066 and 152065 with 100% identity.

2109_g_at 493.2 P

Saccharomyces cerevisiae chromosome VIII, complete chromosome sequence. Found forward in NC_001140 between 151066 and 152065 with 100% identity.

2110_s_at 172.1 P

Saccharomyces cerevisiae chromosome VIII, complete chromosome sequence. Found forward in NC_001140 between 152066 and 153065 with 100% identity.

2111_s_at 585.5 P

Saccharomyces cerevisiae chromosome VIII, complete chromosome sequence. Found forward in NC_001140 between 153066 and 154065 with 100% identity.

2112_s_at 529.5 P

Saccharomyces cerevisiae chromosome VIII, complete chromosome sequence. Found forward in NC_001140 between 154066 and 155065 with 100% identity.

2113_s_at 640.7 A

Saccharomyces cerevisiae chromosome VIII, complete chromosome sequence. Found forward in NC_001140 between 155066 and 156065 with 100% identity.

2114_s_at 1970.1 P

Saccharomyces cerevisiae chromosome VIII, complete chromosome sequence. Found forward in NC_001140 between 156066 and 156943 with 100% identity.

2115_at 127.5 A
Saccharomyces cerevisiae chromosome VIII, complete chromosome sequence. Found forward in NC_001140 between 299647 and 300646 with 100% identity.
2116_at 557.6 P
Saccharomyces cerevisiae chromosome VIII, complete chromosome sequence. Found forward in NC_001140 between 300647 and 301646 with 100% identity.
2117_at -774.4 A
Saccharomyces cerevisiae chromosome VIII, complete chromosome sequence. Found forward in NC_001140 between 301647 and 302646 with 100% identity.
2118_at 1676.3 P
Saccharomyces cerevisiae chromosome VIII, complete chromosome sequence. Found forward in NC_001140 between 302647 and 303646 with 100% identity.
2119_g_at 564.3 A
Saccharomyces cerevisiae chromosome VIII, complete chromosome sequence. Found forward in NC_001140 between 302647 and 303646 with 100% identity.
2120_s_at 67.2 P
Saccharomyces cerevisiae chromosome VIII, complete chromosome sequence. Found forward in NC_001140 between 303647 and 304646 with 100% identity.
2121_s_at -1751.6 P
Saccharomyces cerevisiae chromosome VIII, complete chromosome sequence. Found forward in NC_001140 between 304647 and 305646 with 100% identity.
2122_s_at 358.1 P
Saccharomyces cerevisiae chromosome VIII, complete chromosome sequence. Found forward in NC_001140 between 305647 and 306646 with 100% identity.
2123_s_at 484.9 P
Saccharomyces cerevisiae chromosome VIII, complete chromosome sequence. Found forward in NC_001140 between 306647 and 307646 with 100% identity.
2124_s_at 559.5 P
Saccharomyces cerevisiae chromosome VIII, complete chromosome sequence. Found forward in NC_001140 between 307647 and 308646 with 100% identity.
2125_s_at 907.4 P
Saccharomyces cerevisiae chromosome VIII, complete chromosome sequence. Found forward in NC_001140 between 308647 and 309646 with 100% identity.
2126_s_at 2333.7 P
Saccharomyces cerevisiae chromosome VIII, complete chromosome sequence. Found forward in NC_001140 between 309647 and 310646 with 100% identity.
2127_s_at 977.5 P
Saccharomyces cerevisiae chromosome VIII, complete chromosome sequence. Found forward in NC_001140 between 310647 and 311646 with 100% identity.
2128_s_at 1491.0 P
Saccharomyces cerevisiae chromosome VIII, complete chromosome sequence. Found forward in NC_001140 between 311647 and 312646 with 100% identity.
2129_s_at 4433.4 P
Saccharomyces cerevisiae chromosome VIII, complete chromosome sequence. Found forward in NC_001140 between 312647 and 313497 with 100% identity.
2130_at -19.8 P
Saccharomyces cerevisiae chromosome VIII, complete chromosome sequence. Found forward in NC_001140 between 430206 and 431205 with 100% identity.
2131_at -608.8 A
Saccharomyces cerevisiae chromosome VIII, complete chromosome sequence. Found forward in NC_001140 between 431206 and 432205 with 100% identity.
2132_at -492.4 A
Saccharomyces cerevisiae chromosome VIII, complete chromosome sequence. Found forward in NC_001140 between 432206 and 433205 with 100% identity.
2133_at -15.9 A
Saccharomyces cerevisiae chromosome VIII, complete chromosome sequence. Found forward in

NC_001140 between 433206 and 434205 with 100% identity.
2134_at 256.6 P
Saccharomyces cerevisiae chromosome VIII, complete chromosome sequence. Found forward in NC_001140 between 434206 and 435205 with 100% identity.
2135_at -918.1 A
Saccharomyces cerevisiae chromosome VIII, complete chromosome sequence. Found forward in NC_001140 between 435206 and 436205 with 100% identity.
2136_at 2383.2 A
Saccharomyces cerevisiae chromosome VIII, complete chromosome sequence. Found forward in NC_001140 between 436206 and 437169 with 100% identity.
2137_at 472.9 P
Saccharomyces cerevisiae chromosome VIII, complete chromosome sequence. Found forward in NC_001140 between 522872 and 523871 with 100% identity.
11394_at 469.0 P
Saccharomyces cerevisiae chromosome VIII, complete chromosome sequence. Found forward in NC_001140 between 523872 and 524871 with 100% identity.
11395_at 129.6 A
Saccharomyces cerevisiae chromosome VIII, complete chromosome sequence. Found forward in NC_001140 between 524872 and 525871 with 100% identity.
11396_g_at 461.6 A
Saccharomyces cerevisiae chromosome VIII, complete chromosome sequence. Found forward in NC_001140 between 524872 and 525871 with 100% identity.
11397_f_at 667.8 M
Saccharomyces cerevisiae chromosome VIII, complete chromosome sequence. Found forward in NC_001140 between 525872 and 526871 with 100% identity.
11398_s_at 281.4 P
Saccharomyces cerevisiae chromosome VIII, complete chromosome sequence. Found forward in NC_001140 between 526872 and 527871 with 100% identity.
11399_s_at 4722.3 P
Saccharomyces cerevisiae chromosome VIII, complete chromosome sequence. Found forward in NC_001140 between 527872 and 528114 with 100% identity.
11400_s_at 165.1 P
Saccharomyces cerevisiae chromosome VIII, complete chromosome sequence. Found forward in NC_001140 between 532177 and 533176 with 100% identity.
11401_at -344.5 A
Saccharomyces cerevisiae chromosome VIII, complete chromosome sequence. Found forward in NC_001140 between 533177 and 534176 with 100% identity.
11402_at 143.8 A
Saccharomyces cerevisiae chromosome VIII, complete chromosome sequence. Found forward in NC_001140 between 534177 and 535176 with 100% identity.
11403_at 675.0 P
Saccharomyces cerevisiae chromosome VIII, complete chromosome sequence. Found forward in NC_001140 between 535177 and 536176 with 100% identity.
11404_at -17.0 A
Saccharomyces cerevisiae chromosome VIII, complete chromosome sequence. Found forward in NC_001140 between 537177 and 537754 with 100% identity.
11405_at 3850.2 P
Saccharomyces cerevisiae chromosome VIII, complete chromosome sequence. Found forward in NC_001140 between 543488 and 544487 with 100% identity.
11406_f_at -17.5 A
Saccharomyces cerevisiae chromosome VIII, complete chromosome sequence. Found forward in NC_001140 between 544488 and 545487 with 100% identity.
11407_f_at -62.4 A
Saccharomyces cerevisiae chromosome VIII, complete chromosome sequence. Found forward in NC_001140 between 546488 and 547487 with 100% identity.
11408_f_at 4611.7 P

Saccharomyces cerevisiae chromosome VIII, complete chromosome sequence. Found forward in NC_001140 between 547488 and 548487 with 100% identity.
11409_f_at -16.3 A
Saccharomyces cerevisiae chromosome VIII, complete chromosome sequence. Found forward in NC_001140 between 548488 and 549487 with 100% identity.
11410_at -25.8 A
Saccharomyces cerevisiae chromosome VIII, complete chromosome sequence. Found forward in NC_001140 between 549488 and 549898 with 100% identity.
11411_at -34.6 A
Saccharomyces cerevisiae chromosome IX, complete chromosome sequence. Found forward in NC_001141 between 9696 and 10695 with 100% identity.
11412_at -104.9 A
Saccharomyces cerevisiae chromosome IX, complete chromosome sequence. Found forward in NC_001141 between 10696 and 11695 with 100% identity.
11413_s_at 797.2 P
Saccharomyces cerevisiae chromosome IX, complete chromosome sequence. Found forward in NC_001141 between 11696 and 12695 with 100% identity.
11414_s_at 88.8 P
Saccharomyces cerevisiae chromosome IX, complete chromosome sequence. Found forward in NC_001141 between 12696 and 13695 with 100% identity.
11415_f_at 1308.6 P
Saccharomyces cerevisiae chromosome IX, complete chromosome sequence. Found forward in NC_001141 between 13696 and 14695 with 100% identity.
11416_at 2035.5 P
Saccharomyces cerevisiae chromosome IX, complete chromosome sequence. Found forward in NC_001141 between 106607 and 107606 with 100% identity.
11417_at -206.0 A
Saccharomyces cerevisiae chromosome IX, complete chromosome sequence. Found forward in NC_001141 between 107607 and 108606 with 100% identity.
11418_at 216.4 A
Saccharomyces cerevisiae chromosome IX, complete chromosome sequence. Found forward in NC_001141 between 108607 and 109606 with 100% identity.
11419_at 129.9 A
Saccharomyces cerevisiae chromosome IX, complete chromosome sequence. Found forward in NC_001141 between 109607 and 110606 with 100% identity.
11420_at -660.0 A
Saccharomyces cerevisiae chromosome IX, complete chromosome sequence. Found forward in NC_001141 between 110607 and 111606 with 100% identity.
11421_at 32.2 A
Saccharomyces cerevisiae chromosome IX, complete chromosome sequence. Found forward in NC_001141 between 111607 and 112606 with 100% identity.
11422_at -35.5 A
Saccharomyces cerevisiae chromosome IX, complete chromosome sequence. Found forward in NC_001141 between 112607 and 113606 with 100% identity.
11423_at 60.0 A
Saccharomyces cerevisiae chromosome IX, complete chromosome sequence. Found forward in NC_001141 between 113607 and 114606 with 100% identity.
11424_g_at 1989.8 P
Saccharomyces cerevisiae chromosome IX, complete chromosome sequence. Found forward in NC_001141 between 113607 and 114606 with 100% identity.
11425_s_at 1699.2 A
Saccharomyces cerevisiae chromosome IX, complete chromosome sequence. Found forward in NC_001141 between 114607 and 115606 with 100% identity.
11426_s_at 1233.5 P
Saccharomyces cerevisiae chromosome IX, complete chromosome sequence. Found forward in NC_001141 between 115607 and 116404 with 100% identity.

11427_at	-1574.8	A	Saccharomyces cerevisiae chromosome IX, complete chromosome sequence. Found forward in NC_001141 between 204053 and 205052 with 100% identity.
11428_at	199.1	M	Saccharomyces cerevisiae chromosome IX, complete chromosome sequence. Found forward in NC_001141 between 205053 and 206052 with 100% identity.
11429_at	31.2	A	Saccharomyces cerevisiae chromosome IX, complete chromosome sequence. Found forward in NC_001141 between 365963 and 366962 with 100% identity.
11430_at	2.4	A	Saccharomyces cerevisiae chromosome IX, complete chromosome sequence. Found forward in NC_001141 between 366963 and 367962 with 100% identity.
11431_at	-367.0	A	Saccharomyces cerevisiae chromosome IX, complete chromosome sequence. Found forward in NC_001141 between 367963 and 368962 with 100% identity.
11432_at	4117.5	P	Saccharomyces cerevisiae chromosome IX, complete chromosome sequence. Found forward in NC_001141 between 368963 and 369962 with 100% identity.
11433_at	-277.3	A	Saccharomyces cerevisiae chromosome IX, complete chromosome sequence. Found forward in NC_001141 between 369963 and 370962 with 100% identity.
11434_g_at	412.5	A	Saccharomyces cerevisiae chromosome IX, complete chromosome sequence. Found forward in NC_001141 between 369963 and 370962 with 100% identity.
11435_s_at	1285.3	P	Saccharomyces cerevisiae chromosome IX, complete chromosome sequence. Found forward in NC_001141 between 370963 and 371962 with 100% identity.
11436_s_at	724.9	P	Saccharomyces cerevisiae chromosome IX, complete chromosome sequence. Found forward in NC_001141 between 371963 and 372495 with 100% identity.