Expression Analysis: Pivot Tab

	JJ52 rich	JJ52 rich	JJ52 rich	JJ52 rich	JJ52 rich	JJ52 rich	JJ52 rich	Descriptions
	Avg Diff	Abs Call	Diff Call	Avg Diff Change	B=A	Fold Change	Sort Score	
AFFX-MurIL2_at	17.7	A						M16762 Mouse interleukin 2 (IL-2) gene, exon 4
AFFX-MurIL10_at	-12.4	A						M37897 Mouse interleukin 10 mRNA, complete cds
AFFX-MurIL4_at	306.4	A						M25892 Mus musculus interleukin 4 (Il-4) mRNA, complete cds
AFFX-MurFAS_at	-126.0	A						M83649 Mus musculus Fas antigen mRNA, complete cds
AFFX-BioB-5_at	176787.0	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	253845.0	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	226116.0	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	262629.7	P						J04423 E coli bioC protein (-5 and -3 represent transcript regions 5 prime and 3 prime respectively)
AFFX-BioC-3_at	204890.1	P						J04423 E coli bioC protein (-5 and -3 represent transcript regions 5 prime and 3 prime respectively)
AFFX-BioDn-5_at	252648.0	P						J04423 E coli bioD gene dethiobiotin synthetase (-5 and -3 represent transcript regions 5 prime and 3 prime respectively)
AFFX-BioDn-3_at	118007.7	P						J04423 E coli bioD gene dethiobiotin synthetase (-5 and -3 represent transcript regions 5 prime and 3 prime respectively)
AFFX-CreX-5_at	250670.8	P						X03453 Bacteriophage P1 cre recombinase protein (-5 and -3 represent transcript regions 5 prime and 3 prime respectively)
AFFX-CreX-3_at	265636.0	P						X03453 Bacteriophage P1 cre recombinase protein (-5 and -3 represent transcript regions 5 prime and 3 prime respectively)
AFFX-BioB-5_st	3424.9	P						J04423 E coli bioB gene biotin synthetase (-5, -M, -3 represent transcript regions 5 prime, Middle, and 3 prime respectively)
AFFX-BioB-M_st	9166.9	P						J04423 E coli bioB gene biotin synthetase (-5, -M, -3 represent transcript regions 5 prime, Middle, and 3 prime respectively)
AFFX-BioB-3_st	6380.4	P						J04423 E coli bioB gene biotin synthetase (-5, -M, -3 represent transcript regions 5 prime, Middle, and 3 prime respectively)
AFFX-BioC-5_st	1506.5	M						J04423 E coli bioC protein (-5 and -3 represent transcript regions 5 prime and 3 prime respectively)
AFFX-BioC-3_st	2656.6	P						J04423 E coli bioC protein (-5 and -3 represent transcript regions 5 prime and 3 prime respectively)
AFFX-BioDn-5_st	10664.2	P						J04423 E coli bioD gene dethiobiotin synthetase (-5 and -3 represent transcript regions 5 prime and 3 prime respectively)
AFFX-BioDn-3_st	18132.9	P						

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

AFFX-CreX-5_st 1333.5 P

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

AFFX-CreX-3_st 809.3 P

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

AFFX-DapX-5_at 101.0 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 235.4 A

L38424 B subtilis dapB, jojF, jojG genes corresponding to nucleotides 1358-3197 of L38424 (-5, -M, -3 represent transcript regions 5 prime, Middle, and 3 prime respectively)

AFFX-DapX-3_at -126.8 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-LysX-5_at 49.2 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 -115.8 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 259.3 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 -168.7 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-M_at -61.2 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-3_at 34.8 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 296.7 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 -6.8 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 -39.0 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 -514.7 A

K01391 B subtilis TrpE protein, TrpD protein, TrpC protein corresponding to nucleotides 1883-4400 of K01391 (-5, -M, -3 represent transcript regions 5 prime, Middle, and 3 prime respectively)

AFFX-TrpnX-M_at -486.2 A

K01391 B subtilis TrpE protein, TrpD protein, TrpC protein corresponding to nucleotides 1883-4400 of K01391 (-5, -M, -3 represent transcript regions 5 prime, Middle, and 3 prime respectively)

AFFX-TrpnX-3_at -186.8 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 19463.6 P

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

AFFX-YFL039CM_at 40954.8 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 86637.8 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 1522.8 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 2850.5 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 6668.1 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 46.0 A

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 273.4 A

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 532.5 A

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 111370.5 P

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

AFFX-18srRnab_at 160956.5 P

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

AFFX-18srRnac_at 35804.7 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 45685.7 P

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

AFFX-18srRnae_at 56643.9 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-25srRnaa_at 197319.8 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 27638.3 P

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

AFFX-25srRnac_at 29526.4 P

Saccharomyces cerevisiae /REF=J01355 /DEF=Z73326 SGD:YLR154C Yeast S.cerevisiae 25S ribosomal RNA corresponds to complement of 4212-7605 in Z73326 /LEN=3394 (regions a-e represent transcript regions 5 prime to 3 prime respectively)
AFFX-25srRnad_at 22560.6 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 109930.2 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_at5288.8 P
X61388 SGD: YEL002C Yeast S.cerevisiae WBP1 Oligosaccharyltransferase beta subunit
AFFX-YEL018w/_at 627.7 A
U18530 SGD:YEL018W Yeast S. cerevisiae Protein of unknown function
AFFX-YEL024w/RIP1_at 1279.9 P
M23316 SGD:YEL024C Yeast S.cerevisiae RIP1 Rieske iron-sulfur protein of the mitochondrial cytochrome bc1 complex .
AFFX-YEL021w/URA3_at3857.3 P
K02207 SGD:YEL021W Yeast S.cerevisiae URA3 gene coding for OMP decarboxylase
11378_at -58.6 A
Aldehyde dehydrogenase 1, mitochondrial
11379_at -39.0 A
Suppressor of Sulfoxyde Ethionine resistance
11380_at 114.0 A
hypothetical protein
11381_at -7.6 A
putative pseudogene
11382_at 7.2 A
putative pseudogene
11383_at -81.0 A
putative pseudogene
11384_at -107.2 A
hypothetical protein
11385_s_at 191.2 A
putative Flo1p homolog
11386_at 513.6 A
NADP-linked glutamate dehydrogenase
11387_at 11.9 A
similarity to alcohol/sorbitol dehydrogenase
11388_at 2999.2 P
similarity to alcohol/sorbitol dehydrogenase
11389_at 1232.5 P
ExtraCellular Mutant
11390_at -367.6 A
Calnexin and calreticulin homolog
11391_at 82.1 A
questionable ORF
11392_at 419.6 P
similarity to hypothetical protein YOR371c
11393_at 974.8 P
hypothetical protein
11356_at 752.9 M
inducible acetyl-coenzyme A synthetase
11357_at 4068.7 P
strong similarity to hypothetical proteins YOR365c,YGL139w,YPL221w

11358_at 822.9 P
peroxisome proliferating transcription factor
11359_at 2772.7 P
weak similarity to Legionella small basic protein sbpA
11360_at 153.6 A
weak similarity to GTP-binding proteins
11361_at 354.4 A
Spc72p interacts with Stu2p in the two-hybrid assay\; Spc72p localizes to the spindle pole bodies. Molecular weight is 72 kD
11362_at 716.9 P
hypothetical protein
11363_at 172.3 A
hypothetical protein
11364_at 11274.2 P
H-protein subunit of the glycine cleavage system
11365_at 1706.6 P
pre-tRNA processing
11366_at -171.8 A
questionable ORF
11367_at 5926.8 P
Function unknown now
11368_at 994.3 P
Guanine nucleotide exchange factor (a.k.a. GDP-release factor) for cdc42
11369_at 1525.5 P
G(sub)1 cyclin
11370_at 2115.3 P
cytochrome c heme lyase (CCHL)
11371_at 198177.8 P
Pyruvate kinase
11372_at 229.9 A
strong similarity to GTP-binding proteins
11373_at 8512.2 P
Function unknown now
11374_at 20549.9 P
97 kDa protein
11375_at 273.8 A
questionable ORF
11376_at 81.0 A
hypothetical protein
11377_at 75.3 A
Function unknown now
11333_at 819.9 P
An integral subunit of RNase P and apparent subunit of RNase MRP
11334_at 244.8 A
Function unknown now
11335_at 0.1 A
FUN21
11336_at 366.9 A
homolog of Snc2p, vesicle-associated membrane protein (synaptobrevin) homolog, forms a complex with Snc2p and Sec9p
11337_at 3329.8 P
homolog of Snc2p, vesicle-associated membrane protein (synaptobrevin) homolog, forms a complex with Snc2p and Sec9p
11338_at 1761.6 P
myosin
11339_at -0.3 A

```
similarity to hypothetical protein YOR324c
11340_at    -96.7       A
hypothetical protein
11341_at    1072.4      P
Membrane-spanning Ca-ATPase (P-type),member of the cation transport (E1-E2) ATPases
11342_at    1925.6      P
putative nuclear protein
11343_at    236.7       A
putative GTP-exchange protein
11344_at    17572.6     P
dolichyl phosphate-D-mannose:protein O-D-mannosyltransferase
11345_at    1142.6      P
predicted membrane protein
11346_at    2010.8      P
95 kDa containg leucine rich tandem repeats
11347_at    259.1       A
Protein with similarity to human RCC1 protein
11348_at    1163.9      P
Shows homology to SNF2 transcriptional regulator
11349_at    64.2        A                                                                3
transmembrane domains
11350_at    2041.8      P
Serine\/threonine kinase
11351_at    4974.7      P
protein phosphatase 2A regulatory subunit A
11352_at    306.3       A
DNA glycosylase
11353_at    638.4       P
protein of unknown function
11354_at    1140.2      P
regulation of phospholipid metabolism
11355_at    18924.2     P
cystathionine gamma-lyase
11310_at    137.5       A
possible mitochondrial transit peptide
11311_at    27.6        A
Mitochondrial outer membrane protein involved in mitochondrial morphology and inheritance
11312_at    591.5       P
sporulation protein
11313_at    1127.7      P
protein of unknown function
11314_at    2650.9      P
p24 protein involved in membrane trafficking
11315_i_at  157893.5    P
Heat shock protein of HSP70 family, cytoplasmic
11316_r_at  115445.3    P
Heat shock protein of HSP70 family, cytoplasmic
11317_s_at  65474.6     P
Heat shock protein of HSP70 family, cytoplasmic
11318_at    541.9       A
strong similarity to A.klebsiana glutamate dehydrogenase
11319_at    26462.0     P
Translation elongation factor EF-1beta, GDP\/GTP exchange factor for Tef1p\/Tef2p
11320_at    55988.1     P
Translation elongation factor EF-1beta, GDP\/GTP exchange factor for Tef1p\/Tef2p
11321_at    845.7       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 708.9 P
transcription factor tau (TFIIIC) subunit 138
11323_at 308.8 A
transcription factor tau (TFIIIC) subunit 138
11324_at 3361.4 P
protein of unknown function
11325_at 4368.1 P
p24 protein involved in membrane trafficking
11326_at 346.0 A
beta transducin domain
11327_at 4043.1 P
69 kDa subunit of the heterotrimeric RPA (RF-A) single-stranded DNA binding protein, binds URS1 and CAR1
11328_at 935.6 P
34kDa subunit of the tetrameric tRNA splicing endonuclease
11329_at 1685.1 P
maximal growth
11330_at 5440.6 P
phosphoribosyl amino imidazolesuccinocarbozamide synthetase
11331_at 587.5 P
protein kinase
11332_at 538.8 P
protein kinase domain
11287_f_at 6909.5 P
strong similarity to members of the srp1p/Tip1p family
11288_at 114.7 A
membrane protein
11289_at 755.5 A
membrane protein
11290_at 460.5 A
membrane protein
11291_at -5.9 A
membrane protein
11292_at 335.2 A
hypothetical protein
11293_at 418.6 A
membrane protein
11294_g_at 843.6 P
membrane protein
11295_r_at 284.8 A
membrane protein
11296_s_at 597.9 A
membrane protein
11297_at 102.5 A
Outer carnitine acetyltransferase, mitochondrial
11298_at 35.4 A
ankyrin repeat
11299_at 698.7 P
Shows homology to the human oxysterol binding protein (OSBP)
11300_at 72.2 A
predicted nuclear targeting signal
11301_i_at 620.1 P
FLO1 putative cell wall glycoprotein
11302_at 230.2 A

predicted membrane protein
11303_s_at 176.0 A
strong similarity to hypothetical protein YHR212c
11304_at 170.7 A
putative pseudogene
11305_s_at 66.9 A
putative pseudogene
11306_at 24.2 A
Potential membrane protein
11307_s_at 726.5 P
identical to YHR214w hypothetical protein, similarity to Sta1p
11308_s_at 7263.0 P
Potential membrane protein
11309_at -163.1 A
Potential membrane protein
11261_at 23.7 A
potential mitochondrial transit peptide
11262_s_at 49652.6 P
Acid phosphatase, secreted
11263_f_at 5573.1 P
strong similarity to IMP dehydrogenases
11264_f_at 11754.0 P
strong similarity to IMP dehydrogenases
11265_i_at -223.9 A
hypothetical protein
11266_f_at 2217.7 P
hypothetical protein
11267_at 344.3 A
identified by SAGE
11268_at 327.7 A
hypothetical protein
11269_at 232.2 A
non-annotated SAGE orf Found forward in NC_001133 between 101217 and 101354 with 100% identity. See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251
11270_at -64.7 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 296.9 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 478.4 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 132.3 A
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 679.3 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 232.2 A
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 94.7 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 50.7 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 -0.2 A
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 231.8 A
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 -61.4 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 -173.3 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 -2709.5 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 211.1 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
11284_f_at 11012.9 P
non-annotated SAGE orf Found reverse in NC_001133 between 182850 and 183005 with 100% identity.
See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251
11285_at -95.9 A
non-annotated SAGE orf Found forward in NC_001133 between 198205 and 198339 with 100% identity.
See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251
11286_at 66.6 A
non-annotated SAGE orf Found reverse in NC_001133 between 199737 and 199886 with 100% identity.
See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251
11238_at 188.0 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 228.4 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 268.5 A
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 93.7 A
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 286.5 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 96.8 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 510.3 A
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 -236.9 A
Centromere
11246_r_at -157.0 A
Centromere
11247_s_at 6674.6 P
strong similarity to members of the Sir1p/Tip1p family

11248_s_at 151.6 A
strong similarity to members of the Sir1p/Tip1p family
11249_f_at -992.9 A
strong similarity to members of the Srp1p/Tip1p family
11250_s_at 366.4 A
strong similarity to Pep1p
11251_s_at 286.9 A
homology to maltase(alpha-D-glucosidase)
11252_s_at -145.3 A
questionable ORF
11253_s_at 78.5 A
High-affinity hexose transporter
11254_at 274.5 P
strong similarity to E.coli galactoside O-acetyltransferase
11255_at 302.4 A
hypothetical protein
11256_at 84.3 A
strong similarity to Mal62p
11257_at -46.2 A
hypothetical protein
11258_at -103.5 A
High-affinity hexose transporter
11259_at 597.6 P
similarity to Methanobacterium aryldialkylphosphatase related protein
11260_at 317.7 P
strong similarity to S.pombe isp4 protein
11215_at 259.3 A
questionable ORF
11216_at 1886.5 P
CH3HC4 zinc-binding integral peroxisomal membrane protein
11217_at 1801.6 P
Protein required for COB mRNA stability or 5 processing
11218_at 495.4 A
mitochondrial nuclease
11219_at 1049.3 P
weak similarity to rat omega-conotoxin-sensitive calcium channel alpha-1 subunit rbB-I
11220_at 359.8 P
similarity to YIL130p and Put3p
11221_at 1105.6 P
involved in secretion of proteins that lack classical secretory signal sequences
11222_at 649.5 A
weak similarity to Tor2p
11223_at 331.0 A
RNA splicing factor
11224_at 197.2 A
questionable ORF
11225_at 472.8 A
ExtraCellular Mutant
11226_at 12405.1 P
strong similarity to aconitate hydratase
11227_at 590.5 P
hypothetical protein
11228_at 3417.9 P
strong similarity to Pho87p
11229_at 948.6 P
ubiquitin carboxyl-terminal hydrolase

11230_at	5960.8	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	248.1	A	questionable ORF
11232_at	366.6	A	Protein involved in initiation of DNA replication
11233_at	703.4	P	similarity to Sly41p
11234_at	1103.8	P	hypothetical protein
11235_at	3577.4	P	Ribosomal protein S14B (rp59B)
11236_at	64673.6	P	Ribosomal protein S22A (S24A) (rp50) (YS22)
11237_at	43126.7	P	Ribosomal protein L39 (L46) (YL40)
11192_at	5353.2	P	questionable ORF
11193_at	998.1	P	protein kinase homolog
11194_at	1257.2	P	putative mannosyltransferase
11195_at	-29.3	A	hypothetical protein
11196_at	1068.0	P	hypothetical protein
11197_at	3181.9	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	-64.5	A	questionable ORF
11199_at	770.2	P	similarity to hypothetical protein YJR030c
11200_at	292.4	A	essential for assembly of a functional F1-ATPase
11201_at	813.8	P	Putative homolog of subunit 1 of bovine prefoldin, a chaperone comprised of six subunits
11202_at	1731.4	P	hypothetical protein
11203_i_at	22852.0	P	Ribosomal protein L17B (L20B) (YL17)
11204_s_at	42250.8	P	Ribosomal protein L17B (L20B) (YL17)
11205_i_at	66068.9	P	Ribosomal protein L17B (L20B) (YL17)
11206_f_at	55270.8	P	Ribosomal protein L17B (L20B) (YL17)
11207_at	275.5	A	transcription factor
11208_at	198.8	A	questionable ORF
11209_at	4517.9	P	Cell wall beta-glucan assembly
11210_at	2998.8	P	subunit 3 of replication factor-A

11211_at	1833.2	P	carboxypeptidase yscS
11212_at	3074.6	P	similarity to YBR162c
11213_at	-42.6	A	An a-specific gene that is induced to a higher expression level by alpha factor
11214_at	-81.5	A	questionable ORF
11170_at	233.8	A	transcription factor containing a SET domain
11171_at	15375.9	P	Farnesyl diphosphate synthetase (FPP synthetase)
11172_at	7266.9	P	Ubiquinol cytochrome-c reductase subunit 8 (11 kDa protein)
11173_at	818.9	P	Protein kinase homolog, mutant is salt and pH sensitive
11174_at	674.3	P	putative catalytic subunit of cAMP-dependent protein kinase
11175_at	346.6	P	hypothetical protein
11176_at	69.3	A	weak similarity to dnaJ proteins
11177_at	112.0	A	hypothetical protein
11178_at	90.4	A	member of the Pir1p/Hsp150p/Pir3p family
11179_at	43257.8	P	Heat shock protein, secretory glycoprotein
11180_at	28091.6	P	Protein with homology to Hsp150p and Pir1p, Pir2p, and Pir3p
11181_at	4223.7	P	Factor arrest protein
11182_at	827.1	P	sensitive to sulfonylurea herbicides on complex media (YPD)
11183_at	721.0	P	Fructose-2,6-bisphosphatase
11184_at	935.8	P	Protein involved in vacuolar sorting
11185_at	117.6	A	L-myo-inositol-1-phosphate synthase
11186_at	731.6	A	questionable ORF
11187_at	6728.2	P	similarity to hypothetical protein YDL123w
11188_at	85.6	A	questionable ORF
11189_at	863.0	P	similarity to hypothetical protein YDR131c
11190_at	2350.8	P	RNA polymerase I subunit, not shared (A34.5)
11191_at	349.2	A	weak similarity to C.elegans hypothetical protein C43G2.4
11147_at	654.9	P	IME2-Dependent Signalling
11148_at	2221.9	P	weak similarity to T.pacificus retinal-binding protein

11149_at 444.4 A
hypothetical protein
11150_at 2658.9 P
16.5 kDa inner membrane protein required for import of mitochondrial precursor proteins
11151_at 328.4 A
questionable ORF
11152_g_at 1217.4 P
questionable ORF
11153_at 235.0 A
Serine-threonine protein kinase
11154_at 1268.8 P
fourth-largest subunit of RNA polymerase II
11155_at 985.3 P
Probable glycosyltransferase of KRE2\/KTR1\/YUR1 family\; located in the Golgi
11156_s_at 36215.6 P
translation initiation factor eIF4A
11157_at 576.0 P
self-glucosylating initiator of glycogen synthesis\; similar to mammalian glycogenin
11158_i_at 84678.4 P
Ribosomal protein S21B (S26B) (YS25)
11159_s_at 43247.5 P
Ribosomal protein S21B (S26B) (YS25)
11160_at 208.2 A
questionable ORF
11161_at 2058.8 P
putative plasma membrane transporter capable of transporting sphingoid long chain bases into cells
11162_at 434.8 M
mitochondrial carrier protein
11163_at 147.6 A
weak similarity to human phospholipase D
11164_at 266.0 A
weak similarity to nonepidermal Xenopus keratin, type I
11165_at 43642.8 P
carbamoyl-phophate synthetase, aspartate transcarbamylase, and glutamine amidotransferase
11166_at 768.5 P
180 kDa high affinity potassium transporter
11167_at 1075.4 P
MAP kinase kinase (MEK), may act as a scaffolding protein for Sho1p, Ste11p, and Hog1p
11168_at 138.7 A
negative transcriptional regulator
11169_at 242.8 A
Nit2 nitrilase
11124_at 1005.2 P
translational repressor of GCN4
11125_at 659.6 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 6137.4 P
weak similarity to D.melanogaster troponin T and human nucleolin
11127_at 1599.4 P
weak similarity to dog-fish transition protein S2
11128_at 4342.5 P
D-ribulose-5-Phosphate 3-epimerase
11129_at -42.5 A
questionable ORF
11130_at -677.7 A

questionable ORF
11131_at 660.9 P
hypothetical protein
11132_at 6618.0 P
Putative inorganic phosphate transporter
11133_at 1260.7 P
With NCA2, regulates proper expression of subunits 6 (Atp6p) and 8 (Atp8p) of the Fo-F1 ATP synthase
11134_at 2387.1 P
Anti-silencing protein that causes depression of silent loci when overexpressed
11135_at 714.5 P
similarity to Met30p and N.crassa sulfur controller-2
11136_at 1853.6 P
Component of Chaperonin Containing T-complex subunit seven
11137_at 555.9 P
GATA zinc finger protein 3 homologous to Dal80 in structure and function
11138_at 6538.0 P
weak similarity to ATPase Drs2p
11139_at 1409.3 P
strong similarity to hypothetical S. pombe protein
11140_at 74.0 A
similarity to hypothetical S. pombe protein
11141_at 430.1 A
Serine\/Threonine protein kinase, positively regulated by IME1
11142_at -12.3 A
similarity to hypothetical protein YKR029c
11143_at 671.0 P
weak similarity to C.elegans hypothetical protein F45G2.c
11144_at 85.3 A
putative regulatory protein
11145_at 705.9 P
mitochondrial elongation factor G-like protein
11146_at 1282.4 P
gamma-glutamylcysteine synthetase
11102_at 1323.7 P
similarity to hypothetical C. elegans protein C56A3.8
11103_at 755.5 A
Involved in chitin biosynthesis and\/or its regulation
11104_at 1249.6 P
SIT4 associated protein, MW of 185 kDa
11105_at 2414.6 P
similarity to hypothetical C. elegans protein T15B7.2
11106_at 862.6 P
ribosomal protein YmL49, mitochondrial
11107_at 662.3 P
putative 163 kDa protein kinase
11108_at 905.7 P
similarity to E.hirae NaH-antiporter NapA
11109_at 491.6 A
outward-rectifier potassium channel
11110_at 712.8 P
DNA helicase
11111_at 1571.7 P
weak similarity to human G protein-coupled receptor
11112_at 414.6 P
Part of the DNA polymerase II complex, acts in a checkpoiint pathway during S-phase
11113_at 157.3 A

shows homology to DNA binding domain of Gal4p, has a leucine zipper motif and acidic region\; lexA-Sip4p activates transcription
11114_at	427.4	P
Ornithine carbamoyltransferase
11115_at	261.4	A
tRNA ligase
11116_at	-239.1	A
questionable ORF
11117_at	584.5	A
70 kD component of the Exocyst complex\; required for exocytosis
11118_at	-832.3	A
similarity to hypothetical protein YKR021w
11119_at	487.1	A
similarity to hypothetical protein YKR019c
11120_at	1315.1	P
strong similarity to hypothetical protein YKR018c
11121_at	2566.6	P
54.8 kDa actin-related protein
11122_at	10408.6	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	1751.5	P
Similar to plant PR-1 class of pathogen related proteins
11079_at	1743.8	P
Similar to plant PR-1 class of pathogen related proteins
11080_at	202.8	A
hypothetical protein
11081_at	5295.2	P
Establishes Silent omatin\; homolog of TOF2
11082_at	928.8	P
questionable ORF
11083_at	926.9	P
required for structural maintenance of chromosomes
11084_at	823.1	P
DnaJ-like protein of the endoplasmic reticulum membrane
11085_at	582.3	P
hypothetical protein
11086_at	515.4	A
Acetylglutamate Synthase
11087_at	-27.6	A
similarity to AMP deaminases
11088_at	2403.2	P
similarity to C.elegans hypothetical protein
11089_at	2176.8	P
strong similarity to human esterase D
11090_at	108.9	A
questionable ORF
11091_at	399.6	P
hypothetical protein
11092_at	1244.5	P
weak similarity to DNA-directed DNA polymerase II chain C
11093_at	-49.9	A
hypothetical protein
11094_at	1418.8	P
Mitochondrial ribosomal protein MRPL8 (YmL8) (E. coli L17)
11095_at	1474.2	P

similarity to S.pombe SPAC13G6.3 protein
11096_at 295.8 A
82-kDa protein, with putative coiled-coil domain, has carboxy-terminal domain, containing heptad repeats, that binds Nsp1p\; nucleoporin
11097_at 972.1 A
similarity to kynurenine aminotransferase and glutamine-phenylpyruvate transaminase
11098_at 437.4 P
Homolog of human CLN3
11099_at 146.9 A
strong similarity to hypothetical protein YBR270c
11100_at 98.6 A
probable serine\/threonine kinase
11101_at 577.9 A
Metalloregulatory protein involved in zinc-responsive transcriptional regulation
11057_at 5851.5 P
similarity to R.fascians hypothetical protein 6
11058_at 795.0 P
Translocase for the insertion of proteins into the mitochondrial inner membrane.
11059_at 506.4 P
Vacuolar protein similar to mouse gene H<beta>58
11060_at 8881.0 P
Glyceraldehyde-3-phosphate dehydrogenase 1
11061_g_at 193376.5 P
Glyceraldehyde-3-phosphate dehydrogenase 1
11062_at 1134.7 P
hypothetical protein
11063_at 2349.3 P
DEAD-box family helicase required for mRNA export from nucleus
11064_at 382.6 A
hypothetical protein
11065_at 1608.7 P
similarity to hypothetical protein YBR273c
11066_at 66.3 A
Regulator of Ty1 Transposition
11067_at 77.5 A
similarity to E.coli lipoate-protein ligase A
11068_at 7.5 A
strong similarity to succinate dehydrogenase flavoprotein
11069_at 284.4 A
GTPase-activating protein for Ypt6
11070_at -1830.9 A
similarity to hypothetical protein YKR015c
11071_at 2514.2 P
Putative microtubule-associated protein (MAP)
11072_at 3370.6 P
Nucleoskeletal protein found in nuclear pores and spindle pole body
11073_at 559.6 P
similarity to human protein interacting with human nuclearpore protein Nup93
11074_at 128.8 A
strong similarity to hypothetical protein YJL037w
11075_at 823.1 P
strong similarity to hypothetical protein YJL038c
11076_at 254.1 A
weak similarity to Mvp1p
11077_at 396.2 P
weak similarity to P.gingivalis PgaA and B.japonicum nitrogen fixation protein

11078_at 28445.8 P
Homologue of mammalian BiP (GPR78) protein\; member of the HSP70 gene family
11034_at 1480.1 P
putative RNA helicase
11035_at 428.6 A
questionable ORF
11036_at 467.5 A
Geranylgeranyltransferase Type II alpha subunit (PGGTase-II, alpha subunit)
11037_at 525.5 P
spindle-assembly checkpoint protein
11038_at 959.5 P
similarity to C.elegans hypothetical protein T05G5.8
11039_at 221.3 A
hypothetical protein
11040_at -65.4 A
hypothetical protein
11041_at 7516.3 P
small subunit of ribonucleotide reductase
11042_at 393.8 A
member of yeast Pol I core factor (CF) also composed of Rrn11p, Rrn6p and TATA-binding protein
11043_at -218.2 A
similar to Aps1p and mammalian small subunit (sigma-2 adaptin) of plasma membrane-associated clathrin assembly complex (AP-2)
11044_at -645.3 A
Nuclear gene encoding mitochondrial protein
11045_at 73.5 A
questionable ORF
11046_at 2220.2 P
weak similarity to S.pombe hypothetical protein SPAC23A1.16
11047_at 232.4 A
similarity to P.falciparum glutamic acid-rich protein
11048_at 72.6 A
hypothetical protein
11049_g_at -64.7 A
hypothetical protein
11050_at 994.1 P
questionable ORF
11051_at 291.3 A
hypothetical protein
11052_at 1624.8 P
weak similarity to hypothetical protein YNL278w and YLR187w
11053_at 107.6 A
questionable ORF
11054_at 4013.4 P
Cytoplasmic chaperonin subunit gamma
11055_at 324.9 A
Checkpoint protein required for cell cycle arrest in response to loss of microtubule function
11056_at 21768.7 P
weak similarity to regulatory protein PHO81
11010_at 1095.9 P
weak similarity to chicken hypothetical protein
11011_at 1627.7 P
weak similarity to C.elegans hypothetical protei ZK792.5
11012_at 1934.2 P
questionable ORF
11013_at 3043.8 P

Component of Chaperonin Containing T-complex subunit eight
11014_at -22.1 A
hypothetical protein
11015_at 424.5 P
cyclin-related subunit of the kinase complex that phosphorylates the RPO21 CTD (carboxy-terminal domain)\; also called CTDK-I beta subunit
11016_at 849.9 P
adenylate cyclase
11017_at 444.2 P
Multicopy suppressor of ypt6 null mutation
11018_at 379.2 A
hypothetical protein
11019_at 7756.2 P
64-kDa, alpha subunit of oligosaccharyltransferase complex\; homologous to mammalian ribophorin I
11020_i_at 1765.8 P
Subunit of 20S proteasome
11021_f_at 1665.8 P
Subunit of 20S proteasome
11022_at 9275.4 P
Subunit of 20S proteasome
11023_at 4297.4 P
weak similarity to A.thaliana aminoacid permease AAP4
11024_at 1540.2 P
Protein component of the U3 small nucleolar ribonucleoprotein (snoRNP)
11025_at 542.9 P
hypothetical protein
11026_at 38924.7 P
alpha-agglutinin
11027_at 936.4 A
beta-adaptin, large subunit of the clathrin-associated protein complex
11028_at 313.0 A
DNA-directed DNA polymerase delta, 55 KD subunit
11029_at 1526.0 P
Translation initiation factor eIF-2 alpha subunit
11030_at 280.8 A
similarity to S.pombe hypothetical protein
11031_s_at 280927.4 P
glyceraldehyde 3-phosphate dehydrogenase
11032_at 1169.7 P
ATP sulfurylase
11033_at 392.9 A
Homologue of the SPC12 subunit of mammalian signal peptidase complex. Protein is important for efficient signal peptidase activity.
10988_at 306.9 A
hypothetical protein
10989_at 228.6 A
hypothetical protein
10990_at 957.6 P
similarity to C.elegans B0491.1 protein
10991_at 4599.7 P
strong similarity to S.pombe hypothetical protein SPBC16C6.05
10992_at 1065.2 P
strong similarity to Sng1p
10993_at 17245.2 P
dihydroxyacid dehydratase
10994_at 3582.9 P

Peptidyl-prolyl cis\/trans isomerase (PPIase)
10995_at 688.5 P
questionable ORF
10996_at 786.0 P
peroxisomal acyl-CoA thioesterase
10997_at 28.5 A
questionable ORF
10998_at 346.0 A
meiotic recombination protein
10999_at -223.3 A
meiotic recombination protein
11000_at 443.5 P
Sm-like protein
11001_at 125.2 A
hypothetical protein
11002_at 1677.1 P
weak similarity to C.elegans Z49131_E ZC373.5 protein
11003_at 2289.1 P
3-hydroxyanthranilic acid dioxygenase
11004_at 461.2 A
similarity to hypothetical protein YJL181w
11005_at 690.3 P
Component of a complex guanine nucleotide exchange activity for the ADP-ribosylation factor ARF
11006_at 543.3 P a
cyclophilin related to the mammalian CyP-40\; physically interacts with RPD3 gene product
11007_at 401.4 A
similarity to Drosophila DmX gene
11008_at 424.2 A
Required for assembly of active cytochrome c oxidase
11009_at 550.2 P
DNA-dependent ATPase, homologous to human Cockayne syndrome B gene ERCC6, that is a putative helicase
10965_at 188.8 A
similarity to human E6-associated protein
10966_at -161.5 A
questionable ORF
10967_at 104.9 A
questionable ORF
10968_at 412.5 A
hypothetical protein
10969_at 1143.5 P
putative transport protein involved in intracellular iron metabolism
10970_at 1437.8 P
hypothetical protein
10971_at 1921.4 P
Protein in nuclear pore complex\; may function in nuclear envelope integrity\; may also be involved in tRNA biogenesis
10972_at 72.8 A
third (55 kDa) subunit of DNA polymerase delta
10973_at 2867.0 P
weak similarity to putative transport protein YKR103w
10974_at 1828.6 P
Mitochondrial matrix protein involved in protein import\; subunit of SceI endonuclease
10975_at 699.4 P
weak similarity to Xenopus vimentin 4
10976_at 771.8 P

anaerobically expressed form of translation initiation factor eIF-5A
10977_at 7082.4 P
iso-1-cytochrome c
10978_at 753.5 P
Associated with ferric reductase
10979_at 360.4 A
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 2176.2 P
osmotic growth protein
10981_at 1545.7 P
Nucleotide excision repair protein involved in G(sub)2 repair of inactive genes
10982_at 54.5 A
hypothetical protein
10983_at 1000.1 P
similarity to hypothetical protein YML047c
10984_at 236.2 A
Protein required for growth at high temperature
10985_at 426.6 A
hypothetical protein
10986_at 531.5 A
thymidylate kinase
10987_at 2819.4 P
Clathrin-associated protein, small subunit
10943_at 1559.4 P
Putative serine\/threonine protein kinase that enhances spermine uptake
10944_at 420.8 A
basic helix-loop-helix protein
10945_at 146.8 A
similarity to Mnn4p
10946_at 423.5 A
52-kDa amidase specific for N-terminal asparagine and glutamine
10947_at 1696.9 P
A12.2 subunit of RNA polymerase I
10948_at 5718.2 P
subunit of chaperonin subunit epsilon
10949_at 7053.2 P
actin-related gene
10950_at 755.9 P
phosphatidylinositol kinase homolog
10951_at 224.8 A
Essential protein of unknown function
10952_at 1140.4 P
Subunit 2 of Replication Factor C\; homologous to human RFC 37 kDa subunit
10953_at 1588.2 P
controls 6-N-hydroxylaminopurine sensitivity and mutagenesis
10954_at 9278.4 P
similarity to C.elegans hypothetical protein C14A4.1
10955_at -228.2 A
questionable ORF
10956_at 3684.6 P
strong similarity to C.elegans hypothetical protein and similarity to YLR243w
10957_at 2638.0 P

Methylene-fatty-acyl-phospholipid synthase (unsaturated phospholipid N-methyltransferase)
10958_at 1091.0 P
Protein interacts with Gsp1p
10959_at 694.8 P
putative mannosyltransferase
10960_at 1793.9 P
Component of 10 nm filaments of mother-bud neck
10961_at 10419.8 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 794.6 P
similarity to mammalian indoleamine 2,3-dioxygenase
10963_at 843.4 P
questionable ORF
10964_at 933.3 P
hypothetical protein
10920_at 43.3 A
questionable ORF
10921_at 315.3 A
hypothetical protein
10922_at 306.5 A
hypothetical protein
10923_at 677.3 A
weak similarity to S.pombe hypothetical protein SPAC1B3.08
10924_at 7870.7 P
hypothetical protein
10925_at 655.4 P
gamma subunit of G protein coupled to mating factor receptors
10926_at 350.6 A
questionable ORF
10927_at 703.3 P
weak similarity to S.pombe hypothetical protein SPBC14C8.18c
10928_at 329.2 A
hypothetical protein
10929_at 1131.1 P F
box protein with several leucine rich repeats
10930_at 880.7 P
Benomyl dependent tubulin mutant
10931_at 1065.7 A
Component of a pre-mRNA polyadenylation factor that interacts with poly(A) polymerase
10932_at 447.0 A
meiotic gene expression\; meiosis inducing protein
10933_at 27384.3 P
Ribosomal protein L43B
10934_at -36.1 A
protein related to mitochondrial carriers
10935_at 971.6 P
similarity to Corynebacterium 2,5-diketo-D-gluconic acid reductase and aldehyde reductases
10936_at 497.0 A
weak similarity to Caj1p
10937_at 231.1 A
weak similarity to Bacillus licheniformis esterase
10938_at 210.8 A
ubiquitin hydrolase
10939_at 650.4 P

weak similarity to Bud3p
10940_at 758.6 P
weak similarity to superoxide dismutases
10941_at 524.0 P
hypothetical protein
10942_at 2209.8 P
CTP synthase
10897_at 33382.1 P
Cu, Zn superoxide dismutase
10898_at 36685.9 P
strong similarity to human adenosine kinase
10899_at -140.1 A
ExtraCellular Mutant
10900_at 477.6 P
weak similarity to acylglycerol lipase
10901_at 276.0 A
similarity to hypothetical protein YIL014c-a
10902_at 2567.6 P
carbamyl phosphate synthetase
10903_at 209.7 A
similarity to human myotubularin
10904_at 680.3 P
weak similarity to E.coli colanic acid biosynthesis positive regulator RcsB
10905_at 354.3 A
involved in nuclear function
10906_at 2024.1 P
similarity to bacterial, chloroplast and mitochondrial ribosomal protein S7
10907_at 325.4 M
questionable ORF
10908_at -507.3 A
similarity to hypothetical protein YBL043w
10909_at 1601.6 P
similarity to hypothetical protein YPR114w
10910_at 5019.1 P
zinc metallo-protease that catalyzes the first step of N-terminal processing of the yeast a-factor precursor
10911_at 579.6 P
weak similarity to Helicobacter pylori UreD protein
10912_at 96.4 A
similarity to human retinoblastoma binding protein 2
10913_at -207.3 A
hypothetical protein
10914_at 4316.3 P
F(1)F(0)-ATPase complex beta subunit, mitochondrial
10915_at 317.5 A
CCR4 associated factor
10916_at 45875.1 P
Ribosomal protein S5 (S2) (rp14) (YS8)
10917_at 1020.5 P
weak similarity to Staphylococcus multidrug resistance protein
10918_at 1995.9 P
similarity to human KIAA0171 protein
10919_at 985.8 P
similarity to human prostate-specific membrane antigen and transferrin receptor protein
10875_at 1677.9 P
similarity to regulatory protein Ard1p
10876_at -177.7 A

questionable ORF
10877_at 1059.4 P
weak similarity to hypothetical protein YNL024c
10878_at 618.4 P
similarity to O-succinylhomoserine (thiol)-lyase
10879_at 289.0 P
specific alpha-mannosidase
10880_at 999.2 A
Putative Upf1p interacting protein
10881_at 3173.9 P
strong similarity to hypothetical protein YDR399w
10882_at 545.1 P
similarity to paramyosin, myosin
10883_at 185.2 A
Required for maintenance of chromosomes and minichromosomes
10884_at 530.5 A
weak similarity to human 3 ,5 -cyclic-GMP phosphodiesterase
10885_at 1808.6 P
ExtraCellular Mutant
10886_at 398.9 P
similarity to C.elegans hypothetical protein T08A11.1
10887_at 22488.9 P
Homoserine dehydrogenase (L-homoserine:NADP oxidoreductase)
10888_at 1136.6 P
involved in cell-cycle regulation of histone transcription
10889_at 288.9 A
hypothetical protein
10890_at 734.9 P
similarity to thiamin pyrophosphokinase
10891_at 7905.6 P
dolichyl phosphate-D-mannose:protein O-D-mannosyltransferase
10892_at 423.9 A
involved in mitochondrial genome maintenance
10893_s_at 68719.1 P
Ribosomal protein S4A (YS6) (rp5) (S7A)
10894_at 477.0 P
questionable ORF
10895_at -37.5 A
heat shock transcription factor homolog
10896_at 7083.1 P
Branched-Chain Amino Acid Transaminase
10851_at 35.8 A
similarity to 2-nitropropane dioxygenase
10852_at 55.3 A
Protein induced during anaerobic growth
10853_at 514.3 P
similarity to mucin proteins, YKL224c, Sta1p
10854_at 538.1 P
allantoate permease
10855_at -51.3 A
Endo-polygalacturonase
10856_at 85.9 A
hypothetical protein
10857_at 521.7 P
Hypothetical aryl-alcohol dehydrogenase (AAD)
10858_s_at 390.4 P

Thiamine biosynthetic enzyme
10859_at -37.2 A
hypothetical protein
10860_s_at -70.9 A
hexose transporter
10861_s_at 537.7 A
sorbitol-induced sorbitol dehydrogenase
10862_s_at -159.8 A
strong similarity to Mal31p
10863_i_at -254.5 A
identified by SAGE
10864_r_at 362.0 A
identified by SAGE
10865_at 790.5 P
C-terminal part of YJR030c
10866_at 1687.9 P
similarity to human DDP gene, hypothetical protein of S.pombe (YA94_SCHPO) and Mrs11p (YHR005c-a)
10867_s_at 1416.4 P
Co-assembles with Bud3p at bud sites
10868_at 2903.1 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 1794.5 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 378.7 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 4.1 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
10872_at 1202.6 A
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 -304.8 A
non-annotated SAGE orf Found reverse in NC_001142 between 471544 and 471738 with 100% identity. See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251
10874_at 2301.2 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 97.6 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 233.3 A
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 -9.2 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 204.1 A
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 366.6 A
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 123.5 A
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 5176.4 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 825.3 P
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 3052.6 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 -84.9 A
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 26600.9 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 -88.0 A
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 -246.9 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 -84.3 A
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 1273.7 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 -56.3 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 136.3 A
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 -67.8 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 184.2 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 266.7 A
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 1148.9 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 134.8 A
non-annotated SAGE orf Found forward in NC_001142 between 337317 and 337583 with 100% identity.
See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251
10850_at 97.0 A
non-annotated SAGE orf Found reverse in NC_001142 between 416236 and 416439 with 100% identity.
See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251
10806_at 266.7 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 -194.1 A
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 -87.4 A
non-annotated SAGE orf Found forward in NC_001142 between 471954 and 472142 with 100% identity.
See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251
10809_g_at -7.6 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
10810_i_at 105.3 A
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 534.1 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 258.6 A
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 32.4 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 686.1 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 1535.9 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 -34.8 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 509.9 A
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 613.4 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 141.7 A
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 584.3 P
non-annotated SAGE orf Found forward in NC_001142 between 447886 and 448050 with 100% identity.
See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251
10821_g_at 416.8 A
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 183.8 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 173.9 A
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 -570.7 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 358.7 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 180.4 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 488.5 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 1454.0 P
small nuclear RNA128
10783_at -150.3 A
small nuclear RNA190
10784_at 1486.5 P
small nuclear RNA37
10785_at 618.4 P
snRNA
10786_i_at -1019.0 A
Centromere
10787_at 928.9 P
small nuclear RNA3
10788_at 243.7 A
ARS121 Found forward in NC_001142 between 683650 and 683699 with 100% identity.
10789_f_at 381.1 A
strong similarity to members of the Srp1p/Tip1p family
10790_at 339.4 A
weak similarity to transcription factors, similarity to finger proteins YOR162c, YOR172w and YLR266c
10791_at 118.7 A
weak similarity to human X-linked PEST-containing transporter
10792_at -13.4 A
Ferric reductase, similar to Fre1p
10793_at 449.4 P
Protein with similarity to subtelomerically-encoded proteins such as Cos5p, Ybr302p, Cos3p, Cos1p, Cos4p, Cos8p, Cos6p, Cos9p
10794_at 216.2 A
threonine dehydratase
10795_at -55.8 A
carboxylic acid transporter protein homolog
10796_at 23396.2 P
dihydroorotate dehydrogenase
10797_at 904.4 P
similarity to P. aeruginosa hyuA and hyuB
10798_at 1419.1 P
weak similarity to mouse transcriptional coactivator ALY
10799_at 2296.0 P
phospholipase A2-activating protein
10800_at 4992.0 P
integral membrane protein localizing to the ER and Golgi
10801_at 2247.7 P
anthranilate synthase Component II and indole-3-phosphate (multifunctional enzyme)
10802_at 15435.5 P
ubiquitin activating enzyme, similar to Uba2p
10803_at 174.3 A
ABC transporter, glycoprotein, component of a-factor secretory pathway
10804_at 404.1 A
Subunit of complex involved in processing of the 3 end of cytochrome b pre-mRNA
10805_at 2004.5 P

hypothetical protein
10760_at 599.2 P
hypothetical protein
10761_at 1495.2 P
nuclear protein LOS1
10762_at 2229.1 P
probable purine nucleotide-binding protein
10763_at 771.2 P
phosphatidylinositol kinase homolg
10764_at 241.2 A
questionable ORF
10765_at 685.3 P
member of the AAA-protein family
10766_at 2302.3 P
v-SNARE
10767_at 1559.3 P
similarity to rabbit histidine-rich calcium-binding protein
10768_at 271.8 A
mitochondrial threonine-tRNA synthetase
10769_at 703.2 P
Interacts with and may be a positive regulator of GLC7 which encodes type1 protein phosphatase
10770_at 10626.4 P
acyl carrier protein
10771_at 2064.3 P
diphthamide synthesis protein
10772_at 4916.5 P
Type 2B protein phosphatase\; regulatory B subunit of calcineurin
10773_at 1270.9 P
Type 2B protein phosphatase\; regulatory B subunit of calcineurin
10774_at 933.2 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 72.8 A
peroxisomal ABC transporter 2
10776_at 173.5 A
strong similarity to hypothetical protein YLR413w
10777_at 1047.6 P
mRNA transport regulator
10778_at 484.6 P
probable purine nucleotide-binding protein
10779_at 986.4 P
Ornithine decarboxylase
10780_at 934.2 P
hypothetical protein
10781_at 30750.1 P
pentafunctional enzyme consisting of the following domains : acetyl transferase, enoyl reductase, dehydratase and malonyl\/palmityl transferase
10737_at 11649.6 P
ribose-phosphate pyrophosphokinase
10738_i_at 46467.5 P
Ribosomal protein L17A (L20A) (YL17)
10739_f_at 48148.1 P
Ribosomal protein L17A (L20A) (YL17)
10740_at 1674.2 P
kinesin-like protein

10741_at	3629.3	P	a factor recptor
10742_at	365.5	A	questionable ORF
10743_at	915.2	P	hypothetical protein
10744_at	1976.3	P	weak similarity to E.coli hypothetical protein
10745_at	656.4	P	probable transport protein
10746_at	509.9	P	U5 snRNP-specific protein related to EF-2
10747_at	2221.1	P	Nucleolar protein
10748_at	373.5	A	probable serine\/threonine-specific protein kinase (EC 2.7.1.-)
10749_at	508.3	A	mitochondrial ribosomal protein L14
10750_at	293.6	A	questionable ORF
10751_at	250.8	A	probable serine\/threonine-specific protein kinase (EC 2.7.1.-)
10752_at	644.7	P	16 kDa mitochondrial ribosomal large subunit protein
10753_at	588.2	P	cAMP-dependent protein kinase catalytic subunit
10754_at	4158.3	P	Morphogenesis Checkpoint Dependent
10755_at	10671.6	P	Protein containing tandem internal repeats
10756_at	602.2	P	Protein containing tandem internal repeats
10757_at	-122.5	A	hypothetical protein
10758_at	188.2	A	probable serine\/threonine-specific protein kinase (EC 2.7.1.-)
10759_at	6451.3	P	similarity to hypothetical S. pombe protein
10714_at	407.7	A	hypothetical protein
10715_at	274.4	A	hypothetical protein
10716_at	7335.5	P	aminopeptidase yscII
10717_at	10131.6	P	40S ribosomal protein S27A (rp61) (YS20)
10718_at	377.9	A	hypothetical protein
10719_at	560.7	P	signal recognition particle receptor, beta chain
10720_at	5630.2	P	questionable ORF
10721_at	164809.9	P	Phosphoglycerate mutase
10722_at	964.0	P	similarity to C.elegans hypothetical protein R107.2

10723_at 2266.4 P
NADH-cytochrome b5 reductase
10724_at 561.4 P
debranching enzyme
10725_at 1557.7 P
flavoprotein subunit of succinate dehydrogenase
10726_at 48.2 A
questionable ORF
10727_at 2707.7 P
strong similarity to S.pombe hypothetical protein C3H1.09C
10728_at 7028.5 P
putative ATPase, 26S protease subunit component
10729_at 795.5 P
Subunit of RNA polymerase III
10730_at 2553.3 P
low temperature viability protein
10731_at 2498.6 P
mitochondrial ribosomal protein
10732_at 2381.9 P
succinate dehydrogenase cytochrome b
10733_at 950.5 P
triglyceride lipase-cholesterol esterase
10734_at 784.9 P
alpha subunit of the kinase which phosphorylates the RNA polymerase largest subunit CTD (carboxyl-terminal domain)
10735_at 296.9 A
15.5 kDa mitochondrial ribosomal protein YmL31
10736_at 129.9 A
hypothetical protein
10692_at 803.5 P
questionable ORF
10693_at 2402.0 P
Beta-adaptin, large subunit of the clathrin-associated protein (AP-1) complex
10694_at 167.4 A
probable neutral zinc metalloproteinase
10695_at 18.0 A
probable purine nucleotide-binding protein
10696_at 284.2 A
probable folyl-polyglutamate synthetase
10697_at -37.3 A
questionable ORF
10698_at 954.7 P
Required for mother cell-specific HO expression
10699_at 1523.7 P
myosin I
10700_at 3233.4 P
Phospo-mutase homolog
10701_at 3720.0 P
phosphoglucomutase, minor isoform
10702_at 3694.1 P
76.5 kDa Serine\/threonine protein kinase with similarity to protein kinase C, is 90\% identical to Ypk2p
10703_at 797.9 P
DNA-independent RNA Polymerase I transcription factor
10704_at -292.2 A
suppressor of SHR3\; confers leflunomide resistance when overexpressed
10705_g_at 194.2 A

suppressor of SHR3\; confers leflunomide resistance when overexpressed
10706_at 544.6 P
questionable ORF
10707_at 2123.8 P
component of signal recognition particle
10708_at 490.3 P
strong similarity to YMR102c
10709_at 5409.5 P
similarity to mitochondrial uncoupling proteins (MCF)
10710_at 884.8 P
25.2 kDa protein involved in assembly of vacuolar H(+) ATPase
10711_at 118.8 A
questionable ORF
10712_at 11497.2 P
Hsp90 (Ninety) Associated Co-chaperone
10713_at 818.9 P
probable serine\/threonine-specific protein kinase (EC 2.7.1.-)
10669_at 699.3 A
questionable ORF
10670_at 1149.2 P
major apurinic\/apyrimidinic endonuclease\/3 -repair diesterase
10671_at 1924.3 P
42 kDa 5 to 3 exonuclease required for Okazaki fragment processing
10672_at 673.9 P
transcriptional activator and ARS1 binding protein
10673_at 437.9 P
questionable ORF
10674_at 1915.3 P
Protein involved in resistance to K. lactis killer toxin
10675_at 1931.3 P
transcriptional activator protein of CYC1 (component of HAP2\/HAP3 heteromer)
10676_at -4.2 A
DNA replication and checkpoint protein 1
10677_at 69.0 A
weak similarity to S.antibioticus probable oxidoreductase
10678_at 1378.2 P
aspartate aminotransferase, mitochondrial
10679_at 418.6 P
similarity to YMR086w
10680_at 3405.9 P
Glutamine_fructose-6-phosphate amidotransferase (glucoseamine-6-phosphate synthase)
10681_at 1260.8 P
vacuolar aminopeptidase ysc1
10682_at -116.0 A
hypothetical protein
10683_at 197.6 A
Putative protein kinase homologous to S. pombe cdr1\/nim1
10684_at 692.4 P
similarity to C.elegans hypothetical protein
10685_at 839.8 P
similarity to C.elegans hypothetical proteins C18G6.06 and C16C10.2
10686_at 697.5 P
hypothetical protein
10687_at 558.5 A
hypothetical protein
10688_at 120707.3 P

cell wall mannoprotein

10689_at	2797.2	P

cell wall mannoprotein

10690_at	-203.7	A

similarity to C.elegans hypothetical proteins

10691_at	3044.7	P

weak similarity to E.coli hypothetical protein

10646_at	61.5	A

MBR1 protein precursor

10647_at	486.4	A

GTPase-activating protein (GAP) for Rsr1p\/Bud1p

10648_at	245.7	A

strong similarity to Sec14p

10649_at	313.3	P

hypothetical protein

10650_at	497.1	P

Centromere protein required for normal chromosome segregation and spindle integrity

10651_at	302.4	A

similarity to C.tropicalis hal3 protein, to C-term. of Sis2p and to hypothetical protein YOR054c

10652_at	-139.2	A

cytochrome c1 heme lyase

10653_at	325.2	A

hypothetical protein

10654_at	4606.0	P

mitochondrial malate dehydrogenase

10655_at	439.2	A

strong similarity to S.pombe hypothetical protein SPAC29B12

10656_at	2636.6	P

weak similarity to C.elegans hypothetical protein

10657_at	489.6	A

questionable ORF

10658_at	1560.7	P

Translation elongation factor EF-1gamma

10659_at	15323.8	P

Translation elongation factor EF-1gamma

10660_at	6853.0	P

Vacuolar H-ATPas hydrophilic subunit C of V1 sector

10661_at	550.6	P

kinesin heavy chain homolog, but is not believed to act as a kinesin, colocalizes with Myo2p

10662_at	995.3	A

probable ATP-dependent RNA helicase

10663_at	2839.8	P

hypothetical protein

10664_at	178.4	A

questionable ORF

10665_g_at	369.3	A

questionable ORF

10666_at	439.4	A

hypothetical protein

10667_at	589.2	P

involved in early pre-mRNA splicing

10668_at	1564.9	P

novel member of the Hsp70 family of molecular chaperones that localizes to the lumen of the endoplasmic reticulum:

10624_at	175.7	A

Binds Sin3p in two-hybrid assay

10625_at 844.3 P
weak similarity to A.parasiticus nor-1 protein
10626_at 250.5 A
similarity to B.subtilis transcriptional regulatory protein
10627_at 2579.1 P
strong similarity to hypothetical E.coli protein b1832
10628_at 2424.3 P
Nuclear pore complex protein homologous to Nup116p
10629_at 2561.3 P
Nucleoside diphosphate kinase
10630_at 763.9 P
hypothetical protein
10631_at 5045.3 P
Yeast endoplasmic reticulum 25 kDa transmembrane protein
10632_at 655.4 P
overexpression overcomes manganese toxicity
10633_at 837.6 P
weak similarity to mammalian microtubule-associated protein MAP 1B
10634_at 1160.0 P
zinc finger protein
10635_at 193.0 A
hypothetical protein
10636_at 200281.9 P
aldolase
10637_at 1829.9 P
similarity to C.elegans hypothetical protein
10638_at 1549.5 P
Transcription factor IIA, small chain
10639_at 449.0 A
100-kDa protein (predicted molecular weight is 120 kDa) with two leucine zipper motifs, coiled-coil region, and some homology to Nup133p
10640_at 39548.1 P
strong similarity to human IgE-dependent histamine-releasing factor
10641_at -219.3 A
probable acetoacetyl-CoA reductase
10642_at 5787.2 P
similarity to glutenin, high molecular weight chain proteins and Snf5p
10643_at 2000.8 P
similarity to C.elegans hypothetical protein T09A5.7 (12.5 kD)
10644_at 1090.0 P
questionable ORF
10645_at 909.5 P
hypothetical protein
10601_at 588.6 P
hypothetical protein
10602_at 44.8 A
similarity to YMR031c
10603_at 893.8 P
high similarity to histone H3 and to human centromere protein CENP-A
10604_at 609.3 P
protein kinase
10605_at 521.0 P
hypothetical protein
10606_at 4004.1 P
strong similarity to YMR238w
10607_at 502.6 P

p58 polypeptide of DNA primase
10608_at 479.1 A
hypothetical protein
10609_at 2475.9 P
putative transcription factor
10610_at 755.0 P
component of the spindle pole body
10611_at 598.6 P
endosomal Vps protein complex subunit
10612_at 1098.6 P
NifU-like protein B
10613_at 3049.5 P
Putative membrane protein
10614_at 600.3 A
transcriptional repressor and activator
10615_at 452.6 A
weak similarity to C.elegans ubc-2 protein
10616_at -8.1 A
questionable ORF
10617_at 6667.5 P
Uridinephosphoglucose pyrophosphorylase
10618_at 1307.0 P
weak similarity to YOL013c
10619_at 125.6 A
hypothetical protein
10620_at 4311.5 P
intrastrand crosslink recognition protein
10621_at 204.1 A
hypothetical protein
10622_at 179.8 A
questionable ORF
10623_at 5568.8 P
mitochondrial malic enzyme
10579_at 1490.9 P
Large subunit of transcription factor tfIIE
10580_at 978.0 P
similarity to E.coli molybdopterin-converting factor chlN
10581_at 99.0 A
strong similarity to glutathione peroxidase
10582_at 972.3 P
76-kDa subunit of Pab1p-dependent poly(A) ribonuclease (PAN)
10583_at 4709.8 P
uridine-monophosphate kinase (uridylate kinase)
10584_at 586.7 P
weak similarity to human cylicin II
10585_at 520.4 P
putative metal-binding nucleic acid-binding protein, interacts with Cdc23p and Cdc27p to catalyze the conjugation of ubiquitin to cyclin B
10586_at 1443.6 P
contains four beta-transducin repeats
10587_at 760.7 P
suppressor protein
10588_at 1188.7 P
CAAX farnesyltransferase alpha subunit
10589_at 942.0 P
similarity to C.elegans hypothetical protein

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10590_at     801.9      P
DNA helicase A
10591_at     3678.7     P
ATP synthase d subunit
10592_at     860.9      P
zinc-finger transcription factor of the Zn(2)-Cys(6) binuclear cluster domain type
10593_at     3036.8     P
hypothetical protein
10594_at     1869.5     P
Arp Complex Subunit
10595_at     389.1      A
Splicing component that associates with the yeast U1 small nuclear ribonucleoprotein particle
10596_at     219.4      A
cruciform cutting endonuclease
10597_at     1403.5     P
Ubiquitin Fusion Degradation
10598_at     3917.2     P
mRNA turnover 4
10599_at     3569.3     P
strong similarity to Lag1p
10600_at     2520.4     P
alpha subunit of capping protein
10555_at     1162.4     P
required for transport of proteins between an early and a later golgi compartment. possible NSF
attachment protein receptor (V-SNARE)
10556_i_at   31968.5    P
Ribosomal protein L14A
10557_f_at   61889.8    P
Ribosomal protein L14A
10558_s_at   91587.7    P
Ribosomal protein L14A
10559_at     348.7      A
weak similarity to YKR029c and D.melanogaster transcription elongation factor DmS-II
10560_at     4570.3     P
aureobasidin-resistance protein
10561_at     1543.2     P
Mitochondrial ribosomal protein MRP17
10562_at     971.8      P
similarity to hypothetical protein YKL041w
10563_at     745.6      P
adenylylsulfate kinase
10564_at     2707.1     P
putative GTP-binding protein\; similar to mammalian Mx proteins
10565_at     918.8      P
poly(A) polymerase
10566_at     897.8      P
similarity to Kes1p, Hes1p and Osh1p
10567_at     -133.2     A
ExtraCellular Mutant
10568_at     285.0      A
hypothetical protein
10569_at     1078.3     P
mitochondrial ribosomal protein YmL13
10570_at     958.0      P
weak similarity to Streptococcus protein M5 precursor
10571_at     453.9      P
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Member of RSC complex.
10572_at -128.7 A
peroxisomal multifunctional beta-oxidation protein
10573_at 694.5 P
topoisomerase I interacting factor 2
10574_at 404.0 P
hypothetical protein
10575_at 487.0 A
questionable ORF
10576_at 7105.7 P
Similar to plant PR-1 class of pathogen related proteins
10577_at 935.0 P
probable purine nucleotide-binding protein
10578_at -198.0 A
similarity to hypothetical protein YJL043w
10533_at 878.6 P
weak similarity to mysoin heavy chain proteins
10534_at 29.7 A
similarity to human hypothetical KIAA0161 protein
10535_at 4245.6 P
strong similarity to hypothetical protein YJL082w
10536_at 352.0 P
Increased rDNA silencing
10537_at 59.6 A
hypothetical protein
10538_at 497.7 P
strong similarity to hypothetical protein YJL084c
10539_at 283.8 A
hypothetical protein
10540_at 279.0 A
similarity to S.pombe hypothetical protein SPAC23C4
10541_at 1330.2 P
putative RNA helicase
10542_at 832.0 P
hypothetical protein
10543_at 1328.0 P
translation initiation factor eIF2B, 34 KD, alpha subunit\; negative regulator of GCD12, thereby serving indirectly as a positive regulator of GCN4
10544_at 1225.7 P
strong similarity to Chs6p
10545_at 1839.6 P
Type 2A-related protein phosphatase
10546_at 656.4 P
similarity to YJL105w and Lentinula MFBA protein
10547_at 910.6 P
weak similarity to NADH dehydrogenases
10548_at 671.9 P
Phospholipase D
10549_at 153.5 A
hypothetical protein
10550_at 41.1 A
questionable ORF
10551_at -17.4 A
negative regulator of multiple nitrogen catabolic genes
10552_at 1369.8 P
RAD52 Inhibitor (Fifty Two Inhibitor)

10553_at	1430.5	P	CCR4 associated factor
10554_at	299.6	A	component of spindle pole
10510_at	674.9	P	probable calcium-binding protein
10511_at	188.7	A	general amino acid permease
10512_at	562.2	P	questionable ORF
10513_at	197.6	A	hypothetical protein
10514_at	49776.7	P	YOUTH, involved in determining yeast longevity
10515_at	4901.8	P	weak similarity to phosphoglycerate mutase
10516_at	291.0	A	hypothetical protein
10517_at	188.3	A	hypothetical protein
10518_at	9540.8	P	hypothetical protein
10519_at	1174.4	P	questionable ORF
10520_at	6859.4	P	nucleosome assembly protein I
10521_at	594.1	P	hypothetical protein
10522_at	226.3	A	membrane protein\; low affinity potassium transport
10523_at	132.7	A	similarity to C.elegans hypothetical protein
10524_at	426.2	A	mitochondrial carrier protein, highly homologous to Mrs3p
10525_at	327.6	A	DHS-1-P phosphatase
10526_at	780.8	P	heavy chain of cytoplasmic dynein
10527_at	225.4	A	ras homolog--GTP binding protein
10528_at	1358.0	P	endo-exonuclease yNucR
10529_i_at	67338.7	P	Ribosomal protein S21A (S26A) (YS25)
10530_at	190.6	A	self-glucosylating initiator of glycogen synthesis\; similar to mammalian glycogenin
10531_at	222.4	A	hypothetical protein
10532_at	384.5	A	putative mannosyltransferase\; type 2 membrane protein
10487_at	792.2	P	Small subunit of TFIIE transcription factor
10488_at	796.0	P	May regulate expression of genes involved in bud formation and morphogenesis
10489_at	241.9	A	weak similarity to transcription factors

10490_at	1861.2	P	hypothetical protein
10491_at	2486.5	P	Cytochrome-c peroxidase
10492_at	77.3	A	strong similarity to Sct1p
10493_at	2516.6	P	Hydrophilic protein that acts in conjunction with SNARE proteins in targeting and fusion of ER to Golgi transport vesicles
10494_at	544.8	A	siroheme synthase
10495_at	2147.8	P	strong similarity to S. pombe phosphatidyl synthase
10496_at	1576.3	P	weak similarity to C.elegans hypothetical protein
10497_at	2836.6	P	sit4 suppressor
10498_at	235.0	A	hypothetical protein
10499_at	1285.2	P	strong similarity to hypothetical S. pombe protein
10500_at	758.0	P	weak similarity to negative regulator Reg1p
10501_at	829.3	P	ExtraCellular Mutant
10502_at	538.1	P	hypothetical protein
10503_at	455.9	A	similarity to Vps5p
10504_at	438.1	A	similarity to S.pombe hypothetical protein SPAC1D4.10
10505_at	2401.8	P	NAD-dependent 5,10-methylenetetrahydrafolate dehydrogenase
10506_at	4936.3	P	hypothetical protein
10507_at	1642.8	P	Nuclear pore complex protein involved in poly(A)+ RNA transport, nuclear pore distribution, and possibly in the biogenesis of functional tRNA
10508_at	272.1	A	weak similarity to S.japonicum paramyosin
10509_at	1723.4	P	Protein related to translation elongation factor EF-1alpha and to Suf12p\/Sup2p\/Gst1p\/Sup35p
10464_at	732.7	P	22.3 kDa mitochondrial ribosomal large subunit protein YmL20\; homologous to L17 of E. coli
10465_at	299.1	P	putative ATP-binding protein
10466_at	963.3	P	similarity to hypothetical Myxococcus xanthus protein
10467_at	1236.5	P	weak similarity to b.subtilis spore germination protein II
10468_at	1820.0	P	strong similarity to YOR081c
10469_at	1053.3	P	similarity to chicken Lim protein kinase and Islet proteins
10470_at	1403.0	P	Suppressor of rad53 lethality

10471_at 4349.0 P
nucleolar protein that is immunologically and structurally related to rat Nopp140, a nonribosomal protein of the nucleolus and coiled bodies.
10472_at 1889.8 P
Peptide transporter
10473_i_at 7328.0 P
Ribosomal protein L40B
10474_s_at 115356.0 P
Ribosomal protein L40B
10475_at 810.9 P
myosin-like protein
10476_at 492.6 P
similarity to mitochondrial aldehyde dehydrogenase Ald1p
10477_g_at 531.0 P
similarity to mitochondrial aldehyde dehydrogenase Ald1p
10478_at 58.7 A
phosphoenolpyruvate carboxylkinase
10479_at 365.7 A
Ubiquitin-specific protease
10480_at 351.3 A
Transcription factor regulating basal and induced activity of histidine and adenine biosynthesis genes
10481_at 519.4 P
cause growth inhibition when overexpressed
10482_at 366.9 M
repressor of silent mating loci
10483_at 119.7 A
Protein with similarity to flocculation protein Flo1p
10484_at 17.7 A
similarity to multidrug resistance proteins
10485_at -4.1 A
similarity to multidrug resistance proteins
10486_s_at -151.9 A
strong similarity to Sge1p and hypothetical protein YCL069w
10442_s_at 267.9 A
regulates the mannosylphosphorylation
10443_at -45.9 A
hypothetical protein identified by SAGE
10444_at 1049.0 P
hypothetical protein
10445_s_at 1332.9 P
regulates the mannosylphosphorylation
10446_s_at 1195.5 P
Protein of unknown function
10447_s_at 466.5 P
probable serine\/threonine-specific protein kinase (EC 2.7.1.-)
10448_s_at 1781.0 P
strong similarity to holacid-halidohydrolase
10449_at -51.6 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 361.5 A
non-annotated SAGE orf Found forward in NC_001143 between 94073 and 94228 with 100% identity. See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251
10451_at 218.0 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 1338.6 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 -74.5 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 -19.0 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 95.2 A
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 944.2 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 -132.3 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 -61.7 A
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 712.8 M
non-annotated SAGE orf Found reverse in NC_001143 between 164674 and 164820 with 100% identity.
See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251
10460_at 617.6 A
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 51.2 A
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 3780.8 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 309.6 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 258.1 A
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 3900.5 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 978.6 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 423.0 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 -70.7 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 -459.5 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 4472.8 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 3.2 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 250.7 A
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 -281.9 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 254.3 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 -8.7 A
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 256.0 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 -59.5 A
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 62.2 A
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 244.2 A
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 509.9 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 -88.7 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 76.1 A
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 -252.8 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 237.2 A
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 238.2 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 35.9 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 146.2 A
non-annotated SAGE orf Found reverse in NC_001143 between 468759 and 468899 with 100% identity.
See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251
10397_at 493.1 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 -159.8 A

non-annotated SAGE orf Found forward in NC_001143 between 533255 and 533518 with 100% identity. See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251
10399_at 102.4 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 65.9 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 267.3 A
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 407.4 A
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 -84.2 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 129.3 A
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 235.4 A
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 786.6 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 136.9 A
snRNA
10408_at 371.5 P
snRNA
10409_at 758.4 P
snRNA
10410_at -54.2 A
snRNA
10411_f_at 65.6 A
Growth INhibitory protein
10412_f_at 933.3 P
strong similarity to members of the Srp1/Tip1p family
10413_at 340.8 A
transacetylase
10414_at -75.4 A
weak similarity to M.leprae metH2 protein
10415_at 243.4 A
strong similarity to amino acid transport protein Gap1p
10416_at 360.3 A
Glutathione transferase
10417_at -162.8 A
hypothetical protein
10418_at 487.3 A
similarity to N.crassa O-succinylhomoserine (thiol)-lyase
10373_at 42.1 A
similarity to E.coli dioxygenase
10374_at 191.7 A
weak similarity to Y.pseudotuberculosis CDP-3,6-dideoxy-D-glycero-L-glycero-4-hexulose-5-epimerase
10375_at 274.3 A
similarity to Dal5p

10376_at 329.4 A
similarity to transcription factor Pip2p
10377_at 1479.7 P
similarity to water channel proteins
10378_at 803.9 P
member of mip family transmembrane channels
10379_at 961.8 A
similar to FRE2
10380_at 11239.5 P
Cofilin, actin binding and severing protein
10381_at 208.8 A
hypothetical protein
10382_at 4101.4 P
yeast bile transporter, similar to mammalian bile transporter
10383_at -24.5 A
questionable ORF
10384_at 109.9 A
ribonucleoprotein 1
10385_i_at 63655.8 P
Ribosomal protein L8B (L4B) (rp6) (YL5)
10386_s_at 35954.3 P
Ribosomal protein L8B (L4B) (rp6) (YL5)
10387_at 3703.7 P
questionable ORF
10388_at 3227.0 P
Suppressor of tps1\/fdp1 and member of the MIP family of transmembrane channels\; may be involved in glycerol efflux
10389_at -8.6 A
hypothetical protein
10390_at 153.1 P
Succinate dehydrogenase (ubiquinone) iron-sulfur protein subunit
10391_at 1235.9 P
involved in regulating membrane traffic
10392_at 1571.1 P
ubiquitin
10393_at 174.8 A
weak similarity to YJR125c and YDL161w
10394_at 206.2 A
weak similarity to human platelet-activating factor receptor
10395_at 1426.7 P
RNA splicing factor
10351_at -168.1 A
hypothetical protein
10352_at 3588.7 P
similarity to mammalian valosin
10353_at -37.2 A
hypothetical protein
10354_at 252.4 A
hypothetical protein
10355_at 1926.3 P
similarity to hypothetical protein YJL062w
10356_at 49.5 A
hypothetical protein
10357_at 1501.8 P
similarity to M.jannaschii X-Pro dipeptidase and S.pombe hypothetical protein
10358_at -24564.8 A

similarity to multidrug resistance proteins
10359_at 1302.3 P
similarity to H.influenzae and E.coli hypothetical proteins
10360_at 3303.4 P
heat shock protein 104
10361_f_at 10008.6 P
strong similarity to members of the Srp1p/Tip1p family
10362_at 65588.0 P
member of 70 kDa heat shock protein family
10363_at 3761.9 P
similarity to hypothetical protein YLR064w
10364_at 1000.9 P
Hat1 Interacting Factor 1
10365_at 1305.4 P
spindle pole antigen
10366_i_at 1623.5 P
questionable ORF
10367_r_at 2040.5 P
questionable ORF
10368_s_at 1668.0 P
questionable ORF
10369_at 296.2 A
protein kinase homolog
10370_at 22459.0 P
Aspartyl-tRNA synthetase, cytosolic
10371_at 94.2 A
maybe part of SCD25
10372_at -166.0 A
homologous to cdc25
10328_at 840.4 P
similarity to metal resistance proteins
10329_at 2332.2 P
hypothetical protein
10330_at 618.6 P
similarity to Drosophila pumilio protein
10331_at 3311.5 P
similarity to triacylglycerol lipases
10332_at 1841.2 P
56 kDa nucleolar snRNP protein that shows homology to beta subunits of G-proteins and the splicing factor Prp4
10333_at 812.2 P
strong similarity to hypothetical protein YLR019w
10334_at 1075.0 P
cysteine-rich cytoplasmic protein
10335_at 1428.4 P
putative ATP dependent RNA helicase
10336_at 181.2 A
hypothetical protein
10337_at 449.7 A
mitochondrial outer membrane protein
10338_at 117.3 A
similarity to A.thaliana hyp1 protein
10339_at 643.6 P
Third subunit of the origin recognition complex
10340_at 438.5 A
protein of unknown function

10341_at	198.8	A	Killed in Mutagen, sensitive to diepoxybutane and\/or mitomycin C
10342_at	586.8	P	Dynamin-related protein
10343_at	750.7	P	hypothetical protein
10344_at	1818.3	P	similarity to hypothetical C. elegans protein
10345_at	1269.4	P	hypothetical protein
10346_at	168.0	A	similarity to allantoate transport protein
10347_at	5017.3	P	Component of RNA polymerase transcription factor TFIIH
10348_at	482.4	A	Two-component signal transducer that with Sln1p regulates osmosensing MAP kinase cascade(suppressor of sensor kinase)
10349_at	294.8	A	hypothetical protein
10350_at	1022.8	P	similarity to hypothetical protein YNL328c
10305_at	1805.1	P	similarity to ribosomal protein L24.e.B
10306_at	475.8	P	weak similarity to Aquifex aeolicus adenylosuccinate synthetase
10307_at	-288.1	A	weak similarity to E.coli hypothetical 20.4 kDa protein
10308_at	-561.6	A	hypothetical protein
10309_at	196.1	A	weak similarity to nitrogen regulatory proteins
10310_at	618.6	P	zinc-finger transcription factor of the Zn(2)-Cys(6) binuclear cluster domain type
10311_at	511.8	P	weak similarity to S.pombe hypothetical protein SPBC13G1
10312_at	373.7	M	hypothetical protein
10313_at	2399.2	P	Protein that regulates ADH2 gene expression
10314_at	470.6	P	hypothetical protein
10315_at	819.2	P	strong similarity to YLL010c
10316_at	745.2	P	similarity to triacylglycerol lipase
10317_at	727.3	P	hypothetical protein
10318_at	497.2	P	similarity to C.elegans and M.jannaschii hypothetical proteins
10319_at	1209.3	P	similarity to S.pombe hypothetical protein SPAC30D11.11
10320_at	122.5	A	similarity to ubiquitin--protein ligase Ubr1p
10321_at	2055.3	P	involved in derepression of SUC2 in response to glucose limitation
10322_at	570.4	A	

Sed5p is a t-SNARE (soluble NSF attachment protein receptor) required in ER to Golgi transport.
10323_at 12773.0 P
aspartate aminotransferase, cytosolic
10324_at 6344.7 P
5-aminoimidazole-4-carboxamide ribonucleotide (AICAR) transformylase\/IMP cyclohydrolase
10325_at 22888.6 P
Ribosomal protein L15A (YL10) (rp15R) (L13A)
10326_g_at 42770.9 P
Ribosomal protein L15A (YL10) (rp15R) (L13A)
10327_at 90.3 A
hypothetical protein
10283_at 50.4 A
similarity to hypothetical protein YMR124w
10284_at 410.2 A
putative ATPase\/DNA helicase
10285_at 344.6 A
hypothetical protein
10286_at 3934.3 P
strong similarity to SMF2 protein
10287_at 311.3 P
similarity to human mutL protein homolog
10288_at 749.4 P
similarity to YIL089w
10289_f_at 1388.4 P
strong similarity to members of the Srp1p/Tip1p family
10290_at 5450.1 P
subunit VIb of cytochrome c oxidase
10291_at 964.0 P
involved in transcription of ribosomal proteins and ribosomal RNA
10292_at 9120.9 P
weak similartity to hypothetical protein YIL011w
10293_at 328.6 A
questionable ORF
10294_at 639.4 P
hypothetical protein
10295_at 14849.8 P
thioredoxin
10296_at 185712.1 P
pyruvate decarboxylase
10297_at 976.6 P
May play a role in attachment, organization, and\/or dynamics of microtubule ends at the spindle pole body
10298_at 214.6 A
strong similarity to Rta1p and Rtm1p protein
10299_at -79.4 A
similarity to hypothetical protein YGL160w
10300_f_at 11582.0 P
Ribosomal protein S0B
10301_at 63367.6 P
Ribosomal protein S0B
10302_g_at 70006.1 P
Ribosomal protein S0B
10303_at -4.9 A
hypothetical protein
10304_at 4571.7 P
weak similarity to human MAC30 C-terminus

10260_at	836.7	P
similarity to human acidic 82 kDa protein
10261_at	736.7	P
hypothetical protein
10262_at	142.1	A
hypothetical protein
10263_at	477.6	A
hypothetical protein
10264_at	2304.4	P
transcription factor, probable member of histone acetyltransferase SAGA complex
10265_at	26981.2	P
C-5 sterol desaturase
10266_at	951.9	P
weak similarity to mouse alpha-mannosidase
10267_at	10061.0	P
serine hydroxymethyltransferase
10268_at	2933.0	P
suppressor of rna12/yme2
10269_at	18817.0	P
Phenylalanyl-tRNA synthetase, alpha subunit, cytoplasmic
10270_at	71569.3	P
Ribosomal protein L22A (L1c) (rp4) (YL31)
10271_at	2143.6	P
questionable ORF
10272_at	255.8	A
ser/thr protein kinase
10273_at	1590.3	P
weak similarity to Anopheles NADH-ubiquinone oxidoreductase, chain 4
10274_at	3219.9	P
hypothetical protein
10275_at	1024.0	P
signal peptidase subunit
10276_at	-104.7	A
Involved in expression of mitochondrial COX1 by regulating translation of COX1 mRNA and by affecting transcription or stability of COX1 mRNAs
10277_at	26.9	A
hypothetical protein
10278_at	1416.0	P
mitochondrial elongation factor G-like protein
10279_at	262.7	A
strong similarity to sugar dehydrogenases
10280_at	1717.5	P
component of RNA polymerase II holoenzyme\/mediator complex, interacts with Sin4p, Gal11p, and a 50 kd polypeptide
10281_at	682.1	P
similarity to YFL042c, YFL043c, YDR326c and YHR080c
10282_at	360.1	A
hypothetical protein
10238_at	2094.2	P
weak similarity to human zinc finger protein
10239_at	99035.3	P
Ribosomal protein L10\; Ubiquinol-cytochrome C reductase complex subunit VI requiring protein
10240_at	5029.3	P
questionable ORF
10241_at	-2.8	A
weak similarity to Xenopus RCC1 protein

10242_at 772.2 P

necessary for vesicular transport from the ER to the Golgi complex

10243_at 653.7 P

P40 inhibitor of Cdc28p-Clb5 protein kinase complex

10244_at 265.3 A

strong similarity to Emp47p

10245_at 161.2 P

galactose permease

10246_at 119.1 A

Suppressor of rad53 lethality

10247_at 6149.5 P

integral membrane protein\; p24a protein

10248_at 1783.9 P

weak similarity to S.pombe hypothetical protein SPAC6F6

10249_at 795.2 P

Actin-related protein

10250_at 282.5 A

Smc4 protein, member of SMC family

10251_at 527.4 P

hypothetical protein

10252_at 1504.0 P

Possible component of GPI:protein transamidase

10253_at 5263.4 P

strong similarity to alanine transaminases

10254_at 1374.4 P

Homolog of E. coli DnaJ, closely related to Ydj1p

10255_at 125.4 A

hypothetical protein

10256_at 233.1 A

high affinity sulfate permease

10257_at 366.1 A

vacuolar v-SNARE

10258_at 221.8 A

hypothetical protein

10259_at 2531.1 P

hypothetical protein

10215_at 2580.3 P

Serine\/threonine protein kinase

10216_at 293.8 M

hypothetical protein

10217_at -81.1 A

DNA-binding transcriptional activator or CHA1

10218_at 13636.5 P

similarity to YDR125c

10219_at 7460.1 P

similarity to rat ovarian specific protein

10220_at 416.1 A

questionable ORF

10221_at 266.6 A

subunit of the anaphase promoting complex (APC)

10222_at 532.0 P

omosomal DNA replication initiation protein

10223_at 652.6 P

hypothetical protein

10224_at 792.0 P

tRNA splicing endonuclease subunit

10225_at	948.0	P	similarity to Kaposi s sarcoma-associated herpes-like virus ORF73 homolog gene
10226_at	788.4	P	similarity to Pan troglodytes prot GOR
10227_at	363.5	P	strong similarity to YDR132c
10228_at	37035.4	P	similarity to C.boidinii peroxisomal membrane protein 20K A
10229_at	238951.9	P	strong similarity to Flo1p
10230_at	-90.8	A	hypothetical protein
10231_at	578.8	P	hypothetical protein
10232_at	3801.7	P	mitogen-activated protein kinase (MAP kinase)
10233_at	450.5	P	similarity to C.elegans hypothetical protein and YOR054c
10234_at	610.9	P	Component of cleavage factor II (CF II)\; 105-kDa protein associated with polyadenylation factor 1 (PF I)
10235_at	697.1	P	Branchpoint bridging protein -- component of the splicing commitment complex
10236_at	312.4	A	SYnthetic lethal with cdc40 (Forty)
10237_at	1002.4	P	similarity to several esterases
10192_at	-50.1	A	suppressor of rna1-1 mutation
10193_at	2543.6	P	GPI-anchored aspartic protease
10194_at	3353.2	P	GPI-anchored aspartic protease
10195_at	-121.0	A	hypothetical protein
10196_g_at	-95.4	A	hypothetical protein
10197_at	291.9	A	questionable ORF
10198_at	120.4	A	hypothetical protein
10199_at	50.4	A	hypothetical protein
10200_at	213.6	A	weak similarity to P.aeruginosa anthranilate synthase component II
10201_at	229.6	A	subunit of the anaphase promoting complex (APC)
10202_at	628.0	A	similarity to S.pombe hypothetical protein SPBC24E9
10203_at	1388.4	P	DOM34 Interacting Protein
10204_at	1497.4	P	Low-affinity zinc transport protein
10205_at	649.7	P	zinc finger transcription factor
10206_at	377.9	P	hypothetical protein

10207_at 711.0 P
choline kinase
10208_at 3611.8 P
pyruvate decarboxylase
10209_at 466.6 A
hypothetical protein
10210_at 222.2 A
zinc finger containing homolog of mammalian TIS11, glucose repressible gene
10211_at 463.3 P
hypothetical protein
10212_at 1617.6 P
Putative Na+\/H+ antiporter
10213_at -28.5 A
73 kDa mitochondrial integral membrane protein
10214_at -123.2 A
questionable ORF
10170_g_at 1380.3 P
questionable ORF
10171_at 661.2 P
transcription factor, member of UAF (upstream activation factor) along with Rrn9p and Rrn10p
10172_at 17.8 A
proline oxidase
10173_at 523.5 A
weak similarity to Pyrococcus horikoshii hypothetical protein PHBJ017
10174_at 1158.6 P
Identified as an activity necessary for actin polymerization in permeabilized cells
10175_at 637.3 P
hypothetical protein
10176_at 444.7 P
Spermine Synthase
10177_at 1300.4 P
encodes a core snRNP protein
10178_at -271.2 A
vacuolar membrane protein
10179_at 0.4 A
hypothetical protein
10180_at 38339.1 P
specific affinity for guanine-rich quadruplex nucleic acids
10181_at 204.9 A
weak similarity to A.thaliana hypothetical protein ATU78721
10182_at 765.0 P
similarity to YOR3165w and YNL095c
10183_at 28253.5 P
acetyl-coenzyme A synthetase
10184_at 1971.7 P
hypothetical protein
10185_s_at 2762.4 P
nitrogen catabolite-regulated cell-wall L-asparaginase II
10186_s_at 12.8 A
identical to hypothetical proteins YLR161w and YLR159w
10187_at 33652.9 P
hypothetical protein
10188_at 1014.1 P
mitochondrial processing protease subunit
10189_at -170.0 A
strong similarity to Sdh4p

10190_at	310.3	A	weak similarity to H.influenzae hypothetical protein HI0176
10191_at	502.2	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	117080.4	P	Ribosomal protein S31 (S37) (YS24)
10148_at	883.6	P	probably involved in intramitochondrial protein sorting
10149_at	347.2	A	questionable ORF
10150_at	912.4	P	clathrin-associated protein complex, small subunit
10151_at	163.6	A	questionable ORF
10152_at	5633.9	P	S-adenosylmethionine (AdoMet)-dependent methyltransferase of diphthamide biosynthesis
10153_at	-107.0	A	hypothetical protein
10154_at	316.7	A	Cytosolic form of NADP-dependent isocitrate dehydrogenase
10155_at	14053.3	P	major low affinity 55 kDa Centromere\/microtubule binding protein
10156_at	592.1	P	DNA binding protein, homologous to a family of mammalian RFX1-4 proteins which have a novel highly conserved DNA binding domain
10157_at	1095.4	P	similarity to suppressor protein Psp5p
10158_at	455.3	A	suppressor of cdc25
10159_at	5994.6	P	similarity to Tfs1p
10160_at	6462.9	P	S-adenosylmethionine synthetase
10161_g_at	43233.1	P	S-adenosylmethionine synthetase
10162_at	749.7	P	hypothetical protein
10163_at	930.6	P	regulatory protein
10164_at	541.6	A	similarity to YDR501w
10165_at	420.2	A	weak similarity to ribulose-bisphosphate carboxylase
10166_at	80901.4	P	60S ribosomal protein L37A (L43) (YL35)
10167_at	3040.7	P	strong similarity to S.pombe hypothetical protein C18G6.07C
10168_at	676.7	P	similarity to hypothetical protein YNL278w
10169_at	3042.4	P	ATP-binding cassette (ABC) transporter family member
10124_at	1950.4	P	similarity to P.aeruginosa rhamnosyltransferase 1 chain B
10125_at	719.1	P	hypothetical protein

10126_at 610.8 P
Peroxisomal membrane protein that contains Src homology 3 (SH3) domain
10127_at 7827.5 P
weak similarity to fruit fly transcription factor 5 large chain
10128_at 764.5 P
similarity to G.gallus px19 and Msf1p
10129_at 4374.6 P
hypothetical protein
10130_at 2527.8 P
N-myristoyl transferase
10131_at 4452.6 P
Protein with periodic trytophan residues that resembles members of beta-transducin superfamily because of presence of WD-40 repeats
10132_at 4885.8 P
homology to microtubule binding proteins and to X90565_5.cds
10133_at 4509.7 P
questionable ORF
10134_at 1713.1 P
hypothetical protein
10135_at 900.8 P
Polypeptide 6 of a Yeast Non-native Actin Binding Complex, homolog of a component of the bovine NABC complex
10136_at 948.5 P
similarity to hypothetical S. pombe protein
10137_at 141.7 A
questionable ORF
10138_g_at -254.9 A
questionable ORF
10139_i_at 7448.6 P
questionable ORF
10140_r_at 3195.2 P
questionable ORF
10141_at 1063.8 P
Protein involved in maturation of COX1 and COB mRNA
10142_at 2129.9 P
protein of unknown function
10143_at 4552.1 P
hypothetical protein
10144_at 1724.8 P
similarity to human tricohyalin and protein KIAA0171
10145_at 502.4 P
HMG-CoA Reductase Degradation
10146_at 3616.2 P
cytoplasmic protein involved in release of transport vesicles from the ER
10101_at 1865.2 P
strong similarity to purine-nucleoside phosphorylases
10102_at 390.7 A
G(sub)2-specific B-type cyclin
10103_at 328.3 A
hypothetical protein
10104_at 1133.0 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 213.1 A
similarity to UTR2 protein
10106_at 2824.4 P

Ferric (and cupric) reductase
10107_at 298.3 A
strong similarity to rat cell cycle progression related D123 protein
10108_at 6547.0 P a
cyclophilin related to the mammalian CyP-40\; physically interacts with RPD3 gene product
10109_at -100.2 A
questionable ORF
10110_at 565.6 P
hypothetical protein
10111_at 1021.0 P
hypothetical protein
10112_at 834.2 P
Possible transmembrane Ca2+ transporter
10113_at 564.9 P
hypothetical protein
10114_at 1963.6 P
similarity to Dip2p
10115_at 390.9 A
has a weak RNA-dependent ATPase activity which is not specific for rRNA
10116_at 844.6 P
hypothetical protein
10117_at 808.8 P
strong similarity to YDR222w
10118_at 327.6 A
hypothetical protein
10119_at 354.2 A
hypothetical protein
10120_at 817.0 P
strong similarity to YDR213w, weak similarity to Lys14p
10121_at 4066.1 P
member of the Rho subfamily of Ras-like proteins
10122_at -11.0 A
questionable ORF
10123_at 922.0 P
strong similarity to rat kynureninase
10079_at 142.7 A
questionable ORF
10080_at -134.6 A
Telomere elongation protein (ever shorter telomeres)
10081_at -42.3 A
DNA Topoisomerase III
10082_at 331.0 A
questionable ORF
10083_g_at 139.9 A
questionable ORF
10084_at 317.1 A
hypothetical protein
10085_at 1951.3 P
thiamine transporter
10086_at 531.3 P
similarity to YDR200c
10087_at 338.0 A
weak similarity to H.influenzae lipoate biosynthesis protein B
10088_at 984.5 P
phosphatidylinositol 3-kinase
10089_at 825.0 P

similarity to hypothetical S.pombe protein SPAC2G11.09
10090_at 162.0 A
weak similarity to C.elegans R05H5.5 protein and Nup120p
10091_at 1359.2 P
strong similarity to YOR262w
10092_at 3977.0 P
methionine aminopeptidase
10093_at 533.0 A
strong similarity to B.subtilis cytidine deaminase
10094_at 373.3 A
similarity to human DHHC-domain-containing cysteine-rich protein
10095_at 735.9 P
similarity to S.pombe rad8 protein and Rdh54p
10096_at 2562.3 P
Serine\/threonine protein kinase
10097_at 200664.6 P
EF-3 (translational elongation factor 3)
10098_at 638.5 M
secretory protein
10099_at 65.6 A
similarity to peroxisomal rat membrane protein PMP22
10100_at 667.7 P
questionable ORF
10055_at 731.3 P
weak similarity to bacterial aminoglycoside acetyltransferase regulators
10056_at 923.2 P
hypothetical protein
10057_at 97.1 A
hypothetical protein
10058_at 439.0 A
zinc-finger transcription factor of the Zn(2)-Cys(6) binuclear cluster domain type
10059_at 2035.5 P
hypothetical protein
10060_at 645.5 A
Glycogen synthase (UDP-gluocse--starch glucosyltransferase)
10061_at 52498.0 P
heat shock protein 60\; chaperonin protein
10062_at 728.9 P
sphingoid long chain base (LCB) kinase
10063_i_at 311.9 A
questionable ORF
10064_s_at 731.5 P
questionable ORF
10065_at 243.7 A
highly homologous to the human GTPase, Rab6
10066_s_at 2658.3 P
strong similarity to F49C12.11 (Z68227_K) from C. elegans
10067_at 58.9 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 3600.8 P
Ribosomal protein S28B (S33B) (YS27)
10069_f_at 5025.6 P
Ribosomal protein S28B (S33B) (YS27)
10070_at 19.3 A
hypothetical protein

10071_at	178.3	A	weak similarity to transcription factors
10072_at	-360.5	A	Bypass of PAM1
10073_at	756.4	P	Synaptobrevin (v-SNARE) homolog present on ER to Golgi vesicles
10074_at	132.0	A	questionable ORF
10075_at	659.0	P	strong similarity to YOR173w
10076_at	307.0	A	hypothetical protein
10077_at	438.3	A	similarity to human hypothetical ORF
10078_at	155.4	A	Protein similar to Gac1p, a putative type 1 protein phosphatase targeting subunit
10032_at	562.3	P	Member of complex that acts at ARS s to initiate replication
10033_at	313.4	A	U1 snRNP protein of the Sm class
10034_at	2613.1	P	DEAD-Box Protein 9
10035_at	1217.9	P	subunit of Polyadenylation factor I (PF I)
10036_at	204.8	A	weak similarity to regulatory proteins
10037_at	250.1	A	questionable ORF
10038_i_at	262.6	P	questionable ORF
10039_s_at	298.9	A	questionable ORF
10040_at	233.9	A	similarity to polypeptide chain release factors
10041_at	347.9	P	questionable ORF
10042_at	79.5	A	weak similarity to Smc2p
10043_at	-89.1	A	Peroxisomal enoyl-CoA hydratase
10044_at	1267.2	P	hypothetical protein
10045_at	32477.9	P	Endochitinase
10046_at	453.3	A	weak similarity to S.pombe hypothetical protein SPAC22E12
10047_f_at	74297.0	P	Ribosomal protein S30A
10048_at	596.0	P	involved in checkpoint control and DNA repair
10049_at	346.4	A	GTPase
10050_at	1144.6	P	hypothetical protein
10051_at	1954.8	P	translation initiation factor eIF2b, 43 kDa subunit\; negative regulator of GCN4 expression

10052_at 1311.1 P
protein involved in membrane protein insertion into the ER
10053_at 19475.8 P
GTP-binding protein
10054_at 5508.4 P
questionable ORF
10010_at 1969.5 P
ATP synthase subunit h
10011_at -35.5 A
hypothetical protein
10012_at 259.6 A
weak similarity to Vibrio vulnificus VvpC protein
10013_at 477.1 A
U1 snRNP protein required for pre-mRNA splicing
10014_at 685.2 P
gamma-glutamyltransferase homolog
10015_at 18854.3 P
Exo-1,3-beta-glucanase
10016_at 4695.6 P
hypothetical protein
10017_at -161.3 A
questionable ORF
10018_at 19492.6 P
O-Acetylhomoserine-O-Acetylserine Sulfhydralase
10019_at 9092.6 P
Aconitase, mitochondrial
10020_at 1514.6 P
encodes a phosphatidylinositol-4-kinase, homologous to VPC34
10021_at 240.6 A
Ubiquitin-conjugating enzyme
10022_at -672.6 A
Chitin Deacetylase
10023_at 82.4 A
Chitin Deacetylase
10024_at 1373.2 P
similarity to human centromere protein E
10025_at 493.4 A
regulatory protein of adenylate cyclase
10026_at -197.6 A
weak similarity to S.tarentolae cryptogene protein G4
10027_at 96.3 A
hypothetical protein
10028_at 389.5 A
homologous to Spa2p, localizes to sites of polarized growth
10029_at 640.1 P
Component of 10 nm filaments of mother-bud neck
10030_at -55.8 A
weak similarity to rat apolipoprotein A-IV
10031_at 1387.1 P
weak similarity to H.influenzae hypothetical protein HI0906
9986_at 1297.3 P
questionable ORF
9987_at 17.9 A
103 kD basic protein, catalytic subunit of telomerase
9988_at 473.0 A
Actin Interacting Protein

9989_at 420.9 A
hypothetical protein
9990_at 755.1 P
homolog of Snf5p, member of the chromatin remodeling complex, RSC
9991_at 280.4 A
questionable ORF
9992_at 286.9 P
weak similarity to N.crassa uvs2 protein
9993_at 349.8 A
strong similarity to YGR004w
9994_at 35274.0 P
Ribosomal protein L38
9995_at 288.8 A
hypothetical protein
9996_at 374.9 P
strong similarity to Stf2p
9997_at 960.4 P
strong similarity to YGR010w
9998_at -13.2 A
23 kDa protein containing a putative leucine zipper\; meiosis specific recombination protein\; mRNA is induced early in sporulation
9999_at 2015.0 P
Involved in chitin synthase III activity, also required for homozygosis in the first stages of mating
10000_at 133.4 A
questionable ORF
10001_at 1730.6 P
Protein required for mating
10002_i_at 22990.9 P
Ribosomal protein S25B (S31B) (rp45) (YS23)
10003_f_at 27720.6 P
Ribosomal protein S25B (S31B) (rp45) (YS23)
10004_at 33.8 A
questionable ORF
10005_at 2839.5 P
nuclear pore complex protein with central repetitive domain similar to that of NSP1 and NUP1
10006_at 1079.5 P
Suppressor of Glycerol Defect
10007_at 1423.2 P
Proline-rich protein verprolin
10008_at 48.6 A
questionable ORF
10009_at 792.7 P
questionable ORF
9964_at 148532.7 P
60S ribosomal protein P0 (A0) (L10E)
9965_at 8.3 A
hypothetical protein
9966_at 16148.8 P
1,3-beta-D-glucan synthase
9967_at 190.2 A
strong similarity to Gas1p and C.albicans pH responsive protein
9968_s_at 105058.7 P
Ribosomal protein L26A (L33A) (YL33)
9969_at 516.2 P
similarity to Pfk26p and other 6-phosphofructo-2-kinases
9970_at 2788.1 P

weak similarity to YGR035c
9971_at 1250.0 P
95 kDa structural and functional homolog of vertebrate karyopherin beta (importin 90)
9972_at 2969.5 P
mitochondrial dicarboxylate transport protein
9973_at 644.1 P
questionable ORF
9974_at 5679.7 P
strong similarity to YGR038w
9975_at 4046.1 P
Nit3 nitrilase
9976_at 723.2 P
hypothetical protein
9977_at 533.6 P
budding protein
9978_at 8728.1 P
Transaldolase, enzyme in the pentose phosphate pathway
9979_at 31415.7 P
acetohydroxyacid reductoisomerase
9980_at 976.0 A
similarity to SCM4 protein
9981_at 492.5 P
questionable ORF
9982_at 880.2 P
Member of RSC complex.
9983_at 8934.3 P
Adenylosuccinate Lyase
9984_at 9.7 A
protein involved in vacuolar sorting
9985_at 421.3 A
similarity to YOR3329c
9941_at 279.2 P
Ser\/Thr protein kinase\; MEKK homolog
9942_at 43.7 A
putative Upf1p-interacting protein
9943_at 414.7 P
hypothetical protein
9944_at 171.9 A
weak similarity to Udf2p
9945_at 87.2 A
hypothetical protein
9946_at 1381.2 P
Ribosomal protein S22B (S24B) (rp50) (YS22)
9947_i_at 13952.9 P
Ribosomal protein S22B (S24B) (rp50) (YS22)
9948_f_at 16645.0 P
Ribosomal protein S22B (S24B) (rp50) (YS22)
9949_at 512.2 A
hypothetical protein
9950_at 472.0 P
Hsp70 protein
9951_at 764.9 P
Arp2\/3 Complex Subunit
9952_at 2065.8 P
GDP-GTP Exchange Protein (GEP) for the Rho1p Small GTP-binding Protein\; high copy suppressor of cik1 and kar3 deletion mutants.

9953_at	14316.7	P	required for conversion of 24-carbon fatty acids to 26-carbon species
9954_at	1219.3	P	similarity to hypothetical protein YGR071c
9955_at	-184.1	A	questionable ORF
9956_at	2341.5	P	Involved in pre-tRNA splicing and in uptake of branched-chain amino acids
9957_at	192.1	A	hypothetical protein
9958_at	290.2	A	fructose-1,6-bisphosphatase
9959_at	11270.2	P	membrane component of ER protein translocation apparatus
9960_at	-43.8	A	questionable ORF
9961_at	2039.1	P	weak similarity to SEC14 protein
9962_at	287.3	A	hypothetical protein
9963_at	652.3	P	mitochondrial leucyl tRNA synthetase
9918_at	1010.8	P	Protein involved in recombination repair, homologous to S. pombe rad18
9919_at	3213.4	P	confers sensitivity to killer toxin
9920_at	-204.2	A	hypothetical protein
9921_at	823.3	P	similarity to hypothetical S. pombe protein
9922_at	2445.8	P	similarity to YBR267w
9923_f_at	59799.2	P	Ribosomal protein S29A (S36A) (YS29)
9924_at	1094.3	P	protease involved in a-factor processing
9925_at	738.1	P	ExtraCellular Mutant
9926_at	19238.9	P	Secretory Stress Response protein 1
9927_at	79.1	A	hypothetical protein
9928_at	354.3	A	essential for assembly of a functional mitochondrial ATPase complex
9929_at	448.3	A	weak similarity to chicken RING zinc finger protein
9930_at	4294.1	P	Cytochrome-c oxidase chain VIII
9931_at	811.3	P	Vacuolar sorting protein essential for vacuolar morphogenesis and function
9932_at	1596.6	P	homology to the CDC48 gene product
9933_at	1674.1	P	antiviral protein, putative helicase
9934_at	1650.8	P	Bdf1p contains two bromodomains, localizes to the nucleus and to chomosomes in spread meiotic nuclei

but is excluded from the nucleolus
9935_at -10.7 A
hypothetical protein
9936_at 2263.1 P
similarity to A.brasilense nifR3 protein
9937_at 933.6 P
hypothetical protein
9938_at 352.8 A
split zinc finger protein
9939_at -254.3 A
hypothetical protein
9940_at 880.7 P
similarity to A.brasilense nifR3 protein
9895_i_at 22607.8 P
Ribosomal protein L31B (L34B) (YL28)
9896_f_at 27044.6 P
Ribosomal protein L31B (L34B) (YL28)
9897_f_at 63002.3 P
Ribosomal protein L31B (L34B) (YL28)
9898_at 662.3 P
hypothetical protein
9899_at 325.1 M
hypothetical protein
9900_at 2829.9 P
strong similarity to S. pombe beta-transducin
9901_at 4090.4 P
Homologous to S. pombe asp1+
9902_at 4979.9 P
Copper Transporter
9903_at 1190.6 P
weak similarity to Candida maltosa cytochrome P450
9904_at 1775.1 P
strong similarity to YKL187c
9905_at 3881.7 P
weak similarity to YLR413w
9906_at -146.5 A
questionable ORF
9907_at 361.3 A
hypothetical protein
9908_at 692.0 P
defective in vacuolar protein sorting
9909_at 1244.7 P
Accessory factor associated with RNA polymerase II by affinity chromatography
9910_at 1193.8 P
similarity to helicases
9911_at 8655.9 P
dihydrooratase
9912_at 2049.1 P
weak similarity to human 42K membrane glycoprotein
9913_at 867.8 P
similarity to human DOCK180 protein
9914_at 392.2 A
hypothetical protein
9915_at -47.3 A
weak similarity to Stu1p
9916_at 1060.8 P

hypothetical protein
9917_at 3142.8 P
weak similarity to 3-oxoacyl-[acyl-carrier-protein] reductase from E. coli
9873_at 515.0 A
weak similarity to 3-oxoacyl-[acyl-carrier-protein] reductase from E. coli
9874_at 1568.7 P
weak similarity to human transcription regulator Staf-5
9875_at -25.5 A
questionable ORF
9876_at 2375.3 P
has homology to the Dictyostelium and human actin-binding protein coronin
9877_at 1398.6 P
component of a nuclear-localized tRNA splicing complex
9878_at 284.2 A
weak similarity to rabbit trichohyalin
9879_f_at 24292.4 P
strong similarity to IMP dehydrogenases, Pur5p and YML056c
9880_at 1507.9 A
Calcineurin subunit A\; type 2B protein serine\/threonine phosphatase catalytic subunit A1\; cytoplasmic
9881_at 322.6 A
questionable ORF
9882_at 397.5 A
hypothetical protein
9883_at 1092.4 P
ExtraCellular Mutant
9884_at 118.8 A
hypothetical protein
9885_at 1990.9 P
ornithine aminotransferase
9886_at 2000.1 P
Putative snRNP protein containing Sm-like domain\; coprecipitates with U4, U5 and U6 snRNAs
9887_at 798.0 P
Mitochondrial 60S ribosomal protein L4
9888_at 1672.7 P
hypothetical protein
9889_i_at 18888.5 P
Ribosomal protein S1A (rp10A)
9890_s_at 42881.6 P
Ribosomal protein S1A (rp10A)
9891_at 1181.2 P
regulator of silent mating loci
9892_at 1013.8 P
ExtraCellular Mutant
9893_at 491.6 A
questionable ORF
9894_at 226.4 A
hypothetical protein
9850_at 86.6 A
weak similarity to hexokinases
9851_at 2552.4 P
36 kDa subunit (D subunit of VO sector) of the vacuolar H(+) ATPase\; required for assembly
9852_at 38222.8 P
60S ribosomal subunit protein L6B (L17B) (rp18) (YL16)
9853_at 6617.5 P
60 kDa nuclear FK506 binding protein
9854_at 4793.5 P

3-hydroxy-3-methylglutaryl-coenzyme A (HMG-CoA) reductase isozyme
9855_at 380.4 P
zinc-finger transcription factor of the Zn(2)-Cys(6) binuclear cluster domain type
9856_at 1543.7 P
Protein involved in desensitization to alpha-factor pheromone
9857_at -131.2 A
Nuclear protein
9858_at 1163.3 P
similarity to YPR117w
9859_at 316.1 A
weak similarity to human G/T mismatch binding protein
9860_at 165.3 A
strong similarity to YPR172w
9861_at -25.9 A
Nap1p-binding protein
9862_at -5.8 A
questionable ORF
9863_at 2075.5 P
cell division control protein
9864_at -139.0 A
similarity to C.carbonum toxD protein
9865_f_at 417.8 P
member of the seripauperin protein\/gene family (see Gene_class PAU)
9866_i_at 201.6 A
questionable ORF
9867_s_at 249.9 A
questionable ORF
9868_at 176.1 A
hypothetical protein identified by SAGE
9869_at 3854.9 P
identified by SAGE
9870_s_at -140.3 A
Mitochondrial ribosomal protein MRPL15 (YmL15)
9871_at 123.7 A
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 253.2 A
non-annotated SAGE orf Found forward in NC_001144 between 320496 and 320642 with 100% identity. See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251
9826_at 1389.9 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 1394.7 P
non-annotated SAGE orf Found forward in NC_001144 between 433871 and 434059 with 100% identity. See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251
9828_at 515.2 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 175.3 A
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 177.7 A
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 170.4 A
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 302.0 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 18.5 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 -151.6 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 1487.0 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 4767.7 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 3217.0 P
non-annotated SAGE orf Found forward in NC_001144 between 451607 and 451783 with 100% identity.
See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251
9838_s_at 26499.2 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 20768.5 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 147.3 A
non-annotated SAGE orf Found reverse in NC_001144 between 596345 and 596530 with 100% identity.
See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251
9841_at -202.1 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 1269.7 P
non-annotated SAGE orf Found reverse in NC_001144 between 849381 and 849677 with 100% identity.
See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251
9843_at -127.7 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 2164.1 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 996.9 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 117.6 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 2169.0 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 22.1 A
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 1567.6 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 301.4 A

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 336.7 A
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 4070.8 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 26.7 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 539.2 A
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 -38.0 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 135.9 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 163.9 A
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 87.1 A
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 238.3 A
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 173.5 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 39.1 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 5619.9 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 -4.7 A
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 -439.3 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 -215.6 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 285.5 A
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 2.2 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 53.5 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 2270.0 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 900.4 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 71.0 A
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 178.2 A
non-annotated SAGE orf Found forward in NC_001144 between 514745 and 514888 with 100% identity. See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251
9780_at 123.3 A
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 216.8 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 -162.6 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 737.6 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 1163.9 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 298.5 A
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 262.1 A
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 2151.4 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 869.2 A
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 620.6 P
non-annotated SAGE orf Found forward in NC_001144 between 1035773 and 1035940 with 100% identity. See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251
9790_i_at -14.1 A
Centromere
9791_f_at 178.8 P
Centromere
9792_s_at 708.7 P
CEN12-associated
9793_at 14.4 A
snRNA
9794_at 185.4 A
snRNA
9795_at 1135.4 P
snRNA
9796_at 214.8 A

snRNA
9797_i_at -21.6 A
snRNA
9798_at 1874.7 P
snRNA
9799_at 231.4 A
snRNA
9800_s_at 342.1 A
hypothetical protein Y .2
9801_at 208.3 A
similarity to human leukotriene b4 12-hydroxydehydrogenase
9802_at 1584.3 P
required for protein disulfide bond formation in the ER
9803_at 1762.7 P
mitochondrial membrane protein
9757_at 249.3 A
C-terminal part starting with aa 262 cause growth inhibition when overexpressed
9758_at 2068.8 P
weak similarity to Los1p
9759_at 17446.6 P
Hydroxymethylglutaryl-CoA Synthase
9760_at 7276.6 P
strong similarity to cytochrome-b5- and nitrate reductases
9761_at 6563.1 P
alpha-tubulin
9762_at 60777.1 P
inorganic phosphate transporter, transmembrane protein
9763_at 299.9 A
hypothetical protein
9764_at 722.8 P
Putative small GTPase
9765_at 724.4 P
mitochondrial NADH ubiquinone 6 oxidoreductase
9766_at 529.0 A
hypothetical protein
9767_at 272.7 A
similarity to YMR285c
9768_at 611.0 P
similarity to YPL184c
9769_g_at 1681.1 P
similarity to YPL184c
9770_at 2829.3 P
questionable ORF
9771_at 520.5 P
predicted protein is very hydrophobic, has many membrane-spanning regions, several potential glycosylation sites, potential ATP-binding site
9772_at 775.6 P
Vanadate resistance protein
9773_at 1749.6 P
hypothetical protein
9774_at 1428.4 P
datin, an oligo(dA).oligo(dT)-binding protein
9775_at 1013.3 P
CTD kinase-I gamma subunit
9776_at 634.6 P
strong similarity to ubiquitination protein Bul1p

9777_at 3327.8 P
DBF2 Interacting Protein
9778_at 668.5 P
multicopy suppressor of a sin4 defect
9734_at -265.2 A
hypothetical protein
9735_at 735.4 P
hypothetical protein
9736_at 12136.4 P
Orotate phosphoribosyltransferase 1
9737_at 2968.0 P
signal recognition particle subunit, homologue of mammalian SRP19
9738_at 857.1 P
Intermediate filament protein involved in organelle inheritance
9739_at 857.5 P
Nucleoporin
9740_at 1383.8 P
p60 subunit of the yeast omatin Assembly Factor-I (CAF-I)
9741_at -124.5 A
questionable ORF
9742_at 3588.7 P
weak similarity to YMR264w
9743_at 2349.8 P
123 kD regulatory subunit of trehalose-6-phosphate synthase\/phosphatase complex\; homologous to TPS3 gene product
9744_at 547.9 P
questionable ORF
9745_at 331.0 A
zinc-finger transcription factor of the Zn(2)-Cys(6) binuclear cluster domain type
9746_at 273.1 A
TFIID subunit
9747_at 1792.0 P
required for Golgi to vacuole trafficking, shares similarity to mammalian ras inhibitors
9748_at 857.0 P
similarity to asparagine synthases
9749_at 288.5 A
Endonuclease (with Rad1p) that degrades single-stranded DNA for repair
9750_at 132.9 A
questionable ORF
9751_at 1531.2 P
Putative homolog of subunit 5 of bovine prefoldin, a chaperone comprised of six subunits
9752_at 1836.8 P
similarity to P.falciparum liver stage antigen LSA-1
9753_at 7453.2 P
proteasome component Y7
9754_at 36.4 A
subunit of mitochondrial RNase P
9755_at -10.0 A
hypothetical protein
9756_at -27.2 A
questionable ORF
9711_at 543.5 P
hypothetical protein
9712_at 76.5 A
strong similarity to YML125c, similarity to cytochrome-b5- and nitrate reductases
9713_at 3024.4 P

D-arabinono-1,4-lactone oxidase
9714_at 4406.2 P
alpha-tubulin
9715_at -229.6 A
hypothetical protein
9716_at -51.5 A
hypothetical protein
9717_at 669.8 P
similarity to N.crassa O-succinylhomoserine (thiol)-lyase
9718_at 1371.5 P
strong similarity to ZMS1 protein
9719_at 787.0 P
similarity to A.brasilense nifR3 protein
9720_at 922.3 P
weak similarity to Synechocystis sp. hypothetical protein sll1188
9721_at 6729.0 P
cyclophilin-3 (cyclosporin-sensitive proline rotamase-3)
9722_at 1220.1 P
Bet5p\/18kD component of TRAPP
9723_at 1125.5 P
weak similarity to transcription factor
9724_at 15585.2 P
3-hydroxy-3-methylglutaryl-coenzyme A (HMG-CoA) reductase isozyme
9725_at 5869.9 P
Prolyl cis-trans isomerase, also called proline rotamase or peptidylprolyl cis-trans isomerase (PPIase)
9726_at 16681.5 P
Ribosomal protein L6A (L17A) (rp18) (YL16)
9727_at 1975.3 P
similarity to YOR3141c and YNL087w
9728_at 962.9 P
hypothetical protein
9729_at 4372.9 P
putative dihydroxyacetone kinase
9730_at 2440.4 P
Binds to catalytic subunit of DNA polymerase alpha (Pol1p)
9731_at 270.0 A
similarity to C.elegans hypothetical protein
9732_at 1956.1 P
weak similarity to YAL042w
9733_at -24.3 A
hypothetical protein
9689_at 611.3 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 509.2 P
GTP-binding protein of the ras superfamily involved in termination of M-phase
9691_i_at 23939.6 P
Ribosomal protein S1B (rp10B)
9692_at 924.1 P
Protein involved in mitochondrial import of fusion proteins
9693_at 655.4 P 5
to 3 DNA helicase
9694_at 676.8 P
43-kDa 8-oxo-guanine DNA glycosylase
9695_at 927.9 P
similarity to C.elegans ZK370.4 protein

9696_at 8496.6 P
Suppressor of mec lethality
9697_at 25.3 A
questionable ORF
9698_at 813.4 P
Catalytic A subunit of calcineurin, type 2B protein serine\/threonine phosphatase\; redundant with Cna1\; cytoplasmic
9699_at 9338.6 P
strong similarity to IMP dehydrogenases
9700_at 3615.4 P
strong similarity to IMP dehydrogenases
9701_at 1892.0 P
subunit of signal peptidase complex, homologous to mammalian protein SPC25
9702_at 226.0 A
Cytochrome b2 [L--lactate cytochrome-c oxidoreductase]
9703_at 967.0 P
hypothetical protein
9704_at 4569.9 P
putative integral membrane protein
9705_at 1660.6 P
regulatory protein
9706_at 113.4 A
weak similarity to potato sucrose cleavage protein
9707_at 881.6 P
RNA splicing and ER to Golgi transport
9708_at 4731.1 P
Glucose Signaling Factor
9709_at 299.6 A
questionable ORF
9710_at 78.4 A
strong similarity to YJR054w
9666_at 1140.3 P
RNA splicing factor associated with U1 snRNP
9667_at 122.9 A
Component of rDNA transcription factor CF, which also contains Rrn6p and Rrn7p, which is required for rDNA transcription by RNA polymerase I
9668_at 198.2 A
Carnitine O-acetyltransferase, peroxisomal and mitochondrial
9669_at 1230.9 P
hypothetical protein
9670_at 1112.7 P
hypothetical protein
9671_at 83.2 A
hypothetical protein
9672_at 799.5 P
weak similarity to C.elegans hypothetical protein CELW03F8
9673_at 1462.9 P
putative alpha-mannosidase
9674_at 107.5 A
questionable ORF
9675_at 306.9 A
similarity to YDR458c
9676_at 651.6 P
similarity to YDR458c
9677_at 1450.6 P
Interacts with Rad51p by two hybrid analysis. mRNA is induced in meiosis during recombination

9678_at	349.6	P	questionable ORF
9679_at	3078.4	P	Nuclear envelope protein with multiple putative transmembrane domains
9680_at	420.7	P	hypothetical protein
9681_at	766.1	P	hypothetical protein
9682_at	110789.8	P	Thiol-specific antioxidant
9683_at	978.8	P	Homeobox-domain containing protein
9684_s_at	49371.5	P	Ribosomal protein S18B
9685_at	1358.1	P	ribosomal protein, mitochondrial
9686_s_at	71423.9	P	Ribosomal protein S17A (rp51A)
9687_at	555.7	P	weak similarity to Nmd2p
9688_at	5605.6	P	Adenine phosphoribosyltransferase
9643_at	1146.9	P	uracil DNA glycosylase
9644_at	264.9	A	hypothetical protein
9645_at	769.7	P	Putative new 37kDa subunit of N-oligosaccharyltransferase complex
9646_at	1551.6	P	similarity to YDR438w
9647_at	220.8	A	Polymerase suppressor 2\; Suppressors of group II intron-splicing defect.
9648_at	833.8	P	serine-threonine phosphatase Z
9649_at	595.5	P	TFIID subunit
9650_at	1020.2	P	similarity to C.elegans hypothetical protein C14B1.5
9651_at	511.2	P	hypothetical protein
9652_at	131.7	A	questionable ORF
9653_at	8892.5	P	Component of the COPII coat of certain ER-derived vesicles
9654_at	637.9	P	hypothetical protein
9655_at	483.5	P	transcription factor
9656_g_at	4301.1	P	transcription factor
9657_i_at	1336.3	P	questionable ORF
9658_r_at	1417.9	P	questionable ORF
9659_at	639.6	P	questionable ORF

9660_at	1959.4	P	Mitochondrial ribosomal protein MRPL39 (YmL39)
9661_at	21282.3	P	S-adenoslymethionine: delta 24-methyltransferase
9662_at	867.3	P	jun-like transcription factor
9663_at	1159.5	P	hypothetical protein
9664_at	211.2	A	similarity to hypothetical S.pombe protein
9665_at	4000.9	P	lactoylglutathione lyase (glyoxalase I)
9620_at	248.8	A	hypothetical protein
9621_at	458.9	A	hypothetical protein
9622_at	2352.9	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	1282.5	P	protein kinase which functions at the G(sub)2\/M boundary
9624_at	4614.5	P	similarity to hypothetical S.pombe and C.elegans proteins
9625_at	410.8	A	hypothetical protein
9626_at	1263.8	P	Protein required for sorting proteins to the vacuole
9627_at	1561.6	P	Protein required for protein synthesis
9628_at	2387.7	P	strong similarity to Plb1p
9629_at	108.6	A	hypothetical protein
9630_at	6728.2	P	Phospholipase B (lypophospholipase)
9631_at	2563.9	P	weak similarity to P.aeruginosa regulatory protein mmsR
9632_at	458.8	P	weak similarity to hypothetical protein YDR352w
9633_at	1524.9	P	high affinity hexose transporter-2
9634_at	8929.3	P	CLU1 is similar to the Dictyostelium cluA gene
9635_at	593.0	P	membrane protein required for core glycosylation
9636_at	610.0	P	weak similarity to S.pombe hypothetical protein SPAC4F10
9637_at	5013.3	P	cytochrome P450 involved in C-22 denaturation of the ergosterol side-chain
9638_at	1063.4	P	displays homologies to several transcription factors
9639_at	40.4	A	DBF2 Interacting Protein\; SNAP 25 homolog
9640_at	-32.1	A	similarity to tetratricopeptide-repeat protein PAS10

9641_at 438.9 P
Binds Sin3p in two-hybrid assay
9642_at 757.8 P
Multicopy suppressor of fenpropimorph resistance (fen2 mutant), shows similarity to Candida albicans corticosteroid-binding protein CBP1
9598_at 87.2 A
metal-binding transcriptional activator
9599_at 1879.5 P
ubiquitin conjugating enzyme
9600_at 530.4 A
putative mitochondrial GTPase
9601_at 512.3 M
Mitochondrial ribosomal protein MRPL3 (YmL3)
9602_at 259.0 A
hypothetical protein
9603_at 418.2 A
C3HC4 zinc-binding integral peroxisomal membrane protein
9604_at 2720.3 P
High level expression reduced Ty3 Transposition
9605_at 84.5 A
42 kDa protein that pysically associates with the PP2A and SIT4 protein phosphatase catalytic subunits
9606_at 374.8 P
weak similarity to human nuclear autoantigen
9607_at 200.8 A
hypothetical protein
9608_at 615.3 A
similarity to YKL050c and human restin
9609_at 6.9 A
questionable ORF
9610_at 550.8 P
Cytokinesis
9611_at 1385.5 P
Actin-related protein
9612_at -28.5 A
weak similarity to YPR201w
9613_at 193.4 A
Inner membrane protease (mitochondrial protein)
9614_at 542.7 A
homolog of S. pombe cdc25
9615_at 785.1 P
zinc finger protein
9616_at 4826.3 P
Homocitrate
9617_at 1787.9 P
suppressor of TFIIB mutations
9618_at 201.0 A
strong similarity to Yet1p
9619_at 33.8 A
weak similarity to Pseudomonas L-fucose dehydrogenase
9575_at 200.6 P
Regulator of arginine-responsive genes with ARG81 and ARG82
9576_at 2132.9 P
putative transcriptional activator of alpha-specific genes
9577_at 1902.7 P
hypothetical protein
9578_at 1742.3 P

Nuclear pore complex protein that is member of GLFG repeat-containing family of nucleoporins and is highly homologous to Nup100p
9579_at 385.9 M
hypothetical protein
9580_at 6796.7 P
weak similarity to A.thaliana PRL1 protein
9581_at 93.6 A
Required for arrest in G1 in response to pheromone
9582_at 227.6 A
questionable ORF
9583_at 84.3 A
Binds Sin3p in two-hybrid assay and is part of large protein complex with Sin3p and Stb1p
9584_at 1512.6 P
vacuolar proton pumping ATPase, 110-kDa subunit\; not in vacuole membrane
9585_at 820.2 P
Protein required for cell cycle arrest in response to loss of microtubule function
9586_at 577.1 P
mitochondrial ADP\/ATP translocator
9587_at -241.9 A
hypothetical protein
9588_at 5181.9 P
multicopper oxidase
9589_at 272.2 A
15kDa subunit of the tetrameric tRNA splicing endonuclease
9590_at 348.9 A
mitochondrial import receptor, heterodimerizes with Tom70p, preferentially recognizes the mature regions of precursor proteins associated with ATP-dependent cytosolic chaperones
9591_at 938.1 P
component of the cleavage and polyadenylation factor CF I involved in pre-mRNA 3 -end processing
9592_at 722.3 P
acetylornithine acetyltransferase
9593_at -116.7 A
Regulator of Rim1p, required for IME1 expression
9594_at 412.9 A
basic, hydrophilic protein of 59 kDa
9595_at 438.7 A
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 276.9 A
Synthesis Of Var
9597_at 2227.4 P
hypothetical protein
9553_at 174.6 A
weak similarity to mouse transcription factor NF-kappaB
9554_at 138.2 A
hypothetical protein
9555_at 839.3 A
2 Cys2-His2 zinc fingers at c-terminus, glutamine and asparagine rich
9556_at 3043.2 P
hypothetical protein
9557_at 5686.5 P
HMG-1 homolog, mitochondrial
9558_at 656.7 P
weak similarity to C-terminal part of cytochrome b5 and b2
9559_at 1577.4 P
strong similarity to hypothetical S. pombe protein

9560_at	650.3	P	weak similarity to human Mi-2 protein
9561_at	274.3	A	questionable ORF
9562_at	1414.2	P	Precocious Dissociation of Sister chromatids
9563_at	483.3	A	similarity to SNF7 protein
9564_at	638.9	P	chromosome transmission
9565_at	4038.9	P	phosphatidylinositol transfer protein
9566_at	526.1	P	putative helicase
9567_at	-167.8	A	May regulate NAM7 function, possibly at level of mRNA turnover
9568_at	65.1	A	hypothetical protein
9569_at	17213.5	P	alcohol dehydrogenase isoenzyme III
9570_at	157.8	A	putative pseudogene
9571_at	-119.2	A	putative pseudogene
9572_at	1050.6	P	similarity to YKL105c
9573_at	201.2	A	questionable ORF
9574_at	-506.4	A	hypothetical protein
9530_at	1553.3	P	similarity to multidrug resistance proteins
9531_at	1890.8	P	mitochondrial membrane ATPase of the CDC48\/PAS1\/SEC18 (AAA) family
9532_at	260.6	A	strong similarity to B. subtilis conserved hypothetical protein yhfK
9533_at	1402.9	P	nuclear protein localization factor
9534_at	3510.5	P	Protein localizes to actin cortical patches. Probable binding site on actin lies on front surface of subdomain 3 and 4.
9535_at	1204.1	P	weak similarity to Pwp2p
9536_at	161.5	A	58 kd component (Cbf3c) of the multisubunit Cbf3 kinetochore protein complex, which binds to the CDE III element of centromeres
9537_at	641.5	P	SNZ1 proximal ORF, stationary phase induced gene
9538_at	2453.3	P	encodes highly conserved 35 kDa protein that shows increased expression after entry into stationary phase
9539_at	420.5	A	weak similarity to M.genitalium hypothetical protein homolog MG442
9540_at	96.0	A	hypothetical protein
9541_at	4277.8	P	

similarity to P.ciliare possible apospory-associated protein
9542_at 546.9 P
Homolog of samB gene of Aspergillus nidulans (deletion of samB results in mislocalization of septa
9543_at -38.0 A
similarity to YBR002c
9544_at 5100.4 P
strong similarity to YKL121w
9545_at 934.4 P
hypothetical protein
9546_at 672.0 P
protein kinase
9547_at 557.1 P
Phosphoglucomutase
9548_at 567.3 A
Ku80 homolog, exhibits DNA binding activity on its own, associates with Hdf1p to form major DNA end-binding complex
9549_at -97.5 A
hypothetical protein
9550_at 6798.9 P
acetolactate synthase
9551_at 2185.0 P
myosin I
9552_at 2915.7 P
similarity to aldehyde dehydrogenase
9507_at 335.2 A
weak similarity to MSN1 protein
9508_at 888.4 P
hypothetical protein
9509_at 1494.8 P
similarity to folylpolyglutamate synthetases and strong similarity to YKL132c
9510_at 244.2 A
similarity to B. subtilis conserved hypothetical proteins yoqW and yoaM
9511_at 642.9 P
similarity to YKL133c
9512_at 74346.3 P
WD repeat protein (G-beta like protein) that interacts with the translational machinery
9513_at 36396.2 P
WD repeat protein (G-beta like protein) that interacts with the translational machinery
9514_at 156.6 A
component of spindle pole
9515_at 142.0 A
strong similarity to succinate dehydrogenase
9516_at 580.7 A
similarity to YNL008c
9517_g_at 1898.1 P
similarity to YNL008c
9518_at 854.1 A
questionable ORF
9519_at 4211.6 P
5-aminoimidazole-4-carboxamide ribonucleotide (AICAR) transformylase\/IMP cyclohydrolase
9520_at 2331.0 P
Ribosomal protein L15B (YL10) (L13B) (rp15R)
9521_at 57.3 A
hypothetical protein
9522_at 3020.3 P
resistance against Pichia farinosa killer toxin (SMK toxin) when expressed by a multi copy plasmid

9523_at	432.8	P	weak similarity to YLR031w
9524_at	2929.2	P	transcriptional activator of glycolytic genes
9525_at	521.9	P	hypothetical protein
9526_at	207.2	A	Protein involved in silencing HMR, homologous to acetyltransferases
9527_at	2562.3	P	ExtraCellular Mutant
9528_at	922.3	P	Nuclear pore membrane glycoprotein
9529_at	389.4	A	similarity to D.melanogaster Dreg-2 protein
9484_at	4655.6	P	similarity to human retinoblastoma-binding protein
9485_at	275.0	A	similarity to hypothetical S. pombe protein
9486_at	-1.3	A	mRNA is induced early in sporulation
9487_at	966.2	P	hypothetical protein
9488_at	623.5	P	hypothetical protein
9489_at	289.9	A	questionable ORF
9490_at	176.1	A	weak similarity to YIR013c and YLR013w
9491_at	-15.3	A	interstrand crosslink repair protein
9492_at	907.0	P	GTP-binding protein
9493_at	929.0	P	Serine\/threonine protein kinase, phosphorylates the mitotic activator IME1
9494_at	302.5	A	hypothetical protein
9495_at	529.2	P	hypothetical protein
9496_at	28205.6	P	Ribosomal protein L13B
9497_i_at	5712.2	P	Ribosomal protein S16A (rp61R)
9498_f_at	22732.7	P	Ribosomal protein S16A (rp61R)
9499_at	-10.6	A	weak similarity to Mlp1p
9500_at	4943.5	P	mitochondrial cytosolically directed NADH dehydrogenase
9501_at	6396.1	P	p39 subunit of translation initiation factor eIF3
9502_at	528.4	P	hypothetical protein
9503_at	1819.7	P	hypothetical protein
9504_at	2996.1	P	oligosaccharyl transferase glycoprotein complex, delta subunit

9505_at 1380.1 P
Inner membrane protease (mitochondrial protein)
9506_at 40.1 A
hypothetical protein
9462_at 700.9 P
mitochondrial inner membrane protease
9463_at 1415.0 P
similarity to Asm4p
9464_at 473.4 P
questionable ORF
9465_at -74.3 A
Involved in proteolytic processing of Rim1p
9466_at 174.7 A
weak similarity to E.coli hypothetical protein f402
9467_at 115.1 A
weak similarity to S.pombe hypothetical protein SPAC23C11
9468_at 1001.6 P
hypothetical protein
9469_at 3.7 A
weak similarity to E.coli ribosomal S8 protein
9470_at -49.4 A
questionable ORF
9471_at -166.8 A
Protein homologous to human Sin3 complex component SAP18, possible coiled-coil protein
9472_at 643.6 P
weak similarity to fruit fly ecdysone-inducible protein
9473_at 564.0 A
Homologous to E coli dnaJ protein
9474_at 398.1 A
similarity to ATPases
9475_at 298.1 A
hypothetical protein
9476_at 587.2 A
Predicted 758 amino acid polypeptide with poly-glutamine and poly-asparagine domains
9477_at 961.8 P
involved in plasmid maintenance
9478_at 715.8 A
similarity to members of the mitochondrial carrier protein family
9479_at -122.0 A
MutL homolog, forms a complex with Pms1p and Msh2p to repair mismatched DNA
9480_at 452.4 A
contains an N-terminal Zn2Cys6 type zinc finger domain, a C-terminal acidic domain and a putative coiled coil dimerization domain
9481_at 164.1 A
Aldehyde Dehydrogenase (NAD(P)+)
9482_g_at 768.0 P
Aldehyde Dehydrogenase (NAD(P)+)
9483_at 772.1 P
aldehyde dehydrogenase, (NAD(P)+), likely cytosolic
9439_at 136.9 A
similarity to YKL124w
9440_at 446.1 A
similarity to MSN1 protein
9441_at -157.0 A
questionable ORF
9442_s_at 10052.9 P

flocculent specific protein\; contains >35 repeats of the amino acid sequence NNNDSYGS
9443_at 17841.6 P
questionable ORF
9444_at 463.2 A
Cytoplasmic inhibitor of proteinase Pep4p
9445_at 30.5 A
protein of unknown function
9446_at 808.3 P
ExtraCellular Mutant
9447_at 805.8 P
Protein involved in mitochondrial iron accumulation
9448_at 143.9 A
similarity to C.elegans hypothetical protein
9449_at 453.3 P
non-specific DNA binding protein
9450_at 247.8 A
similarity to YPL228w
9451_at 494.9 P
similarity to YPL229w
9452_at 277.6 A
Putative transcriptional repressor with proline-rich zinc fingers
9453_at 1208.4 P
SSO1 and SSO2 encode syntaxin homologs\; act in late stages of secretion
9454_at 1412.5 P
hypothetical protein
9455_at 491.2 A
hypothetical protein
9456_at 89640.0 P
constitutively expressed heat shock protein
9457_g_at 59483.2 P
constitutively expressed heat shock protein
9458_at 481.6 P
hypothetical protein
9459_at 384.9 A
weak similarity to bacterial ribosomal protein S17
9460_at 2561.9 P
Glycine decarboxylase complex (P-subunit), glycine synthase (P-subunit), Glycine cleavage system (P-subunit)
9461_at 710.4 P
has DNA helicase signature motifs
9416_at 862.7 P
hypothetical protein
9417_at 101.9 A
similarity to mouse Tbc1 protein
9418_at 925.1 P
Mitochondrial ribosomal protein MRPL24 (YmL24)
9419_at 219.3 A
questionable ORF
9420_i_at 25182.2 P
Ribosomal protein L36A (L39) (YL39)
9421_s_at 41144.1 P
Ribosomal protein L36A (L39) (YL39)
9422_at 1729.9 P
similarity to YPL250c
9423_at 357.9 A
hypothetical protein

9424_at	1340.3	P	Vti1p is a v-SNARE that interacts with two t-SNARES, Sed5p and Pep12p
9425_at	662.0	P	spindle pole body associated protein
9426_at	1273.6	P	G(sub)1 cyclin
9427_at	1966.3	P	putative membrane protein
9428_at	331.2	A	human xeroderma pigmentosum group A DNA repair gene homolog
9429_at	13442.2	P	C-8 sterol isomerase
9430_at	3797.1	P	Mitochondrial outer membrane protein\; forms the outer membrane import channel
9431_at	28.3	A	weak similarity to D.melanogaster hypothetical protein DMC39E1
9432_at	28859.3	P	phosphofructokinase beta subunit
9433_at	-223.6	A	weak similarity to hypothetical protein YNR014w
9434_at	730.3	P	Similar to acetyl-coenzyme A carboxylase
9435_at	5534.9	P	mevalonate kinase
9436_at	327.2	A	hypothetical protein
9437_at	247.8	A	similarity to P.glauca late embryogenesis abundant protein and YBR177c and YPL095c
9438_at	129.1	A	weak similarity to beta tubulins
9394_at	1599.3	P	weak similarity to myosins
9395_at	85.2	A	S. cerevisiae homologue of S. pombe cdc5+
9396_at	2915.9	P	dnaJ homolog
9397_at	3432.2	P	similarity to GAS1 protein
9398_at	877.9	P	Serine Protein Kinase
9399_at	16185.8	P	GMP synthase
9400_at	246.3	A	hypothetical protein
9401_at	534.0	P	Establishes Silent omatin
9402_at	6106.4	P	48 kDa Phosphomevalonate kinase
9403_at	4685.6	P	weak similarity to photosystem II protein D2
9404_at	1757.7	P	similarity to S.pombe dihydrofolate reductase
9405_at	398.5	A	encodes putative deubiquitinating enzyme
9406_at	134.9	A	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 1352.7 P
Mitochondrial ribosomal protein MRPL44 (YmL44)
9408_at 238.2 A
Mitochondrial ribosomal protein MRPL44 (YmL44)
9409_at 16077.9 P
similarity to ketoreductases
9410_at 176.4 A
TFIID subunit
9411_at 569.5 P
Mitochondrial RNA polymerase specificity factor
9412_at 6723.0 P
Protein required for processing of pre-rRNA
9413_f_at 201.2 A
Ribosomal protein S10B
9414_f_at 35264.0 P
Ribosomal protein S10B
9415_at 176.0 A
peripheral vaculor membrane protein\; putative Zn-finger protein
9371_at 260.6 A
involved in cell fusion during mating, also required for the alignment of parental nuclei before nuclear fusion
9372_at 682.5 P
strong similarity to YOR295w
9373_at 93.0 A
ribonuclease H
9374_at 3093.0 P
Protein involved in RNA processing and export from nucleus
9375_at 2944.1 P
TFIID subunit
9376_at 3052.1 P
similarity to CHS6 protein
9377_at 4008.9 P
Protein required for filamentous growth, cell polarity, and cellular elongation
9378_at 575.5 P
Ribonuclease III
9379_at 385.1 A
U2 snRNP protein
9380_at 10950.9 P
DNA-binding protein, mtDNA stabilizing protein, mitochondrial inner membrane protein with low homology to RIM2
9381_s_at 51255.4 P
Ribosomal protein L20A (L18A)
9382_at 5221.1 P
Zinc- and cadmium-resistance protein
9383_at 275.9 A
similarity to Uth1p, Nca3p, YIL123w and Sun4p
9384_at 944.4 P
questionable ORF
9385_at 671.7 P
weak similarity to mouse thyrotropin-releasing hormone receptor
9386_at 4198.2 P
long-chain fatty acid--CoA ligase and synthetase 4
9387_at 1844.0 P
hypothetical protein

9388_at -54.9 A
similarity to glutamate decarboxylases
9389_at 71.4 A
strong similarity to YKR076w and YGR154c
9390_at 41132.5 P
hyperosmolarity-responsive gene
9391_at 276.7 A
hypothetical protein
9392_at 194.0 A
strong similarity to YPL264c
9393_at -62.0 A
hypothetical protein
9349_at 465.2 A
hypothetical protein
9350_at 4686.6 P
subunit VII of cytochrome c oxidase
9351_at 1127.6 A
translational activator of cytochrome c oxidase subunit II
9352_at 433.9 M
hypothetical protein
9353_at 1312.5 P
hypothetical protein
9354_at 4597.6 P
Translation initiation factor eIF1A
9355_at 2177.7 P
115 kD regulatory subunit of trehalose-6-phosphate synthase\/phosphatase complex
9356_at 468.7 P
similarity to S.pombe scn1 protein
9357_at 999.4 P
subunit of the histone deacetylase B complex
9358_at 1269.4 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 221.3 A
hypothetical protein
9360_at 3247.8 P
similarity to A.thaliana hyp1 protein
9361_at 174.7 A
mitochondrial inorganic pyrophosphatase
9362_at 223.7 A
U4\/U6 snRNA-associated splicing factor
9363_at 953.6 P
weak similarity to C.elegans hypothetical protein CELT23B3
9364_at 892.4 P
Upstream activation factor subunit
9365_at 112.2 A
Orotate phosphoribosyltransferase 2
9366_at 6498.9 P
desaturase\/hydroxylase enzyme
9367_at 1220.1 P
Negative regulator of cell polarity
9368_at 31.6 A
Protease involved in ras and a-factor terminal proteolysis
9369_at 1498.6 P
Involved in the ubiquination pathway, possibly by functioning with Rsp5
9370_at 12592.4 P

ubiquitin-like protein
9326_at 1709.2 P
TFIIF interacting Component of CTD Phosphatase
9327_at 993.6 P
similarity to phosphomannomutases
9328_at 190.2 A
strong similarity to aminotriazole resistance protein
9329_at -100.4 A
Zinc-cluster protein involved in activating gluconeogenic genes\; related to Gal4p
9330_at 392.7 P
hypothetical protein
9331_at 476.5 P
basic, hydrophilic 67.5 kDa protein
9332_at -31.3 A
Initiator methionine tRNA 2 -O-ribosyl phosphate transferase
9333_at -189.5 A
DNA binding protein
9334_at 429.9 A
similarity to Ccr4p
9335_at 1676.8 P
Mitochondrial ribosomal protein MRPL33 (YmL33) (E. coli L30)
9336_at 442.1 A
Protein essential for mitochondrial biogenesis
9337_at 629.1 P
strong similarity to hypothetical S.pombe and C.elegans proteins
9338_at 930.7 P
hypothetical protein
9339_at 2688.9 P
Putative RNA-dependent helicase
9340_at -160.7 A
questionable ORF
9341_at 1155.8 P
similarity to ser/thr protein kinase
9342_at 3701.9 P
strong similarity to C.elegans hypothetical protein
9343_at 519.6 P
similarity to amidases
9344_at 218.2 A
Coiled-coil domain protein required for proper nuclear migration during mitosis (but not during conjugation)
9345_at 781.9 P
questionable ORF
9346_at 8322.2 P
similarity to YGR273c
9347_at 10199.0 P
Probable component of serine palmitoyltransferase, which catalyzes the first step in biosynthesis of long-chain sphingolipids
9348_at 9063.2 P
carboxypeptidase Y (proteinase C)
9304_at 2641.5 P
hypothetical protein
9305_at 5.6 A
weak similarity to hypothetical protein YJL062w
9306_at 657.0 M
phosphoribosylpyrophosphate amidotransferase
9307_at 1400.0 P

mitochondrial ABC transporter protein
9308_at 751.1 P
Integral membrane mitochondrial protein
9309_at 1250.8 P
alcohol dehydrogenase II
9310_at 600.8 P
encodes putative deubiquitinating enzyme
9311_at 419.2 P
questionable ORF
9312_at 11106.5 P
member of the glucanase gene family
9313_at -356.1 A
Protein with similarity to Gls1p and Gls2p (GB:Z49212)
9314_at 107.9 A
questionable ORF
9315_at 53943.9 P
cell surface glycoprotein 115-120 kDa
9316_at 14352.6 P
Karyopherin
9317_at 2289.9 P
~100 kDa cytoplasmic protein
9318_at 2046.6 P
similarity to YGR283c
9319_at 1621.7 P
Regulates activity of protein phosphatase 1, Glc7p, which is involved in proper chromosome segregation
9320_at 1552.2 P
hypothetical protein
9321_at 716.1 P
similarity to YKR089c and YOR081c
9322_at 4445.5 P
alpha-type of subunit of 20S proteasome
9323_at 4163.3 P
similarity to hypothetical S. pombe protein
9324_at 2051.1 P
similarity to YOR385w and YNL165w
9325_at 254.2 A
questionable ORF
9281_at -120.2 A
questionable ORF
9282_at 183.1 A
similarity to mucins, glucan 1,4-alpha-glucosidase and exo-alpha-sialidase
9283_at 6074.0 P
strong similarity to alcohol-dehydrogenase
9284_at 650.6 P
Low-affinity Fe(II) transport protein
9285_at 266.9 A
hypothetical protein
9286_s_at 4420.7 P
strong similarity to hypothetical proteins YPL273w and YLL062c
9287_s_at 259.4 A
strong similarity to YPL280w, YOR391c and YDR533c
9288_s_at 346.4 P
strong similarity to phosphopyruvate hydratases
9289_at 266.6 A
strong similarity to YBL108w, YCR103c and YKL223w
9290_f_at 473.0 A

strong similarity to members of the Srp1p/Tip1p family
9291_at	4768.3	P
protein associated to the ATP synthase
9292_at	233.2	A
hypothetical protein identified by SAGE
9293_at	246.1	A
identified by SAGE
9294_at	33371.0	P
hypothetical protein
9295_g_at	28253.5	P
hypothetical protein
9296_at	-160.1	A
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	184.1	A
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	326.3	A
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	143.2	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	24.1	A
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	9.6	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	-104.6	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	79.8	A
non-annotated SAGE orf Found forward in NC_001145 between 769282 and 769425 with 100% identity. See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251
9258_at	-13.1	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	302.7	A
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	-48.6	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	164.1	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	8.1	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	281.4	A
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	150.7	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 454.1 A
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 487.8 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 10257.5 P
non-annotated SAGE orf Found reverse in NC_001145 between 849877 and 850053 with 100% identity.
See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251
9268_at 2009.2 P
non-annotated SAGE orf Found forward in NC_001145 between 863528 and 863674 with 100% identity.
See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251
9269_at 1291.2 P
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 -76.5 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 2698.7 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 90.8 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 -90.9 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 -10.4 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 -72.8 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 65.7 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 -68.4 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 7.1 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 159.3 A
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 137.9 A
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 65.1 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 123.5 A
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 237.4 A
non-annotated SAGE orf Found forward in NC_001145 between 434355 and 434564 with 100% identity.

See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251
9237_at 199.3 A
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 -120.1 A
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 81.7 A
non-annotated SAGE orf Found forward in NC_001145 between 478063 and 478257 with 100% identity.
See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251
9240_at 115.3 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 704.0 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 -204.2 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 -158.0 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 20.1 A
non-annotated SAGE orf Found forward in NC_001145 between 482056 and 482289 with 100% identity.
See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251
9245_at 1024.9 P
non-annotated SAGE orf Found reverse in NC_001145 between 511289 and 511522 with 100% identity.
See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251
9246_at 234.9 A
non-annotated SAGE orf Found reverse in NC_001145 between 556676 and 556891 with 100% identity.
See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251
9247_g_at 68.2 A
non-annotated SAGE orf Found reverse in NC_001145 between 556676 and 556891 with 100% identity.
See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251
9248_at -143.5 A
non-annotated SAGE orf Found reverse in NC_001145 between 556746 and 556970 with 100% identity.
See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251
9249_i_at 86.4 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
9250_f_at -9.1 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
9251_at 154.1 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 3567.0 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 3627.2 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 83.8 A
non-annotated SAGE orf Found forward in NC_001145 between 837034 and 837171 with 100% identity.
See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251
9255_at 77.3 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 -44.5 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 191.6 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 3922.0 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 1264.0 P
non-annotated SAGE orf Found forward in NC_001145 between 49819 and 49965 with 100% identity.
See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251
9211_at 2603.0 P
non-annotated SAGE orf Found reverse in NC_001145 between 62403 and 62543 with 100% identity.
See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251
9212_at -44.7 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 111.9 A
non-annotated SAGE orf Found reverse in NC_001145 between 151565 and 151720 with 100% identity.
See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251
9214_at 32.6 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 27.4 A
non-annotated SAGE orf Found forward in NC_001145 between 271996 and 272136 with 100% identity.
See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251
9216_at 61.2 A
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 -49.9 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 876.2 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 161.8 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
9220_r_at -24.0 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 -182.9 A
non-annotated SAGE orf Found forward in NC_001145 between 483361 and 483495 with 100% identity.
See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251
9222_at 222.9 A
non-annotated SAGE orf Found reverse in NC_001145 between 509507 and 509701 with 100% identity.
See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251
9223_at -175.1 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 761.2 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	-118.7	A	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	426.8	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	11504.3	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	7021.7	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	48.0	A	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	169.8	A	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	24.6	A	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	-37.5	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	125.0	A	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	392.5	P	snRNA
9187_i_at	109.2	A	Centromere
9188_at	120.6	A	snRNA
9189_at	4012.3	P	snRNA
9190_at	234.8	A	snRNA
9191_at	420.1	P	snRNA
9192_at	77.1	A	snRNA
9193_at	467.9	P	snRNA
9194_at	757.5	P	snRNA
9195_at	2638.0	P	snRNA
9196_s_at	118.6	A	similarity to M.verrucaria cyanamide hydratase, identical to hypothetical protein YFL061w
9197_s_at	288.1	A	SNZ2 proximal ORF, stationary phase induced gene
9198_s_at	10.3	A	Snooze: stationary phase-induced gene family
9199_at	1045.3	P	Hypothetical aryl-alcohol dehydrogenase
9200_at	1410.4	P	

histone deacetylase
9201_at 537.5 P
Member of the AAA-protein family that includes NSFp and PEX1p
9202_at 20.8 A
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 3146.3 P
Cell-cycle regulation protein, may be involved in the correct timing of cell separation after cytokinesis
9204_at 705.4 P
similarity to YOL003c, YLR246w and C.elegans hypothetical protein ZK757.1
9205_at 458.4 A
FIG4 expression is induced by mating factor.
9206_at -167.6 A
hypothetical protein
9207_at 448.4 A
strong similarity to YCR094w and YNR048w
9208_at 4802.3 P
Cell wall beta-glucan assembly
9163_at 932.9 P
weak similarity to Vcx1p
9164_at 1030.5 P
strong similarity to S.pombe Bem46 protein
9165_at -198.5 A
questionable ORF
9166_at -174.0 A
hexose transport protein
9167_at 346.6 A
similarity to A.thaliana PRL1/2 protein
9168_at 313.9 A
prephenate dehydratase
9169_at 1240.7 P
essential for assembly of a functional F1-ATPase
9170_at 109.1 A
positive regulator of allophanate inducible genes
9171_at 2114.0 A
similarity to C.elegans hypothetical protein
9172_at 1479.9 P
subunit 2 of replication factor RF-A\; 29\% identical to the human p34 subunit of RF-A
9173_at 369.0 A
hypothetical protein
9174_at 678.4 A
similarity to S.pombe hypothetical protein SPAC24H6.02c
9175_at 311.8 A
Binds Sin3p in two-hybrid assay and is present in a large protein complex with Sin3p and Stb2p
9176_at 2968.8 P
similarity to S.pombe and C.elegans hypothetical proteins
9177_at 3565.0 P
43.1 kDa Serine\/threonine\/tyrosine protein kinase
9178_at 1155.1 P
ribosomal protein of the small subunit, mitochondrial
9179_at 2096.0 P
similarity to C-term. of A.nidulans regulatory protein (qutR)
9180_at 677.8 P
similarity to Ypt1p and rab GTP-binding proteins
9181_at 349.7 P
hypothetical protein

9182_s_at 51187.2 P
Ribosomal protein S19B (rp55B) (S16aB) (YS16B)
9183_s_at 53862.4 P
Ribosomal protein L18B (rp28B)
9184_at 4781.2 P
Ribosomal protein L18B (rp28B)
9185_at 7663.4 P
hypothetical protein
9140_at 1071.1 P
exhibits homology to Trf4p and Top1p
9141_at 811.1 P
protein kinase, homologous to Ste20p, interacts with CDC42
9142_at 1956.0 P
similarity to S.pombe hypothetical protein SPAC23D3.13c
9143_at 84.1 A
questionable ORF
9144_at 125.6 A
hypothetical protein
9145_at 637.7 P
hypothetical protein
9146_at 137.7 A
Multicopy Suppressor of Bud Emergence
9147_at 1686.0 P
Pseudouridine synthase
9148_at 990.3 P
N-glycosylated integral plasma membrane protein
9149_at 1021.4 P
Subunit 3 of Replication Factor C\; homologous to human RFC 36 kDa subunit
9150_at 290.6 A
G(sub)1 cyclin that associates with PHO85
9151_at 1880.9 P
strong similarity to C.elegans hypothetical protein
9152_at 6034.1 P
non-clathrin coat protein involved in transport between ER and Golgi
9153_at 456.2 A
Cold sensitive U2 snRNA Supressor
9154_at 4.5 A
hypothetical protein
9155_at 1440.3 P
Mitochondrial ribosomal protein MRPL10 (YmL10)
9156_at 1493.8 P
Putative integral membrane protein containing novel cysteine motif. Similarity to SLG1 (WSC1), WSC3 and WSC4
9157_at 122.3 A
involved in processsing of tRNAs and rRNAs
9158_at 4827.8 P
strong similarity to YDR214w
9159_at 2016.5 P
sterol C-14 reductase
9160_at 596.1 P
hypothetical protein
9161_at 1455.2 P
similarity to YLR187w
9162_at -18.9 A
homoserine O-trans-acetylase
9118_at -91.6 A

questionable ORF
9119_at 539.4 P
similarity to human band 3 anion transport protein
9120_at 259.7 A
similarity to glycerate- and formate-dehydrogenases
9121_at 1346.1 P
topoisomerase I interacting factor 1
9122_at 1225.8 P
Protein with coiled-coil domain essential for vesicular transport
9123_at 1963.1 P
contains formin homology domains\; homologous to BNR1 (BNI1 related protein)
9124_at 292.0 A
Protein highly homologous to permeases Can1p and Lyp1p for basic amino acids
9125_at 53.8 A
hypothetical protein
9126_at 7722.3 P
lysine permease
9127_at 885.5 P
Phosphatidylinositol 4-kinase
9128_at 189.6 A
questionable ORF
9129_at 100.6 A
similarity to human protein KIAA0174
9130_at 457.8 P
weak similarity to Sec14p
9131_at 2707.3 P
YIP1-Interacting Factor, shows similarity to NADH dehydrogenases
9132_at 1144.6 P
DNA polymerase II
9133_at 417.5 A
Fifth largest subunit of origin recognition complex\; contains possible ATP-binding site
9134_at 162.5 A
hypothetical protein
9135_at 1560.9 P
Antioxidant protein and metal homeostasis factor, protects against oxygen toxicity
9136_at 831.2 P
hypothetical protein
9137_at 487.9 A
Interacts with SNF1 protein kinase
9138_at 3316.2 P
similarity to bacterial dihydropteroate synthase
9139_at 4434.7 P
strong similarity to nucleic acid-binding proteins
9095_at -299.5 A
hypothetical protein
9096_at 133.0 A
hypothetical protein
9097_at 1392.3 P
ribosomal protein of the large subunit (YmL30), mitochondrial
9098_at 385.5 A
RNA recognition motif-containing protein that participates in sequence-specific regulation of nuclear pre-mRNA abundance
9099_at 579.8 A
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 262.5 A
similarity to YDR109c
9101_at 3313.3 P
49-kDa alpha subunit of RNA polymerase A
9102_at 3763.9 P
cysteinyl-tRNA synthetase
9103_at 1185.8 P
similarity to D.melanogaster SET protein
9104_at 556.2 P
hypothetical protein
9105_at 9759.1 P
translation initiation factor 3 (eIF3)
9106_at 6186.2 P
transmembrane protein
9107_at 497.9 P
similarity to human hypothetical protein KIAA0404
9108_at 4696.5 P
Glucose-6-phosphate dehydrogenase
9109_at 1261.1 P
strong similarity to K.marxianus LET1 protein
9110_at 2113.2 P
Ca2+-dependent serine protease
9111_at -32.6 A
Yeast putative Transmembrane Protein
9112_at 2434.3 P
component of RNA polymerase II holoenzyme\/mediator complex
9113_at 474.9 M
questionable ORF
9114_at 124.9 A
weak similarity to mouse hemoglobin zeta chain
9115_at 938.3 P
Is required to link Chs3p and Chs4p to the septins
9116_at 1820.5 P
hypothetical protein
9117_at 10816.8 P
weak similarity to Sec14p
9073_at 209.8 A
weak similarity to mammalian transcription elongation factor elongin A
9074_at 1442.8 P
transcriptional regulator, putative glutathione transferase
9075_at 279.2 A
similarity to dnaJ-like proteins
9076_at -29.0 A
questionable ORF
9077_at -56.3 A
questionable ORF
9078_at 616.9 P
chaotic nuclear migration\; predicted mass is 67kDa
9079_at 182.8 A
hypothetical protein
9080_at 365.1 A
Aut2p interacts with Tub1p and Tub2p\; Aut2p forms a protein complex with Aut7p\; Aut2p mediates attachment of autophagosomes to microtubules
9081_at 818.2 P
functionally related to TFIIB, affects start site selection in vivo
9082_at 1015.9 P

Component of nuclear RNase P and RNase MRP
9083_at 6765.0 P
adenylosuccinate synthetase
9084_at 2202.0 P
mannosyltransferase
9085_at 8.6 A
similarity to E.coli hypothetical protein in serS 5 region
9086_at 911.2 P
weak similarity to E.coli bis(5 -nucleosyl)-tetraphosphatase
9087_at 1826.4 P
repressor activator protein
9088_at 709.3 P
similarity to hypothetical S. pombe protein
9089_at 354.0 A
23 kDa peroxisome associated protein, binds Pex14p
9090_at 618.0 P
hypothetical protein
9091_at 2263.1 P
weak simlarity to C.cardunculus cypro4 protein
9092_at 132.3 A
hypothetical protein
9093_at -126.3 A
encodes protein with RNA-binding motifs required for MRE2-dependent mRNA splicing
9094_s_at 110484.8 P
Heat shock protein of HSP70 family, homolog of SSB1
9050_at 19311.2 P
weak similarity to Colletotrichum gloeosporioides nitrogen starvation-induced glutamine rich protein
9051_at 2487.2 P
similarity to M.jannaschii hypothetical protein MJ1073
9052_at 1037.1 P
similarity to structure-specific recognition proteins
9053_at -451.1 A
questionable ORF
9054_g_at -121.9 A
questionable ORF
9055_at -159.4 A
sporulation-specific protein
9056_at -366.2 A
weak similarity to B.subtilis CDP-diacylglycerol--serine O-phosphatidyltransferase
9057_at 307.4 A
peroxisomal 2,4-dienoyl-CoA reductase
9058_at 573.5 P
involved in regulation of carbon metabolism
9059_at 330.7 A
strong similarity to human TGR-CL10C
9060_at 555.0 P
Activates transcription of glycolytic genes\; homologous to GCR1\; may function in complex with Gcr2p
9061_at -19.8 A
questionable ORF
9062_at 29.7 A
Protein involved in regulation of cell size
9063_at -104.4 A
sporulation-specific protein with a leucine zipper motif, regulated by the transcription factor Ume6 and expressed early in meiosis
9064_at 263.7 A
hypothetical protein

9065_at -23.2 A
strong similarity to YDL222c and similarity to Sur7p
9066_at 342.5 A
hypothetical protein
9067_at 2619.7 P
chitin synthase 1
9068_at 940.0 P
similarity to Synechocystis hypothetical protein
9069_at 18203.1 P
hypothetical protein
9070_at 1392.1 P
karyopherin alpha homolog of 60 kDa
9071_at 670.0 P
involved in spindle pole body duplication and karyogamy, interacts with Cdc31p, localizes to the spindle pole body
9072_at -157.1 A
hypothetical protein
9028_at 3491.4 P a
deubiquitinating enzyme
9029_at 595.4 M
ribosomal protein of the large subunit, mitochondrial
9030_at 270.5 A
questionable ORF
9031_at 719.2 P
protein kinase homolog
9032_at 951.6 P
weak similarity to S.pombe hypothetical protein
9033_at 1368.3 P
similarity to hypothetical S. pombe protein
9034_at 95.7 A
hypothetical protein
9035_at 87633.3 P
Ribosomal protein S3 (rp13) (YS3)
9036_at 176.6 A
hypothetical protein
9037_at 639.8 P
weak similarity to Hkr1p
9038_at 3454.7 P
similarity to S.pombe Rnp24p
9039_at 601.0 P
hypothetical protein
9040_at 559.2 P
multicopy suppressor of bem1 mutation, may be involved in G-protein mediated signal transduction
9041_at 536.6 A
Component of the anaphase-promoting complex
9042_at 189.6 A
questionable ORF
9043_at 645.1 A
questionable ORF
9044_at 3424.1 P
Phosphatidylserine Decarboxylase 1
9045_at 1308.3 P
similarity to C.elegans ZK688.3 protein and E.coli hpcEp
9046_at 725.0 A
CREB like repressor, bZIP protein that binds to CRE motifs, interacts with Mig1p
9047_at 371.6 P

hypothetical protein
9048_at 886.8 P
similarity to YOR385w and YMR316w
9049_at 736.4 P
hypothetical protein
9005_at 1257.3 P
translation elongation factor eEF4
9006_s_at 28060.6 P
Ribosomal protein L42A (YL27) (L41A)
9007_at 249.5 A
Protein kinase
9008_at 10658.6 P
YGP1 encodes gp37, a glycoprotein synthesized in response to nutrient limitation which is homologous to the sporulation-specific SPS100 gene
9009_at 389.3 A
hypothetical protein
9010_at 294.1 A
hypothetical protein
9011_at 2678.6 P
weak similarity to S.pombe hypothetical protein SPAC10F6
9012_at 2316.8 P
similarity to YHR133c
9013_at 866.0 A
hypothetical protein
9014_at 1648.5 P
membrane-bound casein kinase I homolog
9015_at 2887.3 P
Putative homolog of subunit 4 of bovine prefoldin, a chaperone comprised of six subunits
9016_at 244.4 A
hypothetical protein
9017_at 1561.3 P
31-kDa subunit of RNA polymerase III (C)\; HMG1 like protein
9018_at 1147.1 P
hypothetical protein
9019_at 2626.8 P
weak similarity to S.pombe hypothetical protein
9020_at 219.5 A
cofactor B
9021_at 1275.6 P
Sm-like protein
9022_at -49.1 A
hypothetical protein
9023_at 182.6 A
mating a-factor pheromone precursor
9024_at 179.8 A
similarity to YHR131c
9025_at 192.0 A
hypothetical protein
9026_at 55.2 A
Ammonia transport protein
9027_at 1668.8 P
Adenosine deaminase\/adenine aminohydrolase
8982_i_at -211.7 A
questionable ORF
8983_s_at 588.9 P
questionable ORF

8984_at 12128.8 P
70-kDa adenylyl cyclase-associated protein
8985_at 1481.3 P
putative mitochondrial S4 ribosomal protein
8986_at 792.6 P
similarity to neurofilament triplet M protein
8987_at 18359.2 P
peptidylprolyl cis-trans isomerase
8988_at 2598.0 P
similarity to C.carbonum toxD gene
8989_at 544.1 P
hypothetical protein
8990_at 888.8 P
similarity to A.ambisexualis antheridiol steroid receptor
8991_at 1688.7 P
Mitochondrial import receptor complex protein
8992_at 4380.4 P
sn-1,2-diacylglycerol cholinephosphotransferase
8993_at 353.3 P
weak similarity to M.pneumoniae uridine kinase udk
8994_at 214.8 A
Similar to human tumor suppressor gene known as TEP1, MMAC1 and PTEN1. Contains sequence motifs characteristic of protein tyrosine phosphatases.
8995_at 530.1 A
similarity to C.elegans hypothetical protein
8996_at -413.6 A
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 1443.3 P
Protein with similarity to mammalian monocarboxylate transporters MCT1 and MCT2
8998_at 1250.0 P
similarity to hypothetical S. pombe protein
8999_at 3018.9 P
weak similarity to C.jejuni serine protease
9000_at 427.2 A
hypothetical protein
9001_at 2552.2 P
70 kDa mitochondrial specialized import receptor of the outer membrane
9002_at 140.8 A
questionable ORF
9003_at 852.8 P
weak similarity to M.jannaschii hypothetical protein MJ1257
9004_at 1078.7 A
essential suppressor of the respiratory deficiency of a pet mutant
8959_at -43.5 A
carbon-catabolite sensitive malate synthase
8960_at 662.6 A
weak similarity to RING zinc finger protein from Gallus gallus
8961_at 1037.8 P
weak similarity to S.pombe hypothetical protein SPAC23C11
8962_at 734.3 A
questionable ORF
8963_at 6183.9 P
subunit common to RNA polymerases I (A) and III (C)
8964_at 1939.8 P
ATP-dependent RNA helicase of DEAD box family

8965_at 7753.2 P
ATP-dependent RNA helicase of DEAD box family
8966_at 7835.6 P
cytochrome b5
8967_at 2226.5 P
weak similarity to fruit fly RNA-binding protein
8968_at 379.8 A
weak similarity to cytochrome-c oxidase
8969_at 765.5 P
strong similarity to YOR110w
8970_at 667.1 P
similarity to human AF-9 protein
8971_at 575.6 A
inositol polyphosphate 5-phosphatase
8972_at 2.6 A
questionable ORF
8973_at 15989.4 P
alpha-isopropylmalate synthase (2-Isopropylmalate Synthase)
8974_at 725.4 P
member of the leucine zipper family of transcriptional activators
8975_at -148.7 A
DNA polymerase I alpha subunit, p180
8976_at 399.7 A
similarity to YKL146w
8977_at 712.5 P
hypothetical protein
8978_at 1788.1 P
similarity to YNL032w, YNL056w and YDR067c
8979_at 2863.7 P
Ras proto-oncogene homolog
8980_at 228.7 A
involved in transcriptional regulation of PHO5
8981_at 16715.6 P
Ribosomal protein S7B (rp30)
8936_at 11052.2 P
Ribosomal protein S7B (rp30)
8937_at 387.1 P
strong similarity to YOR092w
8938_at 733.1 P
similarity to S.pombe hypothetical protein
8939_at -92.7 A
rab5-like GTPase involved in vacuolar protein sorting and endocytosis
8940_at -477.6 A
similarity to hypothetical C. elegans proteins Y48E1C.2 and Y48E1C.c
8941_at 2652.1 P
similarity to chicken h-caldesmon, Uso1p and YKL201c
8942_at 1029.3 P
GTP-binding protein of the rho subfamily of ras-like proteins
8943_at -97.3 A
questionable ORF
8944_at 2533.4 P
topoisomerase II, Top2p localizes to axial cores in meiosis
8945_at 1761.8 P
weak similarity to synaptogamines
8946_at 1260.6 P
hypothetical protein

8947_at 3005.8 P
Protein involved in propagation of M2 dsRNA satellite of L-A virus
8948_at 1016.1 P
Required for endocytosis and organization of the cytoskeleton
8949_at 74.5 A
weak similarity to rabbit peroxisomal Ca-dependent solute carrier
8950_at 322.0 A
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 912.7 P
similarity to ribosomal protein S13
8952_at 1313.4 P
hypothetical protein
8953_at 9313.7 P
tropomyosin I
8954_at 1382.7 P
hypothetical protein
8955_at 138.5 A
similarity to dnaJ protein homolog YDJ1
8956_at 1308.7 P
negative regulator of Ras cAMP pathway, shares weak homology with Spt2p
8957_at 3414.3 P
similarity to YHR088w and C.elegans hypothetical protein F44G4.1
8958_at 609.2 P
Protein of unknown function
8914_at 935.9 P
mitochondrial lysine-tRNA synthetase
8915_at 957.4 A
RNase H(35), a 35 kDa ribonuclease H
8916_at 6174.7 P
Dihydrolipoamide acetyltransferase component (E2) of pyruvate dehydrogenase complex
8917_at 5216.7 P
translocase of the outer mito. membrane
8918_at 39689.3 P
Ribosomal protein L16B (L21B) (rp23) (YL15)
8919_at 818.9 P
Fork Head homolog two
8920_i_at 3034.2 P
Ribosomal protein L9B (L8B) (rp24) (YL11)
8921_s_at 15845.3 P
Ribosomal protein L9B (L8B) (rp24) (YL11)
8922_at 12133.4 P
Protein involved in the aging process
8923_at 547.7 P
similarity to resistance proteins
8924_at 18617.2 P
yeast dnaJ homolog (nuclear envelope protein)\; heat shock protein
8925_at 507.4 P
weak similarity to Mycoplasma protoporphyrinogen oxidase
8926_at 1585.6 P
RNA-binding (zeta) subunit of translation initiation factor 3 (eIF-3)
8927_at 5254.6 P
90-kDa protein, located in nucleolus, that is homologous to a human proliferation-associated nucleolar protein, p120
8928_at 1689.8 P
Actin-related protein

8929_at	1717.5	P	similarity to YIL117c
8930_at	356.4	A	questionable ORF
8931_at	1251.0	P	similarity to YNL032w and YNL099c
8932_at	26618.5	P	Outer mitochondrial membrane porin (voltage-dependent anion channel, or VDAC)
8933_at	1151.9	P	vacuolar protein
8934_at	588.6	A	Tyrosine protein phosphatase involved in adaptation response to pheromone
8935_at	3790.0	P	Cytochrome-c oxidase chain Va
8891_at	253.3	A	hypothetical protein
8892_at	120.6	A	hypothetical protein
8893_at	1212.8	P	putative zinc finger protein
8894_at	1259.6	P	Required for aspargine-linked glycosylation
8895_at	889.2	P	similarity to probable transcription factor Ask10p and hypothetical protein YPR115w, and strong similarity to hypothetical protein YIL105c
8896_at	826.7	P	hypothetical protein
8897_at	2780.1	P	strong similarity to human leukotriene-A4 hydrolase
8898_at	354.9	A	questionable ORF
8899_at	590.1	A	Bypass of PAM1
8900_at	518.4	A	weak similarity to Mlp1
8901_at	289.5	A	weak similarity to M.genitalium alanine--tRNA ligase
8902_at	860.4	P	90 kd subunit of TFIIIB, also called TFIIIB90 or B or B 90 component
8903_at	399.4	A	hypothetical protein
8904_at	2284.5	P	alpha-4-beta-4 subunit of mitochondrial isocitrate dehydrogenase 1
8905_at	936.7	P	involved in secretion of proteins that lack classical secretory signal sequences
8906_at	2743.0	P	hypothetical protein
8907_s_at	129.0	A	nearly identical to YNL018c
8908_s_at	-30.5	A	nearly identical to YNL019c
8909_at	1429.1	P	Tyrosine phosphatase
8910_at	40969.0	P	Histone H3 (HHT1 and HHT2 code for identical proteins)
8911_s_at	34691.1	P	

Histone H4 (HHF1 and HHF2 code for identical proteins)
8912_at 747.2 P
Putative mannosyltransferase of the KRE2 family
8913_at -250.0 A
questionable ORF
8868_at 649.1 P
putative transcription factor
8869_at 1288.3 P
similarity to S.pombe hypothetical protein
8870_at 333.9 A
C-type cyclin associated with the Ssn3p cyclin-dependent kinase
8871_at 943.8 A
weak similarity to YBR271w and YJR129c
8872_at 1202.1 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 1011.2 P
weak similarity to C.burnetii FMU protein
8874_at 644.7 P
histone deacetylase, shares sequence similarity with Rpd3p, Hos1p, Hos2p, and Hos3p
8875_at 329.6 A
Predicted Ser\/thr kinase
8876_i_at 47.2 A
hypothetical protein
8877_r_at 376.6 A
hypothetical protein
8878_s_at -266.0 A
hypothetical protein
8879_at 5130.7 P
poly(A)+ RNA-binding protein
8880_at 1237.6 P
Proteinase inhibitor I2B (PBI2), that inhibits protease Prb1p (yscB)
8881_at 292.3 A
translation elongation factor eEF3 homolog
8882_at 551.5 A
questionable ORF
8883_at 78.2 A
encodes a protein with high similarity to phospholipase B
8884_at 318.6 A
similarity to hypothetical A. thaliana protein T14G11.21
8885_at 6154.4 P
weak similarity to B.subtilis hypothetical protein ykrX
8886_at 77.3 A
peroxisomal NADP-dependent isocitrate dehydrogenase
8887_at 809.9 P
similarity to YMR119w
8888_at 10586.2 P
sit4 suppressor, dnaJ homolog
8889_at 829.1 P
Required for amino acid permease transport from the Golgi to the cell surface
8890_at 965.1 P
Mitochondrial ribosomal protein MRP7 (YmL2) (E. coli L27)
8845_at 1554.7 P
hypothetical RNA-binding protein
8846_at 359.8 A
Member of family of mitochondrial carrier proteins

8847_at 3568.2 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 923.3 A

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 6163.2 P

citrate synthase. Nuclear encoded mitochondrial protein.

8850_at 295.7 A

Putative transmembrane protein

8851_at 428.1 P

34-kDa subunit of RNA polymerase III (C)

8852_at 137.6 A

weak similarity to bovine interferon gamma precursor

8853_at -38.8 A

questionable ORF

8854_at 1002.7 P

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

8855_at 334.7 A

Protein involved in autophagocytosis during starvation

8856_at 1319.0 P

weak similarity to human phosphatidylcholine--sterol O-acyltransferase

8857_at 488.7 P

hypothetical protein

8858_at 574.1 M

Protein required for accurate mitotic chromosome segregation

8859_at 89.9 A

putative RNA-dependent ATPase

8860_at 913.8 P

Uridine kinase

8861_at 3688.7 P

similarity to Pho87p and YJL198w

8862_at -139.5 A

weak similarity to hypothetical protein YMR206w

8863_at 1121.4 P

Suppressor of Mitochondrial Mutation in the tRNAasp gene

8864_at 23693.6 P

acetyl-CoA carboxylase

8865_at 3605.3 P

23 kDa mitochondrial inner membrane protein

8866_at 4547.5 P

hypothetical protein

8867_at 2405.8 P

Acyl-CoA cholesterol acyltransferase (sterol-ester synthetase)

8823_at 327.1 A

hypothetical protein

8824_at 5113.6 P

hypothetical protein

8825_at 314.7 A

weak similarity to protein phosphatases

8826_at 898.4 P

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

8827_at 840.3 P

weak similarity to Rpc31p

8828_at 224.9 A

questionable ORF
8829_at 694.0 P
Guanine nucleotide exchange factor for Sar1p.
8830_at 748.3 P
similarity to human pyridoxal kinase
8831_at 326.0 P
Cyclophilin
8832_at 2180.4 P
similarity to P.denitrificans cobW protein
8833_at 1223.0 P
ExtraCellular Mutant
8834_at 884.8 P A
MAP kinase kinase kinase\; activator of Pbs2p
8835_at 1191.1 P
Serine\/threonine protein phosphatase involved in glycogen accumulation
8836_at 879.2 P
para-aminobenzoate synthase, PABA synthase
8837_at 464.5 A
shows similarity to glucose-6-phosphate dehydrogenase non-catalytic domains\; homologous to Sol2p and Sol3p
8838_at 2863.9 P
Arp Complex Subunit
8839_at 1735.1 P
strong similarity to ribosomal protein S12
8840_at 603.6 P
strong similarity to Mycoplasma ribosomal protein S19
8841_at 1854.6 P
putative RNA helicase
8842_at 967.0 P
weak similarity to Anopheles mitochondrial NADH dehydrogenase subunit 2
8843_at 429.8 A
hypothetical protein
8844_at 1281.4 P
para hydroxybenzoate: polyprenyl transferase
8800_at 314.4 A
hypothetical protein
8801_at 9576.6 P
mevalonate pyrophosphate decarboxylase
8802_at 8109.3 P
anchorage subunit of a-agglutinin
8803_at 297.5 A
translational activator of cytochrome c oxidase
8804_at 2641.7 P
strong similarity to S.pombe hypothetical protein SPAC31A2.02
8805_at 298.3 A
similarity to ser/thr protein kinases
8806_at 408.7 A
strong similarity to YCR094w and YNL323w
8807_at 866.1 A
small hydrophilic protein, enriched in microsomal membrane fraction, interacts with Sec1p
8808_at 31352.1 P
Saccharopine dehydrogenase (NADP+, L-glutamate forming) (saccharopine reductase) (EC 1.5.1.10)
8809_at 1036.8 A
weak similarity to chicken nucleolin
8810_at 2702.4 P
Putative transcription factor

8811_at 4444.6 P
strong similarity to human breast tumor associated autoantigen
8812_at 678.0 M
strong similarity to human breast tumor associated autoantigen
8813_at 1209.0 P
similarity to C.elegans hypothetical protein CEESL47F
8814_at 1351.9 P
Putative ion transporter similar to the major facilitator superfamily of transporters
8815_at 97.7 A
transmembrane regulator of KAPA\/DAPA transport
8816_at 70.3 A
dethiobiotin synthetase
8817_at 387.0 A
7,8-diamino-pelargonic acid aminotransferase (DAPA) aminotransferase
8818_at 504.1 A
similarity to to alpha-1,3-mannosyltransferase
8819_at 262.2 A
similar to FRE2

8820_at 158.5 A
weak similarity to hypothetical protein YDL218w
8821_at -249.0 A
weak similarity to H.influenzae L-lactate permease (lctP) homolog
8822_at 66.9 A
weak similarity to CYC1/CYP3 transcription activator
8776_at 165.3 A
similarity to R.capsulatus 1-chloroalkane halidohydrolase
8777_at 1792.5 P
strong similarity to YJL222w, YIL173w and Pep1p
8778_at 214.3 A
strong similarity to Pep1p
8779_at 4168.5 P
similarity to beta-glucan-elicitor receptor - Glycine max
8780_at 457.8 A
similarity to Bul1p
8781_at 43.2 A
similarity to central part of Bul1p
8782_at -209.3 A
strong similarity to Snq2p
8783_at 110.5 A
strong similarity to UDP-glucose 4-epimerase Gal10p
8784_s_at 350.0 A
strong similarity to E.coli D-mannonate oxidoreductase, identical to YEL070w
8785_at 802.1 P
weak similarity to B.subtilis nitrite reductase (nirB)
8786_f_at 848.4 P
member of the seripauperin protein\/gene family
8787_at 921.3 P
hypothetical protein identified by SAGE
8788_at 143.7 A
hypothetical protein
8789_s_at 4407.2 P
Aminopeptidase of cysteine protease family
8790_s_at 3447.2 P
protein of unknown function
8791_at -452.2 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 -185.7 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 -101.7 A
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 -677.6 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 247.9 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 256.0 A
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 819.4 A
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 137.4 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 127.5 A
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 1042.6 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 423.0 A
non-annotated SAGE orf Found forward in NC_001146 between 547109 and 547366 with 100% identity. See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251
8754_at -30.0 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 1388.6 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 87145.8 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 -166.3 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 -266.8 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 188.8 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 17.9 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 224.0 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	938.0	P
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	-130.2	A
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	297.7	A
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	250.5	A
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	738.6	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	1550.3	A
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	-166.2	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
8769_g_at	-88.8	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	428.9	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
8771_r_at	-49.4	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	6214.4	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	3022.8	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	2189.9	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	271.5	A
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	737.6	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	2472.3	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
8731_at	-312.3	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	45.6	A
non-annotated SAGE orf Found reverse in NC_001146 between 286092 and 286301 with 100% identity.
See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251
8733_at	333.1	A
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 -30.3 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 65.2 A
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 149.1 A
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 -47.7 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 227.2 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
8739_at 37.9 A
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 1808.4 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 504.2 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 1835.9 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 1017.0 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 -49.0 A
non-annotated SAGE orf Found reverse in NC_001146 between 661997 and 662158 with 100% identity.
See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251
8745_at 332.5 A
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 -109.2 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 415.7 A
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 9.7 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 -376.5 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 -259.6 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 246.5 A
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 197.5 A

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 -205.6 A
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 366.1 A
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 39.8 A
non-annotated SAGE orf Found forward in NC_001146 between 452136 and 452276 with 100% identity. See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251
8709_at 780.0 P
non-annotated SAGE orf Found reverse in NC_001146 between 614367 and 614516 with 100% identity. See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251
8710_at 112.5 A
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 -99.9 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 -207.1 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 268.8 A
snRNA
8714_at 241.1 A
snRNA
8715_at 230.9 A
hypothetical protein
8716_s_at 898.4 P
Hypothetical aryl-alcohol dehydrogenase (AAD)
8717_at 119.1 A
similarity to Pseudomonas alkyl sulfatase
8718_at 241.9 A
similarity to P.putida phthalate transporter
8719_at 297.7 A
strong similarity to hypothetical protein YIL166c
8720_f_at -175.1 A
strong similarity to members of the Srp1p/Tip1p family
8721_at -107.8 A
hypothetical protein
8722_at 89.0 A
hypothetical protein
8723_at 4285.5 P
similarity to subtelomeric encoded proteins
8724_at 1116.5 A
similarity to glucan 1,4-alpha-glucosidase Sta1p and YAR066w
8725_g_at 1023.4 P
similarity to glucan 1,4-alpha-glucosidase Sta1p and YAR066w
8726_at 500.1 A
similarity to S.fumigata Asp FII
8727_at -371.4 A
strong similarity to Cps1p
8728_at -71.5 A
similar to FRE2
8683_at 4058.7 P

induced by osmotic stress\; similar to dihydroflavonol 4-reductase from plants
8684_at 244.9 A
questionable ORF
8685_at 265.2 A
Decapping protein involved in mRNA degradation
8686_at 764.9 P
transcription factor, member of the histone acetyltransferase SAGA complex
8687_at 1955.3 P
Peroxisomal membrane protein
8688_at 450.9 P
hypothetical protein
8689_at 673.1 A
CTR9 is required for normal CLN1 and CLN2 G1 cyclin expression
8690_at 1428.8 P
hypothetical protein
8691_at 6421.7 P
6,7-dimethyl-8-ribityllumazine synthase (DMRL synthase)
8692_at 1799.4 P
strong similarity to hypothetical S. pombe protein
8693_at 104.3 A
similarity to YDR435c and C.elegans hypothetical protein
8694_at 436.0 A
Acetylornithine aminotransferase
8695_at 6608.1 P
mRNA cap binding protein eIF-4E
8696_at 394.8 A
hypothetical protein
8697_at 442.1 P
weak similarity to tetracycline resistance proteins
8698_at 358.9 P
6-phosphofructo-2-kinase
8699_at 202.2 A
Stoichiometric member of mediator complex
8700_at 191.1 A
questionable ORF
8701_at 877.7 P
High level expression Reduces Ty3 Transposition
8702_at 132.6 A
similarity to glycophospholipid-anchored surface glycoprotein Gas1p
8703_at -124.8 A
hypothetical protein
8704_at 3039.2 P
ALuminium Resistance 1
8660_at 2746.4 P
similarity to hypothetical S. pombe protein
8661_at 197.6 A
strong similarity to protein kinase Mck1p
8662_at 27807.2 P
Ribosomal protein L25 (rpl6L) (YL25)
8663_at 5558.2 P
cytosolic malate dehydrogenase
8664_at 238.5 A
hypothetical protein
8665_at 573.9 A
weak similarity to M.jannaschii hypothetical protein
8666_at 2492.2 P

Putative polyadenylated-RNA-binding protein located in nucleus\; similar to vertebrate hnRNP A\/B protein family
8667_at 739.7 A
has been localized to both the plasma membrane and the mitochondrial membrane
8668_at 37021.3 P
Ribosomal protein L18A (rp28A)
8669_at 251.3 A
similarity to monocarboxylate transporter proteins
8670_at 29.3 A
hypothetical protein
8671_at 165.1 A
weak similarity to human sodium channel alpha chain HBA
8672_at 534.0 P
43 kDa protein, transcriptional activator
8673_at 654.8 P
homologous to Trf5p and Top1p, associates with Smc1p and Smc2p
8674_at 53.7 A
similarity to human DS-1 protein
8675_at 154.1 A
Serine\/threonine protein kinase with similarity to Ste20p and Cla4p
8676_at 554.9 P
Multicopy Suppressor of Bud Emergence
8677_at 3232.9 P
weak similarity to human ubiquitin-like protein GDX
8678_at 915.1 P
Involved in RAS localization and palmitoylation
8679_at 37026.1 P
Overexpression yields resistance to Zeocin
8680_at 802.6 P
Transcription factor involved in activation of phospholipid synthetic genes
8681_at 488.2 A
weak similarity to human PL6 protein
8682_at 300.8 A
questionable ORF
8638_at 355.6 A
Putative integral membrane protein containing novel cysteine motif. Similarity to SLG1 (WSC1), WSC2 and WSC4
8639_at 160.3 A
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 1536.3 P
myo-inositol transporter
8641_at 823.1 P
tRNA 2 -phosphotransferase
8642_at 553.5 A
similarity to YOL002c and YDR492w
8643_at 143.0 A
Ser\/Thr protein kinase
8644_at -144.3 A
questionable ORF
8645_at 2510.3 P
similarity to hypothetical S.pombe protein
8646_at 9762.4 P
cytoplasmic tryptophanyl-tRNA synthetase
8647_at 339.9 A
3,4-dihydroxy-5-hexaprenylbenzoate methyltransferase

8648_at 267.8 A
Helicase in MItochondria
8649_at 815.7 P
Subunit 4 of Replication Factor C\; homologous to human RFC 40 kDa subunit
8650_at 1398.7 A
similarity to C.elegans hypothetical protein F25H8.1
8651_at 2815.3 P
strong similarity to YBR147w
8652_at 104.8 A
hypothetical protein
8653_at 326.9 A
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 468.4 A
putative transcription factor\; contains a zinc finger
8655_at 622.3 A
protein disulfide isomerase related protein
8656_at 993.9 P
similarity to S.pombe hypothetical protein
8657_at 247782.0 P
Alcohol dehydrogenase
8658_at 134.1 A
hypothetical protein
8659_at 89.1 A
similarity to A.thaliana hyp1 protein
8615_at 341.4 A
similarity to YOL082w
8616_at 1211.5 P
similarity to YOL083w
8617_at 809.3 P
encodes a GTPase activating protein, highly homologous to Ira1p, homologue of neurofibromin
8618_at 972.5 P
strong similarity to X.laevis XPMC2 protein
8619_at 49.6 A
similarity to NADH dehydrogenases
8620_at 639.0 A
hypothetical protein
8621_at 3777.8 P
strong similarity to C.elegans K12H4.3 protein
8622_at 1303.1 P
Dislikes Extra CIN8, (MDM) Mitochondrial distribution and morphology
8623_at 550.9 A
similarity to A.gambiae ATP-binding-cassette protein
8624_at 720.2 P
hypothetical protein
8625_at 841.7 P
hypothetical protein
8626_at 338.0 A
similarity to hypothetical S. pombe protein
8627_at 782.8 P
hypothetical protein
8628_at -59.5 A
53-kDa coiled-coil protein
8629_at 2224.9 P
Homolog of SIR2

8630_at 113.6 A
Transcription factor (bHLH) involved in interorganelle communication between mitochondria, peroxisomes, and nucleus
8631_at 603.1 P
DRAP deaminase
8632_at 376.3 P
inositol polyphosphate 5-phosphatase
8633_at 1684.7 P 3
(2)5 -bisphosphate nucleotidase
8634_at 402.5 A
hypothetical protein
8635_at 804.4 A
Clathrin associated protein, medium subunit
8636_at 4349.5 P
Phosphoribosylpyrophosphate synthetase (ribose-phosphate pyrophosphokinase)
8637_at 716.9 A
similarity to C.elegans hypothetical protein M02F4.4
8592_at 1075.8 P
Glycerol-3-phosphate dehydrogenase (NAD+)
8593_at 3422.6 P
arginosuccinate synthetase
8594_at 414.8 A
similarity to hypothetical C. elegans protein F02E9.6
8595_at 357.6 A
phosphoglycerate mutase
8596_at 472.3 A
similarity to B. subtilis transcriptional activator tenA
8597_at 1144.7 P
weak similarity to transcription factors
8598_at 298.1 A
hypothetical protein
8599_at 1053.5 A
DNA Damage Responsive
8600_at 3761.0 P
S-adenosylmethionine decarboxylase
8601_at 461.4 A
Component of the RNA polymerase II holoenzyme complex, positive and negative transcriptional regulator of genes involved in mating-type specialization
8602_at 228.4 A
questionable ORF
8603_at 2292.3 P
Glutathione Synthetase
8604_at 157.5 A
similarity to YAL018c and YOL047c
8605_at 250.5 A
weak similarity to hypothetical proteins YAL018c and YOL048c
8606_at 142.0 A
questionable ORF
8607_at 789.5 P
similarity to ser/thr protein kinase
8608_at 604.1 A
44 kDa phosphorylated integral peroxisomal membrane protein
8609_at 565.6 A
Endonuclease III-like glycosylase 2
8610_at 269.9 A
similarity to CCR4 protein

8611_at	782.7	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	51106.9	P	40S ribosomal protein S15 (S21) (rp52) (RIG protein)
8613_at	43660.3	P	60S acidic ribosomal protein P2A (L44) (A2) (YP2alpha)
8614_at	9539.1	P	alpha-type of subunit of 20S proteasome
8570_at	-85.1	A	questionable ORF
8571_at	1957.9	P	weak similarity to YMR317w
8572_at	668.9	P	questionable ORF
8573_at	238.5	A	similarity to S.pombe rad18 and rpgL29 genes and other members of the SMC superfamily
8574_at	359.9	A	Mitochondrial glutamyl-tRNA synthetase
8575_at	244.1	A	hypothetical protein
8576_at	800.4	P	weak similarity to Y.lipolytica Sls1 protein precursor
8577_at	9998.4	P	strong similarity to glycoprotein Gas1p
8578_at	1196.2	P	hypothetical protein
8579_at	49.8	A	bZIP protein
8580_at	1923.7	P	similarity to YPR125w
8581_at	2035.3	P	hypothetical protein
8582_at	647.6	A	Affects longevity
8583_at	346.7	A	hypothetical protein
8584_at	453.7	A	mitochondrial initiation factor 2
8585_at	1586.5	P	weak similarity to rat apoptosis protein RP-8
8586_at	2200.9	P	possible component of RCC1-Ran pathway
8587_at	1915.9	P	Tryptophan permease, high affinity
8588_at	1891.8	P	similarity to Rim9p and YFR012w
8589_at	356.5	A	tSNARE that affects a Late Golgi compartment
8590_at	286.6	A	similarity to YFR013w
8591_at	1510.0	P	Calmodulin-dependent protein kinase
8547_at	-95.0	A	weak similarity to YKR015c
8548_at	530.9	P	

hypothetical protein
8549_at 571.6 P
Hmg-coa Reductase Degradation
8550_at 4303.6 P
An evolutionarily conserved member of the histone H2A F\/Z family of histone variants
8551_at 1662.0 P
strong similarity to phospholipases
8552_at 1566.8 P
putative RNA 3 -terminal phosphate cyclase
8553_at 491.9 A
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 355.2 A
hypothetical protein
8555_at 565.2 P
Appears to be a structural component of the chitin synthase 3 complex
8556_at 1058.5 P
topoisomerase I
8557_at 2339.0 P
RNA polymerase II subunit, homologous to S. pombe Rpb11p subunit
8558_at 2503.0 P
DNA binding protein involved in transcriptional regulation
8559_at 696.9 P
similarity to C.elegans hypothetical protein, YDR126w, YNL326c and YLR246w
8560_at 2014.4 P
strong similarity to YDR492w and S.pombe hypothetical protein
8561_at 213.8 A
negative transcriptional regulator
8562_at 1894.2 P
Ribosomal RNA Processing
8563_at 3040.3 P
Required for glucosylation in the N-linked glycosylation pathway
8564_at 773.5 P
subtilisin-like protease III
8565_at 2919.6 P
weak similarity to hypothetical protein YDR339c
8566_at 122.5 A
ATP dependent DNA ligase
8567_at 706.0 P
similarity to M.jannaschii hypothetical protein MJ0708
8568_at 11777.2 P
small glutamine-rich tetratricopeptide repeat containing protein
8569_at 802.9 A
Cell wall integrity and stress response component 1
8525_at -90.2 A
Killed In Mutagen, reduced growth in diepoxybutane and\/or mitomycin C
8526_at 918.8 P
similarity to Tir1p and Tir2p
8527_at 4323.9 P
Cold-shock induced protein of the Srp1p\/Tip1p family of serine-alanine-rich proteins
8528_at 587.6 A
strong similarity to ATP-dependent permeases
8529_at 74.8 A
similarity to YDR391c
8530_g_at 42.4 A
similarity to YDR391c

8531_at	314.1	A	strong similarity to YDR391c
8532_at	1021.2	P	B-type regulatory subunit of protein phosphatase 2A (PP2A)
8533_at	2483.7	P	hypothetical protein
8534_at	590.4	A	p24 protein involved in membrane trafficking
8535_at	1000.4	P	Mitochondrial membrane protein
8536_at	473.7	A	Resistance to o-dinitrobenzene, calcium, and zinc
8537_at	349.1	A	similarity to YDR474c
8538_at	7487.4	P	10 kDa mitochondrial heat shock protein
8539_at	2380.0	P	similarity to Pyrococcus horikoshii hypothetical protein PHBQ041
8540_at	62.6	A	weak similarity to D.melanogaster probable Ca2+ transporter rdgB
8541_at	1314.2	P	hypothetical protein
8542_at	472.6	A	hypothetical protein
8543_at	214.1	A	Homolog of SIR2
8544_at	942.4	P	Protein required for cell cycle arrest in response to loss of microtubule function
8545_at	11385.3	P	Heat shock protein also induced by canavanine and entry into stationary phase
8546_at	113.2	A	bZIP protein, can activate transcription from a promoter containing a Yap recognition site
8502_at	-126.1	A	hypothetical protein
8503_at	-46.0	A	involved in invasive growth upon nitrogen starvation
8504_at	1065.8	P	Metallothionein-like protein
8505_at	167.4	A	myc-family transcription factor homolog
8506_at	717.6	P	Protein that complements a drug-hypersensitive mutation
8507_at	450.3	A	Protein involved in constitutive endocytosis of Ste3p
8508_at	317.7	A	Required for mother cell-specific HO expression
8509_at	62.2	A	integral membrane protein\; c-terminal TMD\; located in endosome
8510_at	439.1	A	cytochrome c mitochondrial import factor
8511_at	1407.9	P	putative repressor protein\; contains nuclear targeting signal
8512_at	1444.2	P	Casein kinase II, beta subunit
8513_at	245.2	A	Mitochondrial glyoxylase-II

8514_at -138.2 A
questionable ORF
8515_at 1416.8 P
weak similarity to YDR273w
8516_at 583.9 A
Protein involved in growth regulation
8517_at 550.9 A
weak similarity to YDR275w
8518_at 5621.9 P
outer mitochondrial membrane protein, component of the mitochondiral protein translocation complex, associates with Isp42p
8519_at 6922.4 P
RNA helicase
8520_at 1284.4 P
homologous to MTH1\; interacts with the SNF1 protein kinase and TBP in two-hybrid and in in vitro binding studies
8521_at 1924.3 P
RNA trafficking protein\; transcription activator
8522_at 2887.1 P
similarity to YER185w, Rta1p
8523_at -209.9 A
hypothetical protein
8524_at 1983.6 P
weak similarity to myosin heavy chain proteins
8480_at 1570.7 P
hypothetical protein
8481_at 496.3 M
similarity to protamines
8482_at 597.0 P
similarity to Sis2p protein and C.tropicalis hal3 protein
8483_at -113.0 A
questionable ORF
8484_at 1192.7 P
weak similarity to human phosphorylation regulatory protein HP-10
8485_at 688.2 P
G2 allele of skp1 suppressor
8486_at 212.8 A
encodes component of the spindle midzone
8487_at 1448.4 P
weak similarity to YGL144c
8488_at 476.4 A
hypothetical protein
8489_at 1656.9 P
alpha subunit of casein kinase II
8490_at 1127.0 A
strong similarity to YKR075c
8491_at 25386.6 P
Ribosomal protein L3 (rp1) (YL1)
8492_at 598.9 M
weak similarity to human retinoblastoma binding protein 2
8493_at 1597.1 P
Cytochrome c1
8494_at 656.5 P
hypothetical protein
8495_at 1498.3 P
glycosyl transferase

8496_at -44.8 A
hypothetical protein
8497_at 619.2 M
GTPase activating protein
8498_at 265.1 A
strong similarity to Thi10p
8499_at 156.0 A
hypothetical protein
8500_at 597.3 A
hypothetical protein
8501_at 69.3 A
endoplasmic reticulum t-SNARE, coprecipitates with Sec20p, Tip1p. and Sec22p
8457_at 733.3 A
similarity to Hbs1p, Sup2p and EF1-alpha
8458_at 289.3 A
similarity to mouse KIN17 protein
8459_at 1352.9 P
weak similarity to YMR172w
8460_at 1574.0 P
Multi-copy suppressor of SOD-linked defects
8461_at 664.2 A
hypothetical protein
8462_at 1788.3 P
strong similarity to YKR089c
8463_at 267.9 A
questionable ORF
8464_at 59.8 A
weak similarity to YKR091w
8465_at 1321.4 P
hypothetical protein
8466_at 2666.8 P
34-kDa, gamma subunit of oligosaccharyl transferase glycoprotein complex
8467_at 2421.8 P
weak similarity to synaptogamines
8468_at 95.2 A
hypothetical protein
8469_g_at 83.3 A
hypothetical protein
8470_at 752.8 P
weak similarity to human calcium influx channel
8471_at 2082.3 P
small GTP-binding protein\; geranylgeranylated\; geranylgeranylation required for membrane association\; also involved in endocytosis post vesicle internalization
8472_at 1461.5 P
similarity to ser/thr protein phosphatases
8473_at 760.4 M
similarity to hypothetical S.pombe protein D83992_G
8474_at 346.6 A
ExtraCellular Mutant
8475_at 138.6 A
similarity to S.pombe hypothetical protein SPAC22F3.04
8476_at 1368.5 P
GTP-binding ADP-ribosylation factor
8477_at 1605.4 P
Ribose-5-phosphate ketol-isomerase
8478_at 23065.4 P

Ribosomal protein S7A (rp30)
8479_at 24273.4 P
Ribosomal protein S7A (rp30)
8434_at 558.2 A
hypothetical protein
8435_at 2784.1 P
nuclear pore complex protein
8436_at 4499.9 P
type 2 membrane protein\; probable secretory protein
8437_at 245.0 A
similarity to mitochondrial carrier proteins
8438_at 862.8 P
ras proto-oncogene homolog
8439_at 1.2 A
questionable ORF
8440_at 475.6 A
16-kDa, epsilon subunit of oligosaccharyltransferase complex\; 40\% identical to vertebrate DAD1 protein
8441_at 442.6 A
hypothetical protein
8442_g_at 306.8 A
hypothetical protein
8443_at 488.4 A
member of the syntaxin family of proteins\; predicted C-terminal TMD
8444_at 102.9 A
weak similarity to human G-0/G-1 switch regulatory protein 8
8445_at 1721.4 P
putative isoform of Leu4p
8446_at 1415.3 A
inositol polyphosphate 5-phosphatase
8447_at 822.0 A
TFIIIC (transcription initiation factor) subunit, 55 kDa
8448_at 61.9 A
weak similarity to B.subtilis maf protein
8449_at 1386.1 P
similarity to C.elegans hypothetical protein
8450_at 111.8 A
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 280.7 A
hypothetical protein
8452_at 1122.6 P
involved in targeting and fusion of ER to golgi transport vesicles
8453_at 1735.7 P
RNA polymerase III large subunit
8454_at 3351.8 P
Probable 26S protease subunit and member of the CDC48\/PAS1\/SEC18 family of ATPases
8455_at 226.0 A
hypothetical protein
8456_at 231.0 A
similarity to a C.elegans ZK632.3 protein
8412_at 482.8 A
Similar to mammalian aldo\/keto reductases
8413_at -203.5 A
questionable ORF
8414_at 10852.0 P
profilin (actin-binding protein)

8415_at 3390.2 P
extremely hydrophilic protein
8416_at 1400.1 P
Ubiquitin-specific protease
8417_at 361.5 A
may encode a protein involved in one or more monoxygenase or hydroxylase steps of ubiquinone biosynthesis
8418_at 769.7 P
isoamyl acetate hydrolytic enzyme
8419_at 855.8 P
rho type GTPase activating protein
8420_at 1628.5 P
phosphoribosylamino-imidazole-carboxylase
8421_at 621.5 P
hypothetical protein
8422_at 149.8 A
mitochondrial integral membrane protein
8423_at 1557.5 P
weak similarity to E.coli hypothetical 27K protein
8424_at 2158.3 P
Peripheral membrane protein required for vacuolar protein sorting
8425_s_at 82403.8 P
translation elongation factor 2 (EF-2)
8426_at 48.1 A
GTPase activating protein (GAP)
8427_at 21.9 A
questionable ORF
8428_at 9874.7 P
NAD+-dependent isocitrate dehydrogenase
8429_at 837.5 A
similarity to YLR361c
8430_at 342.6 A
hypothetical protein
8431_at 283.3 A
questionable ORF
8432_at 381.3 A
Transcription factor
8433_at 703.0 A
Actin-related protein
8389_at 4570.7 P
Succinate-CoA Ligase (ADP-Forming)
8390_at 274.6 A
Thiamin pyrophosphokinase
8391_at 260.5 A
weak similarity to human DNA-binding protein PO-GA and to bacterial H+-transporting ATP synthases
8392_at 2203.2 P
strong similarity to hypothtical S. pombe protein and to hypothetical C. elegans protein
8393_at 320.0 A
questionable ORF
8394_at 400.6 A
similarity to YHR194w
8395_at 460.9 A
required for final stages of splicesome maturation\; promotes step 1 of splicing
8396_at 25.1 A
Involved in plasmid maintenance
8397_at 986.4 P

ribosomal protein of the large subunit, mitochondrial
8398_at 7530.5 P
second largest subunit of RNA polymerase II
8399_at 593.2 A
hypothetical protein
8400_at 81929.0 P
multidrug resistance transporter
8401_at -57.8 A
similarity to hypothetical A. thaliana proteins F19G10.15 and T19F06.21
8402_at 1059.1 P
similarity to 5 -flanking region of the Pichia MOX gene
8403_at 409.1 A
Interacts with C-terminus of CDC12
8404_at 6085.7 P
putative proteasome subunit
8405_at 382.1 A
Mitochondrial ribosomal protein of small subunit
8406_at 601.4 P
homologue of human E core protein
8407_at 967.1 P
Protein involved in mRNA transport from nucleus to cytoplasm
8408_at 39.2 A
similarity to C.elegans cosmid F35C8
8409_at 335.3 A
transcription factor
8410_at 1093.1 P
strong similarity to S.pombe SPAC13G6.14 protein
8411_at 949.0 P
hypothetical protein
8366_at 1819.2 P
similarity to E.histolytica surface lectin
8367_at 162.3 A
hypothetical protein
8368_i_at 19692.2 P
Ribosomal protein S28A (S33A) (YS27)
8369_f_at 39328.1 P
Ribosomal protein S28A (S33A) (YS27)
8370_at 5674.8 P
glutaminyl-tRNA synthetase
8371_at 2574.0 P
questionable ORF
8372_at 91.8 A
questionable ORF
8373_at 291.3 A
sphingoid long chain base (LCB) kinase
8374_at 1278.9 P
similarity to finger protein YKL222c, YOR162c and YLR266c
8375_at -1.1 A
strong similarity to YLR270w
8376_at 738.4 A
Stoichiometric member of mediator complex
8377_at 1178.0 P
similarity to human and murine C3f protein
8378_at 2027.1 P
ferrochelatase (protoheme ferrolyase)
8379_at 222.1 A

weak similarity to rat SCP1 protein
8380_at 238.0 A
Regulatory subunit for Glc7p
8381_at 198.9 A
similarity to BRR5 protein
8382_at 293.6 A
Peroxisomal enoyl-CoA hydratase
8383_at 900.1 A
Actin assembly factor
8384_f_at 81954.7 P
Ribosomal protein S30B
8385_at 146.9 A
hypothetical protein
8386_at 4161.1 P
phosphoserine transaminase
8387_at 845.6 A
GTP binding protein, almost identical to Gsp1p
8388_at -238.9 A
hypothetical protein
8343_at 2715.6 P
Translation elongation factor Tu, mitochondrial
8344_at 686.8 P
Protein that may play a role in polarity establishment and bud formation
8345_at 1126.1 A
weak similarity to chicken nonhistone chromosomal protein HMG-2
8346_at -214.7 A
sporulation-specific exo-1,3-beta-glucanase
8347_at 294.5 A
contains motifs that are present in a family of DNA-dependent ATPases, the SWI2\/SNF2-like proteins
8348_i_at 514.1 P
strong similarity to Thi10p
8349_f_at 373.7 A
strong similarity to Thi10p
8350_at -102.1 A
weak similarity to YPL112c
8351_at 563.1 P
Transcription factor IIA, large chain
8352_at 381.3 A
possible leucine zipper
8353_at 1276.0 P
Involved in lipoic acid metabolism
8354_at 3724.5 P
hypothetical protein
8355_at 3058.2 P
Multicopy suppressor of BFA (Brefeldin A)-induced lethality\; implicated in secretion and nuclear segregation
8356_at -81.3 A
questionable ORF
8357_at 149.5 A
questionable ORF
8358_at 797.8 P
Ribose methyltransferase for mitochondrial 21S rRNA
8359_at 2726.2 P
imidazoleglycerol-phosphate dehydratase
8360_at 789.6 P
questionable ORF

8361_at 3571.7 P
ATP-dependent RNA helicase of DEAD box family\; suppressor of a pre-mRNA splicing mutation, prp8-1
8362_at 676.1 A
hypothetical protein
8363_at 1533.4 P
similarity to Brettanomyces RAD4 and to S.pombe hypothetical protein
8364_at 4468.9 P
second-largest subunit of RNA polymerase III
8365_at 1099.7 P
protein tyrosine phosphatase
8320_at 3630.5 P
homology to bacterial nicotinate phosphoribosyl transferase
8321_at 5000.7 P
RNA polymerase II subunit
8322_at -49.9 A
encodes protein with GTP-binding domain related to dynamin
8323_at 2298.4 P
beta subunit of G protein coupled to mating factor receptor
8324_at 254.3 A
Involved in silencing at telomeres, HML and HMR
8325_at -229.2 A
hypothetical protein
8326_at 589.2 A
similarity to M.xanthus hypothetical protein
8327_at 664.6 M
Relieves uso1-1 Transport Defect
8328_at 2016.4 P
Subunit 1 of Replication Factor C\; homologous to human RFC 140 kDa subunit
8329_at 847.2 P
questionable ORF
8330_at 1750.7 P
dipeptidyl aminopeptidase
8331_at 2056.1 P
hypothetical protein
8332_at 1226.2 P
malonyl-CoA:ACP transferase
8333_at 65.1 A
malonyl-CoA:ACP transferase
8334_at 1018.4 A
similarity to ADP/ATP carrier proteins
8335_at 538.6 A
protein of unknown function
8336_at 5916.7 P
16-kDa RNA polymerase subunit (common to polymerases I, II and III)
8337_at 423.3 A
questionable ORF
8338_at 1628.7 P
NifU-like protein A
8339_at 449.8 A
similarity to microtubule-interacting protein Mhp1p
8340_at 457.2 P
weak similarity to YNR013c
8341_at 1628.7 P
Transcriptional modulator
8342_at 9933.2 P
Transcriptional modulator

8297_at 430.8 A
protein kinase involved in protein kinase C pathway
8298_at 1412.5 P
GrpE homolog, mitochondrial matrix protein
8299_at 1382.9 P
protein kinase
8300_f_at 25257.2 P
Ribosomal protein L33B (L37B) (rp47) (YL37)
8301_at 349.4 A
encodes snRNA U3, SNR17B also encodes snRNA U3
8302_at 1252.7 P
dihydrofolate reductase
8303_at -172.4 A
homology to human oxysterol binding protein
8304_at 569.1 A
similarity to hypothetical S. pombe protein
8305_at 825.0 A
hypothetical protein
8306_at 1492.9 P
similarity to C.elegans ZK1058.5 protein
8307_at 2469.6 P
tetrahydrofolylpolyglutamate synthase
8308_at -19.9 A
Sporulation Specific
8309_at 2281.6 P
similarity to M.jannaschii hypothetical protein MJ0588
8310_at 944.4 A
Acetyltransferase in the SAS gene family
8311_at 1024.6 P
similarity to hypothetical C. elegans proteins
8312_at 1169.8 P
weak similarity to reductases
8313_at 13831.5 P
Suppressor of rad53 lethality
8314_g_at 17300.8 P
Suppressor of rad53 lethality
8315_i_at 3897.2 P
questionable ORF
8316_at 306.2 A
subunit of the anaphase promoting complex
8317_at 899.6 A
CLeavage\/Polyadenylation factor IA subunit\; interacts with Pcf11p in the 2-hybrid system
8318_at 1854.2 P
similarity to thiosulfate sulfurtransferases
8319_at 220.5 A
hypothetical protein
8274_at 550.2 P
hypothetical protein
8275_at 2219.7 P
Protein involved in protein import into ER
8276_at 177.0 A
hypothetical protein
8277_at 726.3 P
strong similarity to secretory protein Ssp134p
8278_at 1717.8 P
calcium-binding protein component of spindle pole bodies, localizes to half-bridges and interacts with

KAR1
8279_at 90.1 A
hypothetical protein
8280_at 4187.7 P
ATPase\; component of the 26S proteasome cap subunit
8281_at 5059.3 P
translation initiation factor eIF2b gamma subunit\; negative regulator in the general control of amino acid biosynthesis
8282_at 2660.8 P
Subunit of the regulatory particle of the proteasome
8283_at 686.8 A
similarity to YLR243w
8284_at 121.0 A
questionable ORF
8285_at 696.2 P
hypothetical protein
8286_at 2024.7 P
Binds to beta-tubulin and may participate in microtubule morphogenesis
8287_at -97.6 A
Pentamidine resistance protein
8288_at 2775.0 P
similarity to ser/thr protein kinases
8289_at -157.9 A
hypothetical protein
8290_at 608.5 A
Required for viability in the absence of the kinesin-related Cin8p mitotic motor.
8291_at 10753.8 P
Vacuolar H-ATPase 100 kDa subunit of membrane (V0) sector, essential for vacuolar acidification and vacuolar H-ATPase activity
8292_at 9873.3 P
strong similarity to Rattus tricarboxylate carrier
8293_at 2323.7 P
microtubule-associated protein
8294_at 1451.4 P
similarity to resistance proteins
8295_at 581.7 A
transfer RNA isopentenyl transferase
8296_at 128.6 A
similarity to A.nidulans palA protein
8252_at 4821.7 P
Binds to eIF4E, the mRNA cap-binding protein, and represses cap-dependent translation initiation by interfering with the interaction of eIF4E and eIF4G
8253_at 503.7 A
questionable ORF
8254_at 539.2 A
uroporphyrinogen III synthase
8255_at 166.0 A
hypothetical protein
8256_at 608.5 A
similarity to S.pombe dihydrofolate reductase
8257_at 1930.4 P
weak similarity to phosducins
8258_at -328.2 A
questionable ORF
8259_at 1920.8 P
weak similarity to phosphoglycerate mutases

8260_at	45.9	A	weak similarity to M.jannaschii hypothetical protein MJ0694
8261_at	8166.6	P	similarity to D.melanogaster heat shock protein 67B2
8262_at	2066.7	P	similarity to D.melanogaster heat shock protein 67B2
8263_at	493.7	P	weak similarity to PITSLRE protein kinase isoforms
8264_at	752.5	P	Disulfide isomerase related protein
8265_at	299.2	A	similarity to C.elegans hypothetical protein
8266_at	2808.8	P	transcriptional regulator
8267_at	1067.1	P	similarity to cation translocating ATPases
8268_at	360.6	A	similarity to human and mouse glomerulosclerosis protein Mpv17
8269_f_at	14759.9	P	Ribosomal protein S10A
8270_f_at	53608.2	P	Ribosomal protein S10A
8271_at	926.9	P	similarity to human hypothetical protein
8272_at	67.8	A	weak similarity to SWI/SNF complex 60 KDa subunit from man and mouse
8273_at	323.3	A	similarity to hypothetical S. pombe protein
8229_at	374.6	A	similarity to Sdh4p
8230_at	-33.0	A	required for meiosis
8231_at	3101.7	P	multiprotein bridging factor
8232_at	1348.7	P	BUD site selection
8233_g_at	822.4	P	BUD site selection
8234_at	114.9	A	questionable ORF
8235_at	252.5	A	hypothetical protein
8236_at	2204.1	P	CPA1 leader peptide
8237_at	4213.6	P	Carbamoyl phosphate synthetase, arginine specific
8238_at	877.0	A	has strong homology to Drosophila ISWI
8239_at	472.4	A	AIP3 binding protein
8240_at	1042.4	A	hypothetical protein
8241_at	1673.5	P	similarity to human X-linked PEST-containing transporter
8242_at	1449.6	P	homolog of chloroplast phosphate transporter

8243_at	453.7	A	weak similarity to YIL149c
8244_i_at	25825.2	P	questionable ORF
8245_r_at	2031.1	P	questionable ORF
8246_s_at	10281.6	P	questionable ORF
8247_at	12158.1	P	57 kDa nucleolar protein
8248_at	1098.6	P	similarity to hypothetical S. pombe protein
8249_at	221.3	A	sporulation-specific protein
8250_at	1173.6	P	hypothetical protein
8251_at	1112.9	P	hypothetical protein
8206_at	898.0	M	Protein involved in cobalt accumulation\; dosage dependent suppressor of cobalt toxicity
8207_at	2339.3	P	long chain fatty acyl:CoA synthetase
8208_at	65.7	A	hypothetical protein
8209_at	166.0	A	homolog of mammalian splicing factor\/U2 snRNP protein
8210_at	975.7	P	hypothetical protein
8211_at	685.0	P	dolichyl phosphate-D-mannose:protein O-D-mannosyltransferase
8212_at	989.9	P	similarity to hypothetical S.pombe protein SPAC1F12.05
8213_at	10306.6	P	gamma-glutamyl phosphate reductase
8214_at	487.4	P	similarity to YAL028w
8215_at	-68.8	A	questionable ORF
8216_at	3554.5	P	myosin-1
8217_at	5464.9	P	vesicle-associated membrane protein (synaptobrevin) homolog
8218_at	2006.5	P	Putative ABC transporter highly similar to Pdr5p
8219_at	653.5	P	Multicopy suppressor of clathrin deficiency and of ts mutants of IPL1
8220_at	1175.9	P	catalytic subunit of mitochondrial DNA polymerase
8221_at	442.9	A	questionable ORF
8222_at	16010.2	P	27-kDa subunit of the vacuolar ATPase\; E subunit of V1 sector
8223_at	58.5	A	questionable ORF
8224_at	304.5	A	splicing factor

8225_at	10465.3	P	Cytoplasmic alanyl-tRNA synthetase gene
8226_at	1593.8	P	Appears to function early in (1,6)-beta-D-glucan synthesis pathway
8227_at	189.0	A	Mutants are defective in Ty1 Enhancer-mediated Activation
8228_at	-244.6	A	similarity to YAL034c
8183_at	22.2	A	strong similarity to E2 ubiquitin-conjugating enzymes
8184_at	1991.2	P	DNA-dependent RNA polymerase I subunit A43
8185_at	6332.9	P	RNA polymerase I subunit 190 (alpha)
8186_at	451.8	A	weak similarity to YAl037w
8187_at	-188.5	A	hypothetical protein
8188_at	1315.5	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	-3.1	A	questionable ORF
8190_at	1357.2	P	deoxycytidyl transferase
8191_at	505.5	P	Pyruvate kinase, glucose-repressed isoform
8192_at	-36.0	A	putative proline-specific permease
8193_at	-19.8	A	Protein involved in chromosome segregation, required for microtubule stability
8194_at	153.9	A	weak similarity to Esp1p and mitochondrial L.illustris cytochrome oxidase I
8195_at	48.2	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	524.4	A	hypothetical protein
8197_at	451.7	P	weak similarity to adenylate cyclases
8198_at	402.3	A	hypothetical protein
8199_at	2255.6	P	nam9-1 suppressor
8200_at	2841.0	P	strong similarity to human electron transfer flavoprotein-ubiquinone oxidoreductase
8201_at	1322.6	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	322.1	A	Component, along with Hap2p and Hap3p, of CCAAT-binding transcription factor

8203_at	1347.7	P	hypothetical protein
8204_at	1131.4	P	low-Km (high-affinity) cAMP phosphodiesterase
8205_at	5042.9	P	translation initiation factor eIF3 subunit
8161_at	4995.7	P	proteasome component YC1 (protease yscE subunit 1)
8162_at	557.9	A	Activator of peroxisome proliferation
8163_at	-77.2	A	hypothetical protein
8164_at	30.5	A	strong similarity to YAL053w
8165_at	182.3	A	questionable ORF
8166_at	1504.7	P	Calponin homolog
8167_at	-61.3	A	encodes a putative 3 ->5 exonuclease
8168_at	97731.9	P	40S ribosomal protein S12
8169_at	6016.6	P	protein of the TCD\/MRS6 family of GDP dissociation inhibitors (Rab escort protein)\; component of Rab geranylgeranyl transferase
8170_at	700.5	P	similarity to YAL056w
8171_at	935.6	P	hypothetical protein
8172_at	725.8	A	nuclesome assembly protein I
8173_at	1792.1	P	aldehyde dehydrogenase (E.C. 1.2.1.5) (sold by SIGMA under the catalogue number A5550, according to A. Blomberg)
8174_at	4854.0	P	NADP-specific glutamate dehydrogenase
8175_at	-274.5	A	hypothetical protein
8176_at	153.2	A	Alcohol acetyltransferase
8177_at	-323.5	A	strong similarity to aminotriazole resistance protein
8178_at	227.8	A	questionable ORF
8179_at	707.9	P	weak similarity to Pdr3p
8180_at	172.8	A	similar to FRE2
8181_at	527.6	P	hypothetical protein
8182_at	1887.7	P	weak similarity to L.mexicana secreted acid phosphatase 2
8138_at	96.6	A	similar to FRE2
8139_at	954.0	P	strong similarity to hypothetical protein YMR316w

8140_at	99.6	A	photolyase
8141_at	4.4	A	strong similarity to YGL258w
8142_s_at	-73.8	A	Protein with similarity to formate dehydrogenases
8143_at	484.1	A	strong similarity to putative pseudogenes YPL277c and YPL278c
8144_g_at	243.1	A	strong similarity to putative pseudogenes YPL277c and YPL278c
8145_s_at	265.8	A	nearly identical to YPL279c
8146_at	-101.4	A	hypothetical protein
8147_s_at	-83.9	A	strong similarity to members of the Srp1p/Tip1p family
8148_at	1.3	A	hypothetical protein identified by SAGE
8149_at	316.2	A	identified by SAGE
8150_s_at	637.9	A	Sorting nexin I homologue
8151_s_at	1101.2	P	Thymidylate synthase
8152_f_at	345.3	A	Thymidylate synthase
8153_at	657.5	A	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	-193.6	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	-15.6	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	-144.1	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	194.9	A	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	2158.7	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	136.2	A	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	180.5	A	non-annotated SAGE orf Found reverse in NC_001147 between 882274 and 882417 with 100% identity. See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251
8112_at	203.0	A	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	28.6	A	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 -191.8 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 735.9 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 1714.2 P
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 52.6 A
non-annotated SAGE orf Found forward in NC_001147 between 703721 and 703864 with 100% identity.
See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251

8118_i_at 203.2 A
non-annotated SAGE orf Found reverse in NC_001147 between 703986 and 704222 with 100% identity.
See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251

8119_f_at 668.0 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

8120_at 817.1 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 298.7 A
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 129.7 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 26.3 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 1281.8 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 337.4 A
non-annotated SAGE orf Found forward in NC_001147 between 254904 and 255071 with 100% identity.
See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251

8126_at 702.3 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 -42.6 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 -0.8 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 507.0 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 127.4 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 81.0 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 3619.9 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 151.6 A

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

8134_at -82.0 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 97.1 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 1263.2 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 5045.1 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 -132.1 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 1400.3 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 220.5 A

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 196.1 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 2428.1 P

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

8093_r_at 1031.4 A

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 762.0 M

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 79.6 A

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

8096_at 227.3 A

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 674.2 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 44.9 A

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

8099_at -7.0 A

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

8100_at -222.3 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 -116.9 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 548.3 A
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 92.3 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 291.2 M
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 98.1 A
non-annotated SAGE orf Found forward in NC_001147 between 226577 and 226801 with 100% identity.
See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251
8106_at 701.7 A
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 75.8 A
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 -136.5 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 203.8 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 84.6 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 39.6 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 311.1 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 81.2 A
non-annotated SAGE orf Found reverse in NC_001147 between 836569 and 836709 with 100% identity.
See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251
8065_at 46.1 A
non-annotated SAGE orf Found reverse in NC_001147 between 854174 and 854314 with 100% identity.
See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251
8066_at 119.5 A
non-annotated SAGE orf Found reverse in NC_001147 between 969027 and 969179 with 100% identity.
See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251
8067_i_at 9039.0 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 221.0 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 91.4 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 105.7 A
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 -44.5 A
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 -113.3 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
8073_f_at -416.5 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 560.0 A
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 1472.6 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 38.9 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 -195.4 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 -52.0 A
non-annotated SAGE orf Found reverse in NC_001147 between 16760 and 16939 with 100% identity. See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251
8079_s_at 433.3 A
non-annotated SAGE orf Found forward in NC_001147 between 27083 and 27217 with 100% identity. See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251
8080_at 732.1 A
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 -156.9 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 185.5 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 122.0 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 -246.1 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 756.7 A
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 -157.7 A
non-annotated SAGE orf Found forward in NC_001147 between 193557 and 193784 with 100% identity. See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251

8087_at 224.0 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 353.9 A
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 384.5 A
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 1448.1 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 130.4 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 130.7 A
non-annotated SAGE orf Found forward in NC_001147 between 692115 and 692309 with 100% identity. See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251
8044_at 1160.5 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 112.6 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 -27.4 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 312.5 A
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 1482.7 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 106.3 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 -34.4 A
non-annotated SAGE orf Found forward in NC_001147 between 1071000 and 1071164 with 100% identity. See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251
8051_i_at 116.8 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 249.0 A
non-annotated SAGE orf Found reverse in NC_001147 between 1074040 and 1074183 with 100% identity. See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251
8053_at -17.1 A
snRNA
8054_at 659.5 A
snRNA
8055_i_at 105.3 A
Centromere

8056_at	1320.3	P
snRNA		
8057_i_at	-7.2	A
snRNA		
8058_r_at	10.8	A
snRNA		
8059_at	168.1	A
snRNA		
8060_at	864.0	P
snRNA		
8061_at	1526.0	P
snRNA		
8062_at	1540.2	P
snRNA		
8016_at	408.5	A
snRNA		
8017_at	1815.1	A
snRNA		
8018_i_at	-358.6	A
strong similarity to hypothetical protein YOR389w/putative pseudogene		
8019_s_at	86.7	A
strong similarity to hypothetical protein YOR389w/putative pseudogene		
8020_s_at	194.3	A
putative formate dehydrogenase/putative pseudogene		
8021_at	218.2	A
strong similarity to amino-acid transport proteins		
8022_at	1759.8	P
weak similarity to M.leprae metH2 protein, and strong similarity to hypothetical protein YLL062c		
8023_at	165.8	A
hypothetical protein		
8024_at	4458.0	P
nuclear gene for ATP synthase epsilon subunit		
8025_at	1336.4	P
ATP-binding cassette (ABC) transporter family member		
8026_at	324.0	A
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	685.5	P
phosphoinositide-specific phospholipase C		
8028_at	432.0	A
weak similarity to C.elegans transcription factor unc-86		
8029_at	2557.6	P
dimethyladenosine transferase		
8030_at	2579.2	P
dicarboxylic amino acid permease		
8031_at	238.2	A
strong similarity to YMR253c		
8032_at	1397.6	P
similarity to Kel2p and Kel3p		
8033_at	8304.8	P
mitochondrial and cytoplasmic fumarase (fumarate hydralase)		
8034_at	108.5	A
questionable ORF		
8035_at	1976.1	P
hypothetical protein		
8036_at	404.2	P

medium subunit of the clathrin-associated protein complex
8037_at	576.9	P
similarity to B.subtilis transcriptional activator tenA, and strong similarity to hypothetical proteins YOL055c and YPR121w
8038_at	-191.0	A
weak similarity to YIL029c
7993_at	1858.2	P
G(sub)1 cyclin
7994_at	121.5	A
Involved in mitotic cell cycle and meiosis
7995_at	330.5	A
transcription factor, member of Ada\/Gcn5 protein complex
7996_at	366.0	A
Cik1p homolog
7997_at	2147.6	P
iron-sulfur protein homologous to human adrenodoxin
7998_at	-301.2	A
questionable ORF
7999_at	3630.2	P
weak similarity to YMR195w
8000_i_at	12977.9	P
Ribosomal protein L36B (L39) (YL39)
8001_at	270.8	A
similarity to mouse Tbc1 protein
8002_at	221.1	A
zinc-finger transcription factor of the Zn(2)-Cys(6) binuclear cluster domain type
8003_at	650.3	P
similarity to human HAN11 protein and petunia an11 protein
8004_at	1994.2	P
weak similarity to mouse proteinase activated receptor 2
8005_at	1308.0	P
weak similarity to human mutL protein homolog
8006_at	2270.8	P
weak similarity to human UDP-galactose transporter related isozyme 1
8007_at	1768.2	P
component of signal recognition particle
8008_at	256.9	A
Homolog of the mammalian IQGAP1 and 2 genes\; probable regulator of cellular morphogenesis, inducing actin-ring formation in association with cytokinesis
8009_at	760.5	A
involvement in microtubule function
8010_i_at	14051.5	P
heat shock protein
8011_at	2622.3	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	849.9	A
questionable ORF
8013_at	3694.3	P
beta subunit of translation initiation factor eIF-2
8014_at	224.8	A
similarity to Prk1p, and serine/threonine protein kinase homolog from A. thaliana
8015_at	3427.4	P
strong similarity to TATA-binding protein-interacting protein 49 from rat
7970_at	4965.1	P
17-kDa subunit C of vacuolar membrane H(+)-ATPase

7971_at 239.3 A
hypothetical protein
7972_at 2169.9 P
SSO1 and SSO2 encode syntaxin homologs\; act in late stages of secretion
7973_at 14294.4 P
alpha subunit of fatty acid synthase
7974_at 3.2 A
Up in StarVation
7975_at 22.9 A
weak similarity to YMR181c
7976_at 416.3 A
mRNA capping enzyme beta subunit (80 kDa), RNA 5 -triphosphatase
7977_at 1372.7 P
UDP-glucose:dolichyl-phosphate glucosyltransferase
7978_at 11444.6 P
similarity to translation elongation factor eEF3
7979_at 3967.3 P
hypothetical protein
7980_at 915.1 P
Protein involved in mitochondrial iron accumulation
7981_at 660.0 P
Induced by osmotic stress
7982_at 85.5 A
similarity to C.perfringens hypothetical protein
7983_at 2046.8 P
Bypass of PAM1
7984_s_at 65563.3 P
Ribosomal protein L1A, forms part of the 60S ribosomal subunit
7985_at 396.6 A
PHO85 cyclin
7986_at 7889.2 P
GTP binding protein
7987_at 1869.1 P
similarity to human hypothetical protein KIAA0187
7988_at 121.4 A
similarity to YGL133w
7989_at 651.5 P
Protein required for assembly of ubiquinol cytochrome-c reductase complex (cytochrome bc1 complex)
7990_at 410.3 A
TMP pyrophosphorylase, hydroxyethylthiazole kinase
7991_at 287.0 A
similarity to A.thaliana U2 snRNP protein A
7992_at 1880.0 P
intranuclear protein which exhibits a nucleotide-specific intron-dependent tRNA pseudouridine synthase activity
7947_at 1326.9 P
Nip7p is required for 60S ribosome subunit biogenesis
7948_at 2362.5 P
component of signal recognition particle
7949_at 223.4 A
Protein kinase
7950_at 968.8 A
similarity to YHL039w
7951_at 2532.3 P
similarity to hypthetical proteins from A. fulgidus, M. thermoautotrophicum and M. jannaschii
7952_at 1709.0 P

weak similarity to glycerophosphoryl diester phosphodiesterases
7953_at 271.9 A
questionable ORF
7954_at 2442.7 P
casein kinase I isoform
7955_at 847.6 P
cAMP-dependent protein kinase catalytic subunit
7956_at 372.2 A
similarity to cell size regulation protein Rcs1p
7957_at 43.1 A
hypothetical protein
7958_at -272.9 A
hypothetical protein
7959_at 3443.7 P
weak similarity to T.cruzi p284 protein
7960_i_at 712.6 P
Ribosomal protein L7B (L6B) (rp11) (YL8)
7961_f_at 4832.7 P
Ribosomal protein L7B (L6B) (rp11) (YL8)
7962_s_at 35547.8 P
Ribosomal protein L7B (L6B) (rp11) (YL8)
7963_at 1514.8 P
questionable ORF
7964_at 336.6 A
weak similarity to S.pombe hypothetical protein SPAC8C9
7965_at 1145.6 P
delta-like subunit of the yeast AP-3 adaptin component of the membrane-associated clathrin assembly complex
7966_at 246.5 A
DNA damage checkpoint gene
7967_at 675.3 P
weak similarity to human centromere protein E
7968_at 227.9 A
hypothetical protein
7969_at 11.6 A
strong similarity to YGL082w
7924_at 907.9 P
polyadenylated RNA-binding protein
7925_at 63.5 A
strong similarity to YGL084c
7926_at 627.2 A
similarity to Utr1p and YEL041w
7927_at 59710.3 P
mating factor alpha
7928_at 116.8 A
weak similarity to Xenopus protein xlgv7
7929_at 12.5 A
questionable ORF
7930_at 2070.1 P
weak similarity to Pub1p
7931_at 1247.4 P
ribosomal protein L36, mitochondrial
7932_at 1769.6 P
similarity to Taf90p
7933_at 247.6 A
questionable ORF

7934_at	323.5	A	weak similarity to YKR029c
7935_at	1044.5	A	weak similarity to human l-caldesmon I
7936_at	1332.3	P	protein phosphatase Q
7937_at	2035.7	P	Small subunit of nuclear cap-binding protein complex
7938_at	2220.2	P	putative DNA binding protein which shows similarity in homeobox domain to human proto-oncogene PBX1
7939_at	1181.3	A	similarity to chinese hamster transferrin receptor protein
7940_at	594.3	A	N-acetylglucosaminyl-phosphatidylinositol biosynthetic protein
7941_at	65.7	A	Nuclear import protein
7942_at	641.5	A	Mitochondrial ribosomal protein MRPL40 (YmL40)
7943_at	643.4	A	Putative farnesyl transferase required for heme A synthesis
7944_at	62.6	A	NAD(P)H dehydrogenase
7945_at	1877.9	P	similarity to C.elegans LIM homeobox protein
7946_at	715.0	A	INvolved in nuclear mRNA export, binds both poly(A)
7902_at	167.3	A	weak similarity to E.coli bfpB protein
7903_at	238.0	A	DNA polymerase
7904_at	-26.3	A	weak similarity to paramyosins
7905_at	-117.9	A	weak similarity to YHR207c
7906_at	-96.0	A	similarity to mismatch repair protein Mlh1p
7907_at	4445.7	P	Serine and threonine rich protein.
7908_at	134.5	A	hypothetical protein
7909_at	435.2	P	Involved in polarity establishment and bud emergence\; interacts with the Rho1p small GTP-binding protein
7910_at	8170.6	P	cytosolic leucyl tRNA synthetase
7911_at	276.0	A	weak similarity to YPR151c
7912_at	1389.1	P	weak similarity to human nucleolin
7913_at	756.8	P	weak similarity to S.pombe hypothetical protein SPAC2G11.15c
7914_at	1650.2	P	weak similarity to YDL010w
7915_at	549.7	P	kinesin-related protein

7916_at 10341.0 P
vacuolar proteinase A
7917_at 260.4 A
protein kinase, Mec1p and Tel1p regulate rad53p phosphorylation
7918_at 218.3 A
Resistant to Rapamycin Deletion 2
7919_at 1521.4 P
strong similarity to A.thaliana PRL1 and PRL2 proteins
7920_at 72.7 A
similarity to ser/thr protein kinases
7921_at 917.0 A
involved in autophagy
7922_at 253.3 A
Phosphopantetheine
7923_at 112.3 A
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 727.0 A
weak similarity to myosin heavy chain proteins
7880_at 2055.6 P
Homologous to human oxysterol-binding protein\; implicated in ergosterol biosynthesis and regulation of Golgi-derived transport vesicle biogenesis
7881_at 1367.7 A
encodes snRNA U3, SNR17A also encodes snRNA U3
7882_f_at 35155.5 P
Ribosomal protein L33A (L37A) (YL37) (rp47)
7883_at 2681.4 P
questionable ORF
7884_at 778.8 P
strong similarity to protein kinase Kin4p
7885_at 439.3 A
protein kinase
7886_at 341.6 A
Transcriptional modulator
7887_at 410.8 A
weak similarity to fruit fly polycomblike nuclear protein
7888_at 985.7 P
similarity to microtubule-interacting protein Mhp1p and to hypothetical protein YOR227w
7889_at -135.6 A
questionable ORF
7890_at 1934.1 P
NifU-like protein A
7891_at 375.8 A
similarity to ADP/ATP carrier proteins
7892_at 295.2 A
weak similarity to transcription factors
7893_at 292.9 A
Putative heme A biosynthetic enzyme involved in forming the formyl group at position 8 of the porphyrin ring
7894_at 131724.6 P
Ribosomal protein L5 (L1a)(YL3)
7895_at 206.9 A
hypothetical protein
7896_at 2054.8 P
TFIIF subunit (transcription initiation factor), 30 kD
7897_at 1134.7 P

TTAGGG repeat binding factor
7898_at 992.1 P
histone H1
7899_at 1443.1 P
weak similarity to fruit fly TFIID subunit p85
7900_at 750.0 P
weak similarity to YDR395w and cellular apoptosis susceptibility protein
7901_at 224.6 A
Nuclear import protein
7857_at 151.2 A
similarity to ribonucleases
7858_at 465.9 P
TFIIH subunit Tfb2\; has homology to CAK and human IIH subunits
7859_at 260.3 A
Meiotic protein required for synapsis and meiotic recombination
7860_at 845.9 P
Required for sorting and delivery of soluble hydrolases to the vacuole.
7861_at 321.6 A
putative ATP-dependent RNA helicase\; Dead box protein
7862_at 1944.9 P
Component of small subunit of the mitochondrial ribosome
7863_at 2616.5 P
Isopentenyl diphosphate:dimethylallyl diphosphate isomerase (IPP isomerase)
7864_at 543.2 A
Protein with similarity to Hda1p, Rpd3p, Hos2p, and Hos1p
7865_at 1716.4 P
has GTPase-activating protein activity toward the essential bud-site assembly GTPase Cdc42
7866_at 76.1 A
questionable ORF
7867_at -14.6 A
similarity to glycerate dehydrogenases
7868_at 1000.3 A
weak similarity to YOR193w
7869_at 2499.9 P
arginase
7870_at 2803.9 P
similarity to C.elegans hypothetical protein, weak similarity to Pho81p
7871_at 93.9 A
similarity to aminoglycoside acetyltransferase regulator from P. stuartii
7872_at 454.7 A
hypothetical protein
7873_at 372.6 A
hypothetical protein
7874_at 29841.8 P
HSP70 family member, highly homologous to Ssa1p and Sse2p
7875_at 865.4 P
similarity to Smy2p
7876_at 764.1 P
Aspartyl-tRNA synthetase, mitochondrial
7877_at 530.1 A
similarity to hypothetical M. tuberculosis protein
7878_at 494.9 A
questionable ORF
7834_at 2124.1 P
hypothetical protein
7835_at 883.6 P

similarity to YFR021w
7836_at 204.1 A
weak similarity to Sulfolobus hypothetical protein
7837_at 3389.1 P
similarity to S.pombe hypothetical protein
7838_at 470.3 A
Tyrosyl-tRNA synthetase
7839_at 1037.4 P
hypothetical protein
7840_at 534.9 A
strong similarity to YBR177c
7841_at 6487.3 P
membrane component of ER protein translocation apparatus
7842_at 3527.0 P
similarity to M.jannaschii GTP-binding protein, GTP1/OBG-family, weak similarity to other GTP-binding proteins
7843_at 276.2 A
sensitive to sulfite
7844_at 5364.2 P
Glutathione oxidoreductase
7845_s_at 51700.5 P
Ribosomal protein S6A (S10A) (rp9) (YS4)
7846_at 2272.4 P
serum response factor-like protein
7847_at 1318.8 P
similarity to aryl-alcohol dehydrogenases
7848_at 2298.5 P
strong similarity to YBR183w
7849_at 1541.7 P
Histone and other Protein Acetyltransferase\; Has sequence homology to known HATs and NATs
7850_at 1174.7 P
multidomain vesicle coat protein that interacts with Sec23p
7851_at 699.5 A
BCK1-like resistance to osmotic shock
7852_at 302.4 A
54kDa subunit of the tetrameric tRNA splicing endonuclease
7853_at 904.4 P
putative helicase
7854_i_at 2930.3 P
Ribosomal protein S9A (S13) (rp21) (YS11)
7855_f_at 9295.3 P
Ribosomal protein S9A (S13) (rp21) (YS11)
7856_at 111.7 A
hypothetical protein
7811_at 52318.0 P
Ribosomal protein L21B
7812_at 1938.9 P
F(1)F(0)-ATPase complex delta subunit, mitochondrial
7813_at -457.2 A
weak similarity to YBR197c
7814_at 282.6 A
Required for synthesis of N-acetylglucoaminylphosphatidylinositol, the first intermediate in synthesis of glycosylphosphatidylinositol (GPI) anchors
7815_at 729.3 A
similarity to Vps4p and YER047c
7816_at 67.2 A

questionable ORF
7817_at	-54.0	A
encodes putative deubiquitinating enzyme
7818_at	303.8	A
hypothetical protein
7819_at	1231.4	P
weak similarity to Vps9p
7820_at	173.5	A
geranylgeranyl diphosphate synthase
7821_at	472.0	P
hypothetical protein
7822_at	1617.5	P
hypothetical protein
7823_at	1247.1	P
hypothetical protein
7824_at	167.3	A
soluble, hydrophilic protein involved in transport of precursors for soluble vauolar hydrolases from the late endosome to the vacuole
7825_at	253.9	A
weak similarity to S.pombe peptidyl-prolyl cis-trans isomerase
7826_at	2411.0	P
similarity to hypothetical protein YLR019w, YLL010c and S.pombe hypothetical protein SPAC2F7.02c
7827_at	57.2	A
hypothetical protein
7828_at	17105.2	P
cytosolic aldehyde dehydrogenase
7829_at	337.9	A
strong similarity to Mrs2p
7830_at	1935.7	P
similarity to glutaredoxins
7831_at	1099.7	P
multidrug resistance transporter
7832_at	854.2	P
Multicopy suppressor of cls2-2\; also suppresses rvs161 mutations
7833_at	564.6	P
hypothetical protein
7788_at	623.5	P
hypothetical protein
7789_at	92.4	A
protein of unknown function
7790_at	3218.7	P
mannosylphosphate transferase
7791_at	477.1	P
hypothetical protein
7792_at	10.7	A
strong similarity to ADP-ribosylation factors
7793_at	1468.2	P
Protein required for complex glycosylation
7794_at	1748.9	P
MAP kinase-associated protein
7795_at	6303.5	P
Calcium and phospholipid binding protein homologous to translation elongation factor 1-gamma (EF-1gamma)
7796_at	212.4	A
hypothetical protein
7797_at	439.7	A

Elongin C transcription elongation factor
7798_at 726.5 P
Vacuolar sorting protein
7799_at 333.1 A
questionable ORF
7800_at 2151.6 P
RNA recognition motif-containing protein
7801_at 190.1 A a
cyclin(SSN8)-dependent serine\/threonine protein kinase
7802_at 238.9 A
hypothetical protein
7803_at 836.7 P
nuclear encoded mitochondrial isoleucyl-tRNA synthetase
7804_at 365.5 A
hypothetical protein
7805_at 928.5 P
zinc finger DNA binding factor, transcriptional regulator of sulfur amino acid metabolism, highly homologous to Met32p
7806_at 19566.3 P
GAL4 enhancer protein, has similarity to human transcription factor BTF3
7807_at 1003.8 A
plasma membrane ATPase
7808_at 87.1 A
questionable ORF
7809_at 197.9 A
questionable ORF
7810_at -67.3 A
weak similarity to YLR426w
7766_at 2921.9 P
styryl dye vacuolar localization
7767_at 1653.3 P
negative transcriptional regulator, protein kinase homolog
7768_at 637.3 P
similarity to C.elegans hypothetical protein
7769_at 478.1 P
putative ATP-dependent helicase
7770_at 16218.9 P
acetoacetyl CoA thiolase
7771_at -63.9 A
hypothetical protein
7772_at 481.0 P
serine\/threonine protein kinase homologous to Ran1p
7773_at 216.4 A
questionable ORF
7774_at 283.2 A
(N)egative regulator of (C)ts1 (E)xpression
7775_at 1881.2 P
putative methylenetetrahydrofolate reductase (mthfr)
7776_at 215.7 A
UV endonuclease
7777_at -58.5 A
ExtraCellular Mutant\; similar to SRD1
7778_at 1854.0 P
weak similarity to Smt4p
7779_at 15712.3 P
strong similarity to YFL004w, similarity to YJL012c

7780_at	3.4	A	Important for chromosome segregation
7781_at	24.4	A	strong similarity to Lpd1p and other dihydrolipoamide dehydrogenases
7782_at	-3.8	A	Zinc-finger transcription factor
7783_at	581.1	A	Homolog of SIR2
7784_at	707.0	A	hypothetical protein
7785_at	2210.5	P	ribosomal protein S16, mitochondrial
7786_at	4999.3	P	hypothetical protein
7787_at	611.7	A	Component of the TAF(II) complex (TBP-associated protein complex)
7743_at	2347.5	P	coatomer complex zeta chain
7744_at	1545.3	A	similarity to M.jannaschii hypothetical protein
7745_at	306.0	A	kinetochore protein in the DEAH box family
7746_at	288.8	A	hypothetical protein
7747_at	2184.5	P	predicted transmembrane protein
7748_at	564.6	A	weak similarity to Nup2p
7749_at	5768.4	P	strong similarity to YGR086c
7750_at	448.6	M	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	584.3	P	appears to be functionally related to SNF7
7752_at	545.3	P	histone acetyltransferase
7753_at	-32.6	A	Mitochondrial isoform of citrate synthase
7754_at	499.2	A	similarity to B.subtilis mmgE protein
7755_at	-82.0	A	similarity to sulphate transporter proteins
7756_at	1977.3	P	strong similarity to electron transfer flavoproteins alpha chain
7757_at	403.5	A	polar 32k Da cytoplasmic protein
7758_at	802.3	P	Isocitrate lyase, may be nonfunctional
7759_at	97.2	A	hypothetical protein
7760_at	567.1	P	similarity to transcription factor
7761_at	625.1	P	similarity to sterol uptake protein Sut1p

7762_at 11531.1 P
RNA polymerase I subunit A135
7763_at 829.2 P
similarity to ADP/ATP carrier proteins and Graves disease carrier protein
7764_at 56.4 A
hypothetical protein
7765_at 467.8 A
similarity to transcription factors
7721_at 81.9 A
hypothetical protein
7722_at 167.9 A
similarity to transcription factors
7723_at 2778.9 P
similar to human translation initiation factor 6 (eIF6)
7724_at 413.7 A
GDP dissociation factor for Sec4p
7725_at 385.7 A
p90 subunit of yeast omatin Assembly Factor-I (CAF-I)
7726_at 1809.7 P
essential for initiation of DNA replication\; homolog of S. pombe CDC21
7727_at 564.3 A
hypothetical protein
7728_at 977.5 A
similarity to human citrate transporter protein
7729_at 819.6 P
weak similarity to fruit fly dorsal protein and Snf5p
7730_at 3670.1 P
similarity to human hypothetical protein
7731_at 731.6 P
Mitochondrial protein of the CDC48\/PAS1\/SEC18 family of ATPases
7732_at 218.7 A
novel cyclin gene\; encodes subunits of TFIIK, a subcomplex of transcription factor TFIIH
7733_at 505.9 A
null mutant is viable\; increased tolerance to dehydration, freezing, and toxic levels of ethanol
7734_at -76.3 A
similarity to YNL019c and YNL033w
7735_at 4284.0 P
Ypt Interacting Protein
7736_at 8726.4 P
Ypt Interacting Protein
7737_at 2166.8 P
Gamma-adaptin, large subunit of the clathrin-associated protein (AP) complex
7738_at 345.4 A
similarity to YBL101c
7739_at 255.2 A
similarity to human zinc-finger protein BR140
7740_at 612.0 A
yeast homolog of the Drosphila tumor suppressor, lethal giant larvae
7741_at 17955.3 P
cytoplasmic and mitochondrial histidine tRNA synthetases
7742_at 1399.4 P
Actin-related protein
7698_at 24527.9 P
glutamine synthetase
7699_at 10468.4 P
54-kDa vacuolar H(+) ATPase subunit of V1 sector

7700_at	1231.8	P	similarity to Erv1p and rat ALR protein
7701_at	84.1	A	questionable ORF
7702_g_at	509.0	P	questionable ORF
7703_at	491.1	P	questionable ORF
7704_at	871.7	P	similarity to C.elegans C02C2.6 protein
7705_at	1689.0	P	Translation initiation factor eIF-5
7706_at	653.0	A	similarity to Jsn1p
7707_i_at	19602.9	P	Ribosomal protein L43A
7708_f_at	90066.2	P	Ribosomal protein L43A
7709_at	8639.1	P	questionable ORF
7710_at	56.9	A	similarity to C.elegans hypothetical protein
7711_at	336.8	A	Required for chromosome segregation
7712_at	128.1	A	alpha subunit of yeast mitochondrial phenylalanyl-tRNA synthetase
7713_at	505.0	A	similarity to M.domestica NADPH--ferrihemoprotein reductase and mammalian nitric-oxide synthases
7714_at	529.6	A	similarity to Uso1p
7715_at	502.2	A	questionable ORF
7716_at	1463.8	P	N-acetyltransferase
7717_at	2176.9	P	11-kDa nonhistone chromosomal protein
7718_g_at	9177.5	P	11-kDa nonhistone chromosomal protein
7719_at	553.1	A	questionable ORF
7720_at	48.4	A	MAP kinase
7675_at	341.6	A	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	391.6	A	Component of RNA polymerase transcription initiation TFIIH (factor b), 37 kDa subunit
7677_at	923.7	P	Protein involved in snRNP biogenesis
7678_at	2425.9	P	putative mitochondrial carrier protein
7679_at	309.7	A	questionable ORF
7680_at	1811.6	P	chorismate mutase
7681_at	83.1	A	

weak similarity to Synechococcus sp. DnaJ protein
7682_at 7146.8 P
cytosine deaminase
7683_at 4332.3 P
hypothetical protein
7684_at 549.2 A
hypothetical protein
7685_at 991.7 P
site-specific DNA binding protein, repressor
7686_at 175.8 A
ubiquitin-like protein activating enzyme
7687_at 900.1 A
weak similarity to F.alni nitrogen fixation protein
7688_at 133.9 A
Protein with similarity to Hda1p, Rpd3p, Hos2p, and Hos3p
7689_at 2957.7 P
putrescine aminopropyltransferase (spermidine synthase)
7690_at 190.8 A
hypothetical protein
7691_at 290.6 A
strong similarity to YIL029c
7692_at 1413.5 P
member of the NOT complex, a global negative regulator of transcription
7693_at 526.8 P
18-kDa phosphotyrosine phosphatase of unknown function
7694_at 32983.2 P
Transketolase 1
7695_at 1206.7 P
imparts Far- phenotype
7696_at -113.8 A
questionable ORF
7697_i_at 135.1 A
questionable ORF
7653_s_at 49.4 A
questionable ORF
7654_at 46.2 A
hypothetical protein
7655_at 609.8 A
weak similarity to human insulin-like growth factor 2 receptor
7656_s_at 226852.9 P
translational elongation factor EF-1 alpha
7657_at 787.8 P
strong similarity to glycyl-tRNA synthetases
7658_at 1257.6 P
S. pombe dim1+ in budding yeast
7659_at 194.7 A
hypothetical protein
7660_at 336.6 A
hypothetical protein
7661_at 497.9 A
hypothetical protein
7662_at 1267.8 P
transcription factor TFIIB homolog
7663_at 1046.8 P
questionable ORF
7664_at 4865.0 P

Signal recognition particle subunit (homolog of mammalian SRP54)
7665_at 33.7 A
questionable ORF
7666_at 3263.0 P
hypothetical protein
7667_at 1020.6 P
weak similarity to C.elegans LIM homeobox protein
7668_at 73.8 A
questionable ORF
7669_at 282.2 A
weak similarity to zinc-finger proteins
7670_at 575.2 P
weak similarity to chicken lim-3 protein
7671_at 480.4 A
Suppressor of Ypt3
7672_at -167.0 A
hypothetical protein
7673_at 2691.1 P
hypothetical protein
7674_at 2895.4 P
hypothetical protein
7629_at 237.7 A
questionable ORF
7630_at 880.9 P
weak similarity to C.elegans hypothetical protein CEC25A1
7631_at -110.3 A
splicing factor
7632_i_at 53892.0 P
Ribosomal protein L11A (L16A) (rp39A) (YL22)
7633_s_at 48550.0 P
Ribosomal protein L11A (L16A) (rp39A) (YL22)
7634_at 8909.4 P
proteasome subunit
7635_at 321.2 A
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 1332.0 P
hypothetical protein
7637_at 827.8 A
protein kinase
7638_at 190.7 A
Yeast 30kDa Homologue
7639_at 6305.9 P
Subunit of the regulatory particle of the proteasome
7640_at 394.9 P
weak similarity to human nicotinic acetylcholine receptor delta chain
7641_at 2849.1 P
RNA polymerase III (C) subunit
7642_at 130.9 A
kinase required for late nuclear division
7643_at 383.6 A
kinase required for late nuclear division
7644_at 952.9 P
similarity to RNA-binding proteins
7645_at 5515.6 P

phosphatidylinositol synthase
7646_at 4745.7 P
similarity to YJR116w
7647_at 896.6 P
similarity to probable transcription factor Ask10p, and to YNL047c and YIL105c
7648_at -116.5 A
hypothetical protein
7649_at 201.2 A
similarity to YLR454w
7650_at 818.9 P
similarity to M.jannaschii translation initiation factor, eIF-2B
7651_at 404.6 A
G(sub)2-specific B-type cyclin
7652_at 702.5 P
B-type cyclin
7607_at 802.3 A
similarity to B.subtilis transcriptional activator tenA, strong similarity to hypothetical proteins YPL258c and YOL055c
7608_at 648.6 A
putative homolog of human insulin-degrading endoprotease
7609_at -170.7 A
questionable ORF
7610_at 1768.1 P
High affinity copper transporter into the cell, probable integral membrane protein
7611_at 2764.7 P
suppressor of mrs2-1 mutation
7612_at 966.2 A
questionable ORF
7613_at 946.7 P
similarity to C-term. of N.tabacum auxin-induced protein
7614_at 2042.3 P
similarity to carrier protein FLX1
7615_at 2229.6 P
multicopy suppressor of clathrin deficiency
7616_at 472.2 P
questionable ORF
7617_at 460.1 P
similarity to N-acetyltransferases
7618_f_at 22854.3 P
Ribosomal protein S23B (S28B) (rp37) (YS14)
7619_s_at 130324.0 P
Ribosomal protein S23B (S28B) (rp37) (YS14)
7620_at 1112.1 P
similarity to C.elegans hypothetical protein
7621_at 2736.8 P
Translocase of the Outer Mitochondrial membrane
7622_at 116.7 A
Protein involved in splicing intron a15beta of COX1
7623_at 2147.8 P
DNA polymerase alpha binding protein
7624_at 91.2 A
questionable ORF
7625_at 2970.7 P
weak similarity to Taf90p
7626_at 903.0 P
NH4+ transporter, highly similar to Mep1p and Mep2p

7627_at 1230.0 P
hypothetical protein
7628_at 970.2 P
similarity to human BTHS gene involved in Barth syndrome
7584_at 703.5 P
kinesin-like nuclear fusion protein
7585_at 97.1 A
questionable ORF
7586_at 615.6 P
hypothetical protein
7587_at 450.6 A
similarity to YDR060w and C.elegans hypothetical protein
7588_at 9180.4 P
asparagine synthetase
7589_at 514.9 A
questionable ORF
7590_at 1140.4 P
hypothetical protein
7591_at 1960.5 P
hypothetical protein
7592_at 2631.9 P
involved in secretion of proteins that lack classical secretory signal sequences
7593_at -69.8 A
questionable ORF
7594_at 209.4 A
weak similarity to YPL159c
7595_at 237.0 A
hypothetical protein
7596_at 271.2 A
hypothetical protein
7597_at 2054.3 P
similarity to chicken growth factor receptor-binding protein GRB2 homolog
7598_at 242.2 A
Regulates proper expression of subunits 6 (Atp6p) and 8 (Atp8p) of the Fo-F1 ATP synthase
7599_i_at -138.8 A
similarity to multidrug resistance proteins
7600_s_at 9398.8 P
similarity to multidrug resistance proteins
7601_at 372.0 A
strong similarity to YGR141w
7602_at 622.2 P
similarity to YGR142w
7603_at 4023.8 P
potential beta-glucan synthase
7604_at 106.1 A
Glycogen phosphorylase
7605_at 771.1 P
CDC28\/cdc2 related protein kinase
7606_at 452.9 A
56-kDa subunit of origin recognition complex (ORC)
7561_at 7024.6 P
Translation initiation factor eIF-4B
7562_at 409.1 P
killed in mutagen, sensitive to diepoxybutane and\/or mitomycin C
7563_at 5443.9 P
GTP-binding protein of the rho subfamily of ras-like proteins

7564_at 1740.9 P
14 kDa mitochondrial ribosomal protein\; homologous to E. coli S14 protein
7565_at 121.4 A 3
phosphoadenylylsulfate reductase
7566_at 34.0 A
negative regulator of URS2 of the HO promoter
7567_at 2716.8 P
hypothetical protein
7568_at 74.5 A
hypothetical protein
7569_at 278.6 A
hypothetical protein
7570_at 155.8 A
strong similarity to YLR456w
7571_at 2532.2 P
defective in vacuolar protein sorting
7572_at 190.5 A
weak similarity to Nbp1p
7573_at 467.1 A
DNA polymerase epsilon, subunit B
7574_at 781.5 P
Geranylgeranyltransferase Type II beta subunit
7575_at -64.2 A
questionable ORF
7576_at 276.8 A
associated with the U4\/U6 snRNP
7577_at 225.8 A
hypothetical protein
7578_at 1088.3 P
Along with Uba2p forms a heterodimeric activating enzyme for Smt3p
7579_at 2268.1 P
cytoplasmic GTPase-activating protein
7580_at 1934.5 P
Sm or Sm-like snRNP protein
7581_at 4412.0 P
dolichol phosphate mannose synthase
7582_at 709.7 A
similarity to human 4-alpha-glucanotransferase (EC 2.4.1.25)/amylo-1,6-glucosidase (EC 3.2.1.33)
7583_at 834.0 P
Autophagy
7538_at 237.2 A
Transcription factor IIIA (TFIIIA) with putative Zn-fingers
7539_at 3479.4 P
subunit common to RNA polymerases I, II, and III
7540_at 529.6 P
similarity to calmodulin and calmodulin-related proteins
7541_at 315.6 P
Contains 8 copies of the TPR domain
7542_at 1408.8 P
82-kDa subunit of RNA polymerase III (C)
7543_at 4779.4 P
40 kDa ubiquinol cytochrome-c reductase core protein 2
7544_at 425.4 P
similarity to plasma membrane and water channel proteins
7545_at 321.3 A
Histone and other Protein Acetyltransferase\; Has sequence homology to known HATs and NATs

7546_at	53.2	A	similarity to S.pombe isp4 protein
7547_at	171.9	A	hypothetical protein
7548_at	225.2	A	strong similarity to regulatory protein Mal63p
7549_g_at	786.4	P	strong similarity to regulatory protein Mal63p
7550_at	-46.9	A	questionable ORF
7551_at	1520.1	P	multi-copy suppressor of gal11 null\; member of drug-resistance protein family
7552_at	770.9	P	Similar to transcriptional regulatory elements YAP1 and cad1
7553_at	-248.1	A	Required for arsenate but not for arsenite resistance
7554_at	-100.9	A	involved in arsenite transport
7555_s_at	1976.2	P	trans-acting positive regulator of the enolase and glyceraldehyde-3-phosphate dehydrogenase gene families
7556_at	476.7	A	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	3686.1	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	-237.5	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	1446.0	A	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	234.0	A	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	1259.1	A	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	1237.7	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	367.4	A	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	-191.0	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	280.1	A	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	567.0	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	43.2	A	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 179.1 A
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 3716.5 P
non-annotated SAGE orf Found reverse in NC_001148 between 592171 and 592326 with 100% identity.
See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251
7521_at 4235.0 P
non-annotated SAGE orf Found reverse in NC_001148 between 624294 and 624434 with 100% identity.
See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251
7522_at -13.7 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 42.1 A
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 966.3 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 705.9 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 517.9 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 138.2 A
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 -862.7 A
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 65.8 A
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 -25.8 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 5049.6 P
non-annotated SAGE orf Found forward in NC_001148 between 883373 and 883558 with 100% identity.
See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251
7532_at 3289.1 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 2798.5 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 -358.6 A
non-annotated SAGE orf Found reverse in NC_001148 between 700274 and 700456 with 100% identity.
See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251
7535_f_at -161.5 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 73.5 A
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 585.6 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 165.0 A
non-annotated SAGE orf Found forward in NC_001148 between 860478 and 860687 with 100% identity.
See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251
7490_at 172.7 A
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 2.5 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 215.5 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 3297.0 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 -158.9 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 120.9 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 365.5 A
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 99.2 A
non-annotated SAGE orf Found reverse in NC_001148 between 588920 and 589057 with 100% identity.
See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251
7498_at -70.5 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 491.1 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 -61.2 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 -6.7 A
non-annotated SAGE orf Found forward in NC_001148 between 775843 and 775980 with 100% identity.
See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251
7502_at 171.1 A
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 209.1 A
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 209.2 A
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 274.9 A
non-annotated SAGE orf Found reverse in NC_001148 between 921211 and 921453 with 100% identity.
See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251
7506_at 289.5 A
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 -348.0 A

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 78.0 A

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 427.3 A

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 672.1 M

non-annotated SAGE orf Found forward in NC_001148 between 427735 and 427896 with 100% identity. See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251

7511_at 221.2 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 -30.9 A

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 -306.9 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 84.4 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 -5.2 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 6327.4 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 51.2 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 569.1 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 132.5 A

snRNA

7474_at 753.6 P

snRNA

7475_at 1616.8 P

snRNA

7476_at 918.5 P

snRNA

7477_at 673.7 P

snRNA

7478_s_at 614.8 P

similarity to subtelomeric encoded proteins

7479_at 798.3 A

hypothetical protein

7480_at 303.1 A

yeast homolog of the Drosphila tumor suppressor, lethal giant larvae

7481_at 1218.7 P

putative protein kinase

7482_at 984.7 M

hypothetical protein

7483_at 215.9 A
Probable cytochrome c subunit, copper binding
7484_at 2628.9 P
suppressor of sed5 ts mutants
7485_at 1776.2 P
ExtraCellular Mutant
7486_at 36.8 A
questionable ORF
7487_at 13890.3 P
mitochondrial F1F0-ATPase alpha subunit
7488_at 1112.3 A
similarity to human and D.melanogaster kynurenine 3-monooxygenase
7443_at 170.0 A
BARREN, a gene with sequence similarity to Drosophila barren and Xenopus XCAP-H, and a functional homolog of human BRRN1
7444_at 1271.5 P
questionable ORF
7445_at 612.0 P
similarity to C.albicans hypothetical protein
7446_at 314.5 A
questionable ORF
7447_at 429.4 A
RNA polymerase II holoenzyme\/mediator subunit
7448_at 50793.8 P
Ribosomal protein L32
7449_at 702.1 A
weak similarity to SCS2
7450_at 6517.9 P
methionine aminopeptidase 2
7451_at 360.5 A
Component of the small subunit of mitochondrial ribosomes
7452_at 654.4 P
weak similarity to A.thaliana aminoacid permease AAP3
7453_at 339.8 A
putative phosphatidylinositol kinase
7454_s_at 102547.6 P
Ribosomal protein L23A (L17aA) (YL32)
7455_at 580.1 P
involved in sugar metabolism
7456_at 944.6 P
BEM1-binding protein
7457_at 1223.9 P
component of the anaphase-promoting complex
7458_i_at 35.4 A
questionable ORF
7459_s_at 1440.0 P
questionable ORF
7460_at 735.9 P
putative Dol-P-Man dependent alpha(1-3) mannosyltransferase involved in the biosynthesis of the lipid-linked oligosaccharide
7461_at 1006.7 P
hypothetical protein
7462_at 77.8 A
62-kDa protein
7463_at 1107.0 P
Nucleoporin highly similar to Nup157p and to mammalian Nup155p (nup170 mutant can be

complemented with NUP155)

7464_at 901.3 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 1699.9 P

questionable ORF

7421_at 10318.8 P

cytoplasmic isoleucyl-tRNA synthetase

7422_at 446.9 A

heat-inducible cytosolic member of the 70 kDa heat shock protein family

7423_at 2.9 A

splices pre mRNA of the MATa1 cistron

7424_at -206.4 A

questionable ORF

7425_s_at 71442.4 P

Ribosomal protein S8A (S14A) (rp19) (YS9)

7426_at 472.5 P

hypothetical protein

7427_at -54.3 A

questionable ORF

7428_at 2024.0 P

ribose-phosphate pyrophosphokinase 4

7429_at 644.0 P

ubiquitin carboxyl-terminal hydrolase

7430_at 26.6 A

putative transcription factor

7431_at 188.2 A

questionable ORF

7432_at 545.1 A

Homolog to thiol-specific antioxidant

7433_at 3.7 A

kinesin related protein

7434_at 566.2 P

questionable ORF

7435_at 1803.7 P

protoplast regeneration and killer toxin resistance gene, may be a post-translational regulator of chitin synthase III activity, interacts with Chs3p

7436_at 404.3 A

hypothetical protein

7437_at 116.3 A

weak similarity to hypothetical protein YER093c-a

7438_at 222.8 A

weak similarity to hypothetical protein YER093c-a

7439_at 5827.1 P

isolated as a suppressor of the lethality caused by overexpression of the phosphoprotein phosphatase 1 catalytic subuniut encoded by GLC7

7440_at 722.8 A

strong similarity to hypothetical S.pombe protein

7441_at 972.4 P

protein phosphatase type 2C

7442_at 1102.4 P

similarity to hypothetical S.pombe protein

7398_at 1393.1 P

Homolog to myb transforming proteins

7399_at 549.5 A
questionable ORF
7400_at 818.6 P
SAS3 for Something about silencing, gene 3. Influences silencing at HMR.
7401_at 4148.9 P
similarity to S.pombe Z66568_C protein
7402_at 3724.0 P
peripheral membrane protein required for vesicular transport between ER and Golgi
7403_at 242.6 A
hypothetical protein
7404_at 384.1 A
hypothetical protein
7405_at 3563.9 P
USO1 homolog (S. cerevisiae), cytoskeletal-related transport protein, Ca++ binding
7406_at 1110.4 P
weak similarity to hypothetical protein YOR054c
7407_at 2781.3 P
44 kDa core protein of yeast coenzyme QH2 cytochrome c reductase
7408_at -104.8 A
hypothetical protein
7409_at 406.5 P
ExtraCellular Mutant
7410_at 5783.0 P
uridine permease
7411_at 6995.4 P
proteasome subunit
7412_at 1466.6 P
encodes the HDEL receptor required for retention of ER proteins
7413_at 9117.4 P
CTP synthase, highly homologus to URA8 CTP synthase
7414_at 797.8 P
Mitochondrial ribosomal protein MRPL16
7415_at 626.8 P
clathrin Associated Protein complex Large subunit
7416_at 1453.7 P
Homolog to twitching motility protein (P. aeroginosa)
7417_at 1506.4 P B
subunit of DNA polymerase alpha-primase complex
7418_at 1033.4 P
suppressor of cold-sensitive tub2 mutation\; shown to be a component of the mitotic spindle
7419_at 2087.9 P
GTP cyclohydrolase II
7420_at 2631.0 P
weak similarity to hnRNP complex protein homolog YBR233w
7374_at 173.4 A
hypothetical protein
7375_at 14752.8 P
mitochondrial ADP\ATP translocator
7376_at 270.4 A
hypothetical protein
7377_at 1734.6 P
involved in mating-type regulation
7378_s_at 51154.6 P
Ribosomal protein L19B (YL14) (L23B) (rpl5L)
7379_i_at -154.0 A
snRNA-associated protein of the Sm class

7380_f_at	221.5	A	snRNA-associated protein of the Sm class
7381_at	1225.4	P	snRNA-associated protein of the Sm class
7382_at	114.0	A	Upstream activation factor subunit
7383_at	4858.1	P	Probable proliferating-cell nucleolar antigen (human p120)
7384_at	2115.2	P	Minichromosome maintenance protein, transcription factor
7385_at	3367.0	P	mitochondrial ATP-dependent protease
7386_at	474.1	A	transcriptional activator protein of CYC1
7387_at	1887.9	P	67 kDa integral membrane protein
7388_at	336.9	P	AP endonuclease
7389_at	503.0	A	integral subunit of RNase P and apparent subunit of RNase MRP
7390_at	4810.9	P	carboxypeptidase Y sorting receptor in late Golgi\; Type I integral membrane protein 166aa cytoplasmic tail, 1300 aa lumenal domain
7391_at	2188.1	P	cdc2+\/CDC28 related kinase with positive role in conjugation
7392_at	797.9	P	acetyl CoA hydrolase
7393_at	456.6	A	member of yeast Pol I core factor (CF) also composed of Rrn11p, Rrn7p and TATA-binding protein
7394_at	177.2	A	Probable met-tRNA formyltransferase, mitochondrial
7395_at	154.1	A	questionable ORF
7396_at	1555.6	P	High copy suppresor of choline-transport mutants
7397_at	83.9	A	hypothetical protein
7352_at	1175.9	P	strong similarity to DNA damage responsive Alk1p
7353_at	253.3	A	putative repressor protein homologous to yeast Tup1p and mammalian retinal transducin\; contains nuclear targeting signal
7354_at	4479.1	P	contains 3 SH3 domains, interacts with Bee1p
7355_at	1630.3	P	hypothetical protein
7356_at	578.2	P	Pleiotropic drug resistance protein 3
7357_at	1985.2	P	weak similarity to Papaya ringspot virus polyprotein
7358_s_at	12740.0	P	Histone H2A (HTA1 and HTA2 code for nearly identical proteins)
7359_at	9948.8	P	Histone H2B (HTB1 and HTB2 code for nearly identical proteins)
7360_at	2676.5	P	ExtraCellular Mutant

7361_at	1684.2	P	Neutral trehalase, highly homologous to Nth1p
7362_at	1772.8	P	strong similarity to hypothetical protein YMR101c
7363_at	1545.8	P	hexaprenyl pyrophosphate synthetase
7364_at	945.9	P	similarity to S.pombe hypothetical protein SPAC18B11.05
7365_at	972.6	A	strong similarity to hypothetical protein YDR003w
7366_at	899.9	P	hypothetical protein
7367_at	950.9	A	Major Facilitator Transporter
7368_i_at	28347.0	P	Histone H3 (HHT1 and HHT2 code for identical proteins)
7369_s_at	6493.7	P	Histone H3 (HHT1 and HHT2 code for identical proteins)
7370_at	28081.5	P	Inorganic pyrophosphatase
7371_at	248.8	A	hypothetical protein
7372_at	102.3	A	hypothetical protein
7373_at	1659.0	P	Glutaredoxin homolog
7328_at	2275.5	P	Type II transmembrane protein
7329_at	11748.0	P	strong similarity to hypothetical proteins YDL012c and YDR210w
7330_at	1922.8	P	karyopherin beta 2, yeast transportin
7331_at	-113.6	A	galactose-1-phosphate uridyl transferase
7332_at	230.9	A	UDP-glucose 4-epimerase
7333_at	-54.4	A	galactokinase
7334_at	951.0	P	uracil permease
7335_at	198.8	A	hypothetical protein
7336_at	3995.5	P	chitin synthase 3
7337_at	263.0	M	SCO1 protein homolog (S. cerevisiae)
7338_at	19305.9	P	probable purine nucleotide-binding protein
7339_at	1296.2	P	Nuclear protein that binds to T-rich strand of core consensus sequence of autonomously replicating sequence
7340_at	284.0	A	hypothetical protein
7341_at	626.8	P	Probable ser\/thr-specific protein kinase, homolog to YKR2 and YPK1 (S. cerevisiae)
7342_at	2749.4	P	

CDP-diacylglycerol synthase, CTP-phosphatidic acid cytidylyltransferase, CDP-diglyceride synthetase
7343_at 299.6 A
involved in inositol biosynthesis
7344_i_at 10288.5 P
Ribosomal protein L4A (L2A) (rp2) (YL2)
7345_s_at 54548.9 P
Ribosomal protein L4A (L2A) (rp2) (YL2)
7346_at -115.5 A
hypothetical protein
7347_at 419.5 P
Probable regulatory Zn-finger protein,\/ homolog to YKL251\/
7348_at 2295.5 P
nuclear protein arginine methyltransferase (mono- and asymmetrically dimethylating enzyme)
7349_at 1839.3 P
pyridoxine (pyridoxiamine) phosphate oxidase
7350_at 3565.7 P
contains 9 or 10 putative membrane spanning regions\; putative Ca2+ binding protein (homology to EF-hand Ca2+ binding site)
7351_at 906.8 P
inner mitochondrial membrane protein
7306_at 1093.7 P
chitin synthase 2
7307_at 3115.4 P
gamma subunit of mitochondrial ATP synthase
7308_at 207.9 A
integral membrane protein
7309_at 1338.6 P
Fatty acid transporter
7310_at 211.8 A
Probable membrane-bound small GTPase
7311_at 1147.9 P
similarity to benomyl/methotrexate resistance protein
7312_at 124.0 A
similarity to chaperonin HSP60 proteins
7313_at 92.9 A
Glc7-interacting protein.
7314_at 815.4 P
Homolog to quinone oxidoreductase (E. coli)
7315_at 176.1 A
hypothetical protein
7316_s_at 50126.1 P
Ribosomal protein S11B (S18B) (rp41B) (YS12)
7317_at 532.2 M
RNA polymerase I enhancer binding protein
7318_at 487.1 A
Possible regulatory subunit for the PP1 family protein phosphatase Glc7p
7319_at 208.9 A
questionable ORF
7320_at 3864.4 P
Homolog to YCR004, obr1 (S. pombe), trp repressor binding protein (E. coli)
7321_at 1168.6 P
similarity to rat regucalcin
7322_at 437.4 P
Homolog to HSP30 heat shock protein YRO1 (S. cerevisiae) 7
7323_at 644.9 P
RNA splicing factor

7324_at	1040.6	P	Homolog to glucan-1,3--glucosidase (EC 3.2.1.5\; S. cerevisiae) 2
7325_at	239.4	A	Muddled Meiosis
7326_at	972.3	P	Ubiquitin-specific protease
7327_at	1399.0	P	Probable protein kinase
7283_at	292.4	P	origin recognition complex subunit 2
7284_at	1226.1	P	Homolog to ftsJ protein (E. coli) ,\/ YCR054\/
7285_at	3846.9	P	similarity to rat neurodegeneration associated protein 1
7286_at	373.1	M	Probable phosphopanthethein-binding protein
7287_at	117.0	A	questionable ORF
7288_at	119.9	A	ExtraCellular Mutant
7289_at	405.7	A	Probable Zn-finger protein
7290_at	19481.0	P	cell wall mannoprotein
7291_at	6149.3	P	probable amino acid permease for leucine, valine, and isoleucine
7292_at	1258.3	P	Probable amino acid transport protein
7293_at	984.5	P	osmotolerance protein
7294_at	478.4	P	hypothetical protein
7295_at	399.7	A	heat shock protein 26
7296_at	2726.8	P	Putative helicase similar to RAD54
7297_at	275.1	A	Homolog to aminopeptidase Y (S. cerevisiae)
7298_at	1055.7	A	hypothetical protein
7299_at	-11.4	A	ExtraCellular Mutant
7300_at	289.4	A	hypothetical protein
7301_at	10210.5	P	Homolog to sporulation specific protein SPS2 (S. cerevisiae)
7302_at	31173.1	P	Homolog to sporulation specific protein SPS2 (S. cerevisiae)
7303_at	6979.3	P	Exhibits significant sequence similarity with a subunit of the mammalian translation initiation factor 3
7304_at	2023.4	P	cytoplasmic protein involved in protein transport between ER and Golgi\; ATPase
7305_at	1106.7	P	transcription factor, member of the histone acetyltransferase SAGA complex
7260_at	9804.1	P	ubiquitin-conjugating enzyme

7261_at 5874.8 P
transcription factor of the TEA\/ATTS DNA-binding domain family, regulator of Ty1 expression
7262_at 3888.0 P
mitochondrial C1-tetrahydroflate synthase
7263_at 691.6 P
mitochondrial ADP\/ATP translocator
7264_at 5017.3 P
Probable transmembrane protein
7265_at 1120.8 P
Subunit 5 of Replication Factor C\; homologous to human RFC 38 kDa subunit
7266_at 2076.7 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 112.5 A
questionable ORF
7268_at 1325.2 P
11-kDa nonhistone chromosomal protein
7269_g_at 1967.7 P
11-kDa nonhistone chromosomal protein
7270_i_at 1484.1 P
questionable ORF
7271_at -22.0 A
questionable ORF
7272_at 839.1 P
Nuclear protein involved in mitochondrial intron splicing
7273_at 54933.0 P
Acid phosphatase, constitutive
7274_at 3019.5 P
Acid phosphatase, repressible
7275_at 808.9 A
weak similarity to pig tubulin-tyrosine ligase
7276_at 1644.7 P
hypothetical protein
7277_at 866.9 P
hypothetical protein
7278_at 730.0 P
Myristoylated Serine\/threonine protein kinase involved in vacuolar protein sorting
7279_at 3.3 A
putative transcriptional (co)activator for DNA damage
7280_at -64.2 A
weak similarity to T.brucei mitochondrion hypothetical protein 6
7281_at 1064.7 P
questionable ORF
7282_at 2387.4 P
weak similarity to S.pombe hypothetical protein SPBC3B9.01
7238_at 116.4 A
hypothetical protein
7239_at 1029.2 P
weak similarity to human U3 snoRNP associated 55 kDa protein
7240_at 1031.8 P
mitochondrial carrier protein
7241_at 593.7 P
involved in fructose-1,6-bisphosphatase degradation
7242_at 13669.6 P
May be a membrane protein involved in inorganic phosphate transport and regulation of Pho81p function
7243_at 272.1 A

weak similarity to N.crassa chitin synthase
7244_at 290.2 A
Probable transcription factor
7245_at 7581.2 P
Calmodulin
7246_at 1013.6 P
beta-1,4-mannosyltransferase
7247_at 4680.0 P
Homolog to serendipity protein (D. melanogaster)
7248_at 1668.9 P
Transcription regulatory protein
7249_at 543.8 A
questionable ORF
7250_at -15.9 A
Radiation repair protein, putative DNA helicase
7251_at 18550.6 P
alpha aminoadipate reductase
7252_at 200.1 A
questionable ORF
7253_g_at 294.2 A
questionable ORF
7254_at 85.7 A
transketolase, homologous to tkl1
7255_at 493.8 P
U1 snRNP A protein
7256_at 221.9 A
Translational activator of COB mRNA
7257_at 16062.6 P
Glycyl-tRNA synthase
7258_at 775.8 P
Mitochondrial ribosomal protein MRPL36 (YmL36)
7259_at 1011.8 P
transcription factor tau (TFIIIC) subunit 95
7215_at 278.8 A
questionable ORF
7216_at 868.4 P
Probable phosphoprotein phosphatase (EC 3.1.3.16)
7217_at 4566.0 P
56 kD synthase subunit of trehalose-6-phosphate synthase\/phosphatase complex
7218_at 24818.2 P
H+-transporting ATPase, vacuolar (EC 3.6.1.35)
7219_at 14.4 A
required for autophagy
7220_at 275.0 A
imparts Far- phenotype
7221_at 2108.4 P
cytoplasmic protein involved in mother-specific HO expression
7222_at 741.3 P
Calcium Caffeine Zinc sensitivity
7223_at 153.4 A
Amino acid permease
7224_at 1012.5 P
Negative regulator of swe1 kinase (which regulates cdc28)
7225_at -53.8 A
questionable ORF
7226_at 1237.4 P

subunit of the Cdc28 protein kinase
7227_at 605.0 A
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 936.0 P
hypothetical protein
7229_at 281.6 A
Unknown
7230_at 1442.3 P
Probable serine-type carboxypeptidase (EC 3.4.16.1)
7231_at 742.1 P
GTPase activating protein
7232_at 385.9 A
hypothetical protein
7233_at 1126.9 P
Probable pre-mRNA splicing RNA-helicase
7234_at 7912.3 P
Ominipotent suppressor protein of nonsense codons
7235_at 48.2 A
hypothetical protein
7236_at 897.4 P
alcohol dehydrogenase isoenzyme V
7237_at 424.6 A
Probable mitochondrial ribosomal protein S9
7193_at 498.9 P
strong similarity to hypothetical protein YOL092w
7194_at 31.7 A
Spore-specific protein
7195_at 1395.1 P
D-arabinose dehydrogenase
7196_at 777.6 P
Probable Zn-finger protein
7197_at 1362.1 P
weak similarity to potato sucrose cleavage protein
7198_at 51.5 A
U4\/U6.U5-associated snRNP protein\; contains a PEST proteolysis motif
7199_at 1462.9 P
Riboflavin biosynthesis protein
7200_at 3626.5 P
25-kDa RNA polymerase subunit (common to polymerases I, II and III)
7201_at 1025.1 P
Stress-inducible riboflavin biosynthetic protein homolog
7202_at 10.4 A
weak similarity to myosins
7203_at 246.9 A
hypothetical protein
7204_at 6208.4 P
hypothetical protein
7205_at 2860.8 P
similarity to human 17-beta-hydroxysteroid dehydrogenase
7206_at 1881.0 P
protein kinase catalytic subunit
7207_at 288.0 A
Homolog to suppressor of reduced viability of starvation (SUR1, S. cerevisiae)
7208_at 10702.8 P
similarity to hypothetical protein YJL171c

7209_at	7453.2	P	Protein that participates in secretory pathway
7210_at	817.0	P	hypothetical protein
7211_at	2071.0	P	ADP-ribosylation factor-like protein 1
7212_at	603.9	P	General positive regulator of CDC34\; Suppress some cdc34 mutations when over-expressed
7213_at	1275.1	P	Prephenate dehydrogenase (NADP+)
7214_at	333.0	A	Pop7 protein, an integral subunit of RNase P and apparent subunit of RNase MRP
7170_at	61.9	A	weak similarity to hypothetical protein YLR324w
7171_at	1155.3	P	HSP70 family member, highly homologous to Sse1p
7172_at	1142.7	P	Suppressor of SEC63 (S.cerevisiae), novel ER translocation component
7173_at	2628.9	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	1566.1	P	Kinesin-related protein suppressing myosin defects (MYO2)
7175_at	1807.2	P	20S proteasome maturation factor
7176_at	29.3	A	questionable ORF
7177_at	1177.9	P	Probable GTP-binding protein
7178_at	654.9	P	Alpha-Ketoisovalerate Hydroxymethyltransferase
7179_at	4904.8	P	Probable membrane receptor
7180_at	-308.4	A	questionable ORF
7181_at	556.1	A	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	-208.8	A	Probable resistance protein
7183_at	248.0	A	Probable DNA-binding transcription factor, Homolog to SRF\/SL-2
7184_at	942.7	P	strong similarity to hypothetical protein YPL087w
7185_at	-32.9	A	alpha-galactosidase
7186_at	392.2	A	respiratory chain assembly protein
7187_at	16.2	A	Putative ATPase
7188_at	4117.2	P	probable membrane protein
7189_at	402.4	A	splicing factor
7190_i_at	23144.4	P	Ribosomal protein S9B (S13) (rp21) (YS11)

7191_f_at 48819.1 P
Ribosomal protein S9B (S13) (rp21) (YS11)
7192_at 126.7 A
questionable ORF
7147_at 53450.4 P
Ribosomal protein L21A
7148_at 613.7 P
Probable carrier protein, mitochondrial
7149_at 492.7 P
Stoichiometric member of mediator complex
7150_at 747.1 P
hypothetical protein
7151_at 341.2 A
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 66131.4 P
Glucose-6-phosphate isomerase
7153_at 228.0 A
weak similarity to hypothetical protein YPL077c
7154_at 2623.3 P
Probable transcription-associated factor protein, probable -transducin type
7155_at 2404.6 P
Putative alpha-1,2-mannosyltransferase
7156_at 508.9 P
contains two SH3 domains
7157_at 1526.8 P
MCM3 protein homolog (S. cerevisiae)
7158_at 127.6 A
hypothetical protein
7159_at 880.7 P
Probable serine-active lipase, peroxisomal (EX 3.1.1.-)
7160_at 2592.4 P
Putative alpha-1,2-mannosyltransferase
7161_g_at 3286.1 P
Putative alpha-1,2-mannosyltransferase
7162_at 3907.5 P
questionable ORF
7163_at 1937.9 P
probable membrane protein
7164_at 475.6 P
Urea amidolyase (contains urea carboxylase and allophanate hydrolase)
7165_at -227.6 A
hypothetical protein
7166_at 844.4 P
strong similarity to D.melanogaster cornichon protein
7167_at 273.9 A
regulator of microtubule stability
7168_at 2389.9 P
negative growth regulatory protein
7169_at 1084.0 A
Effector in the expression of PAPS reductase and sulfite reductase
7124_at 735.9 P
strong similarity to hypothetical protein YGL056c
7125_at 552.3 P
highly charged, basic protein
7126_at 87.1 A

strong similarity to hypothetical protein YGL060w
7127_at -79.3 A
autophagy
7128_at 9936.3 P
pyruvate carboxylase
7129_at 578.3 P
similarity to human acetyl-coenzyme A transporter
7130_g_at 698.3 P
similarity to human acetyl-coenzyme A transporter
7131_at 3918.0 P
beta subunit of pyruvate dehydrogenase (E1 beta)
7132_at 2482.7 P
Probable AMP-binding protein
7133_at 185.2 A
hypothetical protein
7134_at 546.7 A
questionable ORF
7135_at 569.4 A
hypothetical protein
7136_at -59.7 A
questionable ORF
7137_at 1025.0 P
Homolog to ATP-binding protein clpX (E.coli)
7138_at 220.0 A
similarity to hypothetical A.thaliana protein
7139_at 1221.7 P
Homolog to 1,4-a-glucosidase (S.cerevisiae) (EC 3.2.1.3) 3
7140_at 1096.1 P
hypothetical protein
7141_at 817.5 P
similarity to human p97 homologous protein
7142_at 995.9 A
questionable ORF
7143_at 335.6 M
Homolog to human hnRNP complex K protein
7144_at 2803.3 P
similarity to human Arp2/3 protein complex subunit p41-Arc and to human Sop2p-like protein
7145_at 626.4 A
similarity to bumetanide-sensitive Na-K-Cl cotransport protein
7146_at 936.6 P
RNA (guanine-7-)methyltransferase (cap methyltransferase)
7102_at 347.7 A
RNA helicase homolog
7103_at 538.9 P
strong similarity to general chromatin factor Spt16p
7104_at 502.7 P
Probable Zn-finger protein
7105_at 257.2 A
Probable Zn-finger protein
7106_at 1008.6 A
Probable sugar transport protein
7107_at 1353.4 P
Probable ATP\/GTP-binding protein
7108_at 2039.0 P
UDP-N-acetyl-glucosamine-1-P transferase (GPT)
7109_at 361.3 P

Probable glutathione peroxidase (EC 1.11.1.9)
7110_at 1273.8 P
Homolog to SNF2\/SWI2 DNA-binding regulatory protein
7111_at 1246.2 P
hypothetical protein
7112_at 3640.6 P
Putative 57 kDa protein with an apparent MW of 70 kDa by SDS-PAGE
7113_at 4850.5 P
glutamine amidotransferase:cyclase
7114_at 5082.0 P
3-deoxy-D-arabino-heptulosonate 7-phosphate (DAHP) synthase isoenzyme
7115_at 18.3 A
hypothetical protein
7116_at 437.2 A
Probable mitochondrial ribosomal protein S5
7117_at 5858.6 P
dUTP pyrophosphatase (dUTPase)
7118_at 44.4 A
transcription factor, part of Srb\/Mediator complex
7119_at 546.8 A
probable membrane protein
7120_at 162.3 A
hypothetical protein
7121_at 309.7 A
Riboflavin synthase alpha-chain
7122_at 405.4 A
Required for normal 5.8S rRNA processing and for tRNA processing\; associated with RNase MRP and RNase P
7123_at 245.0 A
hypothetical protein
7079_at 129.2 A
hypothetical protein
7080_at 1141.5 P
similarity to C.elegans GTPase-activating protein
7081_at 1754.7 P
similarity to hypothetical S. pombe protein
7082_at 1026.2 P
questionable ORF
7083_at 14048.7 P
Serine hydroxymethyltransferase, mitochondrial
7084_at 1078.2 P
Probable small GTP-binding protein
7085_at 2137.3 P
probable membrane protein
7086_at 997.3 P
Probable mitochondrial protein L37
7087_at 683.9 P
hypothetical protein
7088_at 433.5 A
Probable ATP\/GTP-binding protein
7089_at 1094.8 P
weak similarity to S.pombe uvi22 protein and hypothetical protein YNL024c
7090_at 278.3 A
Hsm3p may be a member of the yeast MutS homolog family
7091_at 576.8 M
similarity to hypothetical protein YJL048c

7092_at 338.8 A
Probable protein kinase (growth factor & cytokine receptor family)
7093_at 459.6 A
RAP1-interacting factor, involved in establishment of repressed chromatin
7094_at 2316.3 P
dual specificity protein phosphatase
7095_at 60.5 A
questionable ORF
7096_at 419.6 A C
and C subunits of DNA polymerase II
7097_at 1297.9 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 260.6 A
hypothetical protein
7099_at 1004.6 P
Probable G-protein, -transducin type
7100_at 830.4 P
Mitochondrial ribosomal protein MRPL27 (YmL27)
7101_at 9552.3 P
Probable SEC61 protein homolog
7057_at 112.7 A
similarity to AMP deaminase
7058_at -27.9 A
hypothetical protein
7059_at 14524.7 P
Aminopeptidase yscIII
7060_at 3364.1 P
similarity to hypothetical S. pombe protein
7061_at 1124.7 P
clathrin associated protein medium chain
7062_at 1398.1 P
transcriptional activator
7063_at 888.1 P
metal homeostasis protein\; putative membrane protein
7064_at 6800.0 P
citrate tranporter in mitochondrial inner membrane
7065_at 410.4 A
hypothetical protein
7066_at 675.1 P
Probable multidrug resistance protein
7067_at -29.0 A
Probable sulfate transport protein
7068_at 311.3 A
Putative P-type Cu(2+)-transporting ATPase
7069_at 2103.6 P
Homolog to phosphate-repressible phosphate permease
7070_at 170.1 A
Maltose fermentation regulatory protein
7071_s_at 182.3 A
maltose permease
7072_s_at 127.8 A
Maltase (EC 3.2.1.20)
7073_at -10.3 A
strong similarity to hypothetical protein YGR293c
7074_f_at 736.4 P

YKL224 c homolog
7075_at 59.8 A
hypothetical membrane protein
7076_at 843.3 M
identified by SAGE
7077_at 2226.8 P
identified by SAGE
7078_at 456.6 A
hypothetical protein
7033_at 337.0 A
questionable ORF - upstream ORF of ALG1
7034_i_at 8441.9 P
identified by SAGE
7035_s_at 7886.7 P
identified by SAGE
7036_s_at 602.9 P
Protein involved in targeting of plasma membrane [H+]ATPase
7037_s_at 297.6 A
Probable aldehyde dehydrogenase (EC 1.2.1.-)
7038_s_at 656.6 P
Degradation in the Endoplasmic Reticulum
7039_at 128.4 A
probable membrane protein
7040_g_at -25.3 A
probable membrane protein
7041_s_at 1012.0 P
Probable Zn-finger protein (C2H2 type)
7042_at 300.8 A
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 747.3 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 -48.3 A
non-annotated SAGE orf Found reverse in NC_001134 between 164788 and 164997 with 100% identity.
See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251
7045_i_at 5219.9 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 5423.9 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 847.4 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 -3.2 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
7049_s_at 15.0 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 1017.4 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 70.4 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 94.8 A
non-annotated SAGE orf Found reverse in NC_001134 between 101483 and 101674 with 100% identity.
See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251
7053_at 84.0 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 -310.5 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 -387.3 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 15.1 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 290.2 A
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 1593.2 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 24244.4 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 205.8 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 1546.7 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 189.7 A
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 522.1 A
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 522.7 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 511.0 A
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 902.5 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 1019.9 A
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 7914.5 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 370.2 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 458.3 A

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 428.7 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 3.0 A
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 498.4 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 7416.5 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 22.6 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 242.6 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 -289.3 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 326.6 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 1534.9 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 -83.5 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 148.8 A
non-annotated SAGE orf Found forward in NC_001134 between 35606 and 35800 with 100% identity. See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251
6987_at 140.7 A
non-annotated SAGE orf Found reverse in NC_001134 between 66854 and 67036 with 100% identity. See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251
6988_at -58.7 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 194.0 A
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 234.1 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 211.6 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
6992_r_at 1.6 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 1742.3 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 535.3 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 515.0 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 148.4 A
non-annotated SAGE orf Found reverse in NC_001134 between 159883 and 160056 with 100% identity.
See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251
6997_at 344.9 A
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 36.6 A
non-annotated SAGE orf Found forward in NC_001134 between 165623 and 165823 with 100% identity.
See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251
6999_at 415.0 A
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 89.0 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 209.4 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 225.5 A
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 -32.5 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 -23.1 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 73.1 A
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 -208.1 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 -346.0 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 717.1 A
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 163.1 A
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 21.0 A
non-annotated SAGE orf Found reverse in NC_001134 between 554921 and 555088 with 100% identity.
See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251
6963_at 47.6 A
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 338.1 A
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 -147.4 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 44.8 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

6967_at 487.7 P

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

6968_at 656.7 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 2112.2 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 190.4 A

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

6971_at 311.5 A

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 177.4 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 -81.0 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 -123.9 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 3580.1 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 3690.7 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 1184.7 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 434.0 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 397.5 A

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 -184.5 A

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

6981_at 1773.3 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 -21.2 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 -54.0 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 144.4 A
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 3477.2 P
Saccharomyces cerevisiae chromosome II, complete chromosome sequence. Found forward in NC_001134 between 1 and 1000 with 100% identity.
6939_g_at 3177.9 P
Saccharomyces cerevisiae chromosome II, complete chromosome sequence. Found forward in NC_001134 between 1 and 1000 with 100% identity.
6940_s_at 168.2 A
Saccharomyces cerevisiae chromosome II, complete chromosome sequence. Found forward in NC_001134 between 1001 and 2000 with 100% identity.
6941_s_at 543.3 A
Saccharomyces cerevisiae chromosome II, complete chromosome sequence. Found forward in NC_001134 between 2001 and 3000 with 100% identity.
6942_at 300.2 A
Saccharomyces cerevisiae chromosome II, complete chromosome sequence. Found forward in NC_001134 between 3001 and 4000 with 100% identity.
6943_g_at 220.5 A
Saccharomyces cerevisiae chromosome II, complete chromosome sequence. Found forward in NC_001134 between 3001 and 4000 with 100% identity.
6944_at 130.4 A
Saccharomyces cerevisiae chromosome II, complete chromosome sequence. Found forward in NC_001134 between 4001 and 5000 with 100% identity.
6945_g_at 702.5 M
Saccharomyces cerevisiae chromosome II, complete chromosome sequence. Found forward in NC_001134 between 4001 and 5000 with 100% identity.
6946_at 711.9 A
Saccharomyces cerevisiae chromosome II, complete chromosome sequence. Found forward in NC_001134 between 5001 and 6000 with 100% identity.
6947_g_at 1202.1 P
Saccharomyces cerevisiae chromosome II, complete chromosome sequence. Found forward in NC_001134 between 5001 and 6000 with 100% identity.
6948_i_at 471.4 P
Saccharomyces cerevisiae chromosome II, complete chromosome sequence. Found forward in NC_001134 between 6001 and 6215 with 100% identity.
6949_f_at 143.4 A
Saccharomyces cerevisiae chromosome II, complete chromosome sequence. Found forward in NC_001134 between 6001 and 6215 with 100% identity.
6950_at 1301.2 A
snRNA
6951_at 1442.0 P
telomerase RNA component
6952_at 2630.3 P
telomerase RNA component
6953_at 276.0 A
snRNA
6954_at -133.8 A
snRNA
6955_s_at -107.0 A
putative pseudo-TY5
6956_s_at -449.0 A
Reverse transcriptase
6957_s_at 276.5 A

Bud site selection
6958_s_at 3090.3 P
Mating type protein alpha-2
6959_s_at 1573.1 A
transcripton factor involved in the regulation of the alpha-specific genes
6960_at -51.5 A
questionable ORF
6961_g_at 2506.8 P
questionable ORF
6915_at 755.5 P
catabolic serine (threonine) dehydratase
6916_at 773.8 P
weak similarity to yeast translation regulator Gcd6p
6917_at 153.0 A
similarity to myosin heavy chain form b from Chicken and Xenopus
6918_at 921.7 P
strong similarity to human Rev interacting protein Rip-1
6919_at 491.9 P
hypothetical protein
6920_at 4497.8 P
Saccharolysin (oligopeptidase yscD)
6921_at 2142.4 P
hypothetical protein
6922_at 780.6 P
May assist Ste12p in pheromone-dependent expression of KAR3 and CIK1
6923_at 1124.0 P
Methyltransferase
6924_at 532.0 P
Protease B Non-derepressible
6925_at 356.9 P
involved in laminarinase resistance
6926_at 4384.1 P
diadenosine 5 ,5 -P1,P4-tetraphosphate phosphorylase I
6927_at 1106.4 P
hypothetical protein
6928_at 64.5 A
strong similarity to sporulation-specific protein Sps2p
6929_at 236.0 A
hypothetical protein
6930_at 1272.9 P
weak similarity to human ORF
6931_at 97.6 A
questionable ORF
6932_at 1318.3 P
hypothetical protein
6933_at 28441.7 P
protein disulfide isomerase
6934_at 139.3 A
questionable ORF
6935_at 677.1 P
questionable ORF
6936_g_at 1512.7 P
questionable ORF
6937_at 6319.1 P
Glucokinase
6893_at 475.5 A

regulatory protein
6894_at 723.1 A
Membrane transporter
6895_at 4500.6 P
SRO9 may overlap in function with tropomyosin and may be involved in organization of actin filaments
6896_at 1913.8 P
similarity to hypothetical protein YDR514c
6897_at 4677.5 P
Glutaredoxin (thiol-transferase)
6898_at 1716.1 P
similarity to hypothetical S.pombe protein
6899_at 843.6 P
Transcription regulator
6900_at 93.1 A
possesses a SAM (sterile alpha motif)\; interacts with G protein and Ste11p
6901_at 1138.9 P
involved in pre-rRNA processing and ribosome assembly
6902_at 16712.1 P
histidinol dehydrogenase
6903_at 351.5 A
Microtubule-binding protein
6904_at 6394.0 P
weak similarity to glutenins, high molecular weight chain
6905_at 1180.5 P
serine\/threonine-rich membrane protein
6906_at 51.1 A
Protein involved in the integration of lipid signaling pathways with cellular homeostatis
6907_at 875.6 P
Amino acid permease
6908_at 51.9 A
questionable ORF
6909_at 3484.6 P
beta-IPM (isopropylmalate) dehydrogenase
6910_at 2350.7 P
NifS-like protein
6911_at 243.4 A
hypothetical protein
6912_at 309.3 A
Cell cycle regulated protein required for axial bud formation\; co-assembles with Bud4p at bud sites
6913_at 512.4 P
part of budding protein Bud3p due to frameshift in DNA sequence
6914_at 5173.9 P
Protein with RNA recognition motifs
6870_at 56.8 A
strong similarity to Saccharomyces pastorianus hypothetical protein LgYCL010c
6871_at 9837.3 P
Small regulatory subunit of Acetolactate synthase
6872_at 538.5 P
Calcofluor White Hypersensitivity
6873_at -80.2 A
questionable ORF
6874_at 170.0 A
strong similarity to Saccharomyces pastorianus hypothetical protein LgYCL005w
6875_at 88.5 A
17-kDa phosphatidylserine synthase
6876_at 706.6 P

strong similarity to Saccharomyces pastorianus hypothetical protein LgYCL002c
6877_at 1013.1 P
Protein involved in retention of membrane proteins, including Sec12p, in the ER\; localized to Golgi, where it may function in returning membrane proteins to the ER
6878_at -230.2 A
similarity to Dom34p
6879_at 84.7 A
hypothetical protein
6880_at 2151.5 P
conserved potential GTP-ginding protein
6881_at 480.5 P
Mitochondrial ribosomal protein MRPL32 (YmL32)
6882_at 3433.3 P
FMN-binding protein
6883_at 6067.4 P
non-mitochondrial citrate synthase
6884_at 130.4 A
hypothetical protein
6885_at 1264.4 P
Ser\/Thr protein kinase
6886_at 2109.3 P
Reduced viability on starvation protein RVS161
6887_at 406.1 A
strong similarity to Y.lipolytica GPR1 protein and Fun34p
6888_at 2146.4 P
Active transport ATPase
6889_at 4767.6 P
weak similarity to M.leprae B1496_F1_41 protein
6890_at 147483.6 P
3-phosphoglycerate kinase
6891_at 194.2 A
DNA polymerase IV
6892_at 37.9 A
hypothetical protein
6848_at 862.9 P
hypothetical protein
6849_at 3533.8 P
similarity to hypothetical S.pombe protein
6850_at 656.2 P
Transcription regulator
6851_at 595.8 P
MAK32 sugar kinase
6852_at -168.1 A
Transcription regulator
6853_at 722.5 P
MAK31 snRNP
6854_at 303.8 A
Protein induced by heat shock, ethanol treatment, and entry into stationary phase\; located in plasma membrane
6855_at 245.6 A
hypothetical protein
6856_at 881.4 P
Membrane transporter
6857_at 543.5 P
Asn-tRNA synthetase
6858_f_at 26343.0 P

Proteolipid associated with plasma membrane H(+)-ATPase (Pma1p)
6859_at -115.0 A
hypothetical protein
6860_at 1026.4 P
Membrane phospho-diesterase
6861_at 370.5 A
GTPase (RAS-related)
6862_at 691.7 A
Amino acid permease
6863_at 3037.1 P
required for mitochondrial DNA replication
6864_at 3035.4 P
required for mitochondrial DNA replication
6865_at 1396.0 P
weak similarity to S.pombe hypothetical protein SPBC4C3.06
6866_at 46923.8 P
Ribosomal protein S14A (rp59A)
6867_at 405.9 A
Beige Protein Homologue 1
6868_at 591.5 P
similarity to mouse nuclear receptor co-repressor N-Cor
6869_at 4465.1 P
Probable subunit of 1,3-beta-glucan synthase\; homolog of ELO1
6825_at 834.7 P
Component of the exosome 3->5 exoribonuclease complex with Rrp4p, Rrp41p, Rrp42p and Dis3p (Rrp44p).
6826_at 1699.9 P
ribokinase
6827_at 1894.1 P
May collaborate with Pho86p and Pho84p in inorganic phosphate uptake\; protein contains 12 predicted transmembrane domains
6828_at 121.6 A
GTP\/GDP exchange factor for Rsr1 protein
6829_at 94.2 A
questionable ORF
6830_at 1018.0 P
TATA binding protein-associated factor (TAF)
6831_at 706.1 A
hypothetical protein
6832_at 273.6 A
involved in manganese homeostasis
6833_at -216.5 A
Protease
6834_at 1265.9 M
required for respiration and maintenance of mitochondrial genome
6835_at 1175.2 P
Protein carboxyl methylase
6836_at -155.6 A
questionable ORF
6837_at 2421.4 P
Acyl-CoA cholesterol acyltransferase (sterol-ester synthetase)
6838_at 192.4 A
questionable ORF
6839_at 1514.9 P
weak similarity to ankyrins
6840_at 1692.6 P

a subunit of RSC, a fifteen-protein chromatin remodeling complex and related to the Swi\/snf Complex.
6841_at 11592.8 P
threonine synthase
6842_at 298.6 A
CTR86 shares a terminator region with THR4. CTR86 contains aGCN4 responsive site suggesting it may also be involved in amino acid biosynthesis.
6843_at 1297.8 P
regulatory protein
6844_at 2443.8 P
weak similarity to hypothetical protein YDL177c
6845_at 1497.8 P
regulatory protein
6846_at 2301.5 P
hypothetical protein
6847_g_at 6713.6 P
hypothetical protein
6803_at 5005.2 P
similarity to Ytp1p protein
6804_at 198.7 A
questionable ORF
6805_at 213.2 A
G10-like protein
6806_at 592.9 P
Transcription factor (fork head domain)
6807_at 169.4 A
Zn finger protein, putative ATPase
6808_at 1773.0 P
Intracellular transport protein
6809_at 216.7 A
similarity to hypothetical S.pombe protein
6810_g_at -20.7 A
similarity to hypothetical S.pombe protein
6811_at 2001.8 P
cyclophilin homolog
6812_at 377.9 A
(required for) Integrity of Mitochondrial Genome 2
6813_at 1006.5 P
regulatory protein
6814_at 523.6 P
protein kinase
6815_at 2095.1 P
shows similarity to glucose-6-phosphate dehydrogenase non-catalytic domains\; homologous to Sol1p and Sol3p
6816_at 444.3 P
ERS1 protein, ER defect supressor
6817_at 1013.4 P
hypothetical protein
6818_at 1316.5 P
Necessary for accurate chromosome transmission during cell division
6819_at 279.8 A
weak similarity to A.thaliana protein phosphatase 2C
6820_at 305.9 A
activation mediator subcomplex of RNA polymerase I holoenzyme
6821_at 2123.4 P
weak similarity to Rbk1p
6822_at 343.9 A

Thioredoxin type II
6823_at 3541.3 P
glucose repression regulatory protein, exhibits similarity to beta subunits of G proteins
6824_at -17.3 A
hypothetical protein
6780_at 404.7 P
hypothetical protein
6781_at 1037.9 P
questionable ORF
6782_at 1150.3 P
nucleic acid-binding protein
6783_at 6454.7 P
Actin binding protein
6784_at 751.5 P
predicted GPI-anchored cell wall protein
6785_at 802.9 P
hypothetical protein
6786_at 172.0 A
Putative serine\/threonine protein kinase most similar to cyclic nucleotide-dependent protein kinase subfamily and the protein kinase C subfamily
6787_at 468.4 A
mutS homolog, forms a complex with Msh2p to repair insertion-deletion mispairs\; redundant with Pms3\/Msh6p in repair of insertion-deletion mispairs
6788_at 1717.5 P
nuclear protein that negatively regulates basal transcription
6789_at 570.5 A
Cell Division Cycle mutant
6790_at 293.0 A
hypothetical protein
6791_s_at 5.7 A
Homeobox-domain containing protein which, together with alpha2, represses transcription of haploid-specific genes in diploid cells
6792_s_at 43.1 A
Homeobox-domain containing protein which, together with alpha2, represses transcription of haploid-specific genes in diploid cells
6793_at 150.5 A
permease involved in the uptake of glycerophosphoinositol (GroPIns)
6794_at -22.4 A
strong similarity to Pep1p
6795_at 223.8 A
strong similarity to Pep1p
6796_at 39.9 A
strong similarity to Pep1p
6797_at 111.1 A
Alcohol dehydrogenase
6798_f_at 590.7 A
member of the seripauperin protein\/gene family (see Gene_class PAU)
6799_at 36.9 A
Alcohol dehydrogenase
6800_at 175.6 A
Transcription regulator
6801_at 73.7 A
hypothetical protein
6802_at 164.7 A
hypothetical protein
6755_i_at 2.6 A

hypothetical protein
6756_at 36.4 A
high-temperature lethal
6757_i_at -25.8 A
Homeobox-domain containing protein which, together with alpha2, represses transcription of haploid-specific genes in diploid cells
6758_at 320.6 A
hypothetical protein identified by SAGE
6759_at 2516.2 P
identified by SAGE
6760_g_at 4333.3 P
identified by SAGE
6761_at -54.6 A
similarity to starvation induced pSI-7 protein of C. fluvum
6762_s_at 256.9 A
Ser\/Thr protein kinase
6763_at 878.7 P
homologous to mouse and human Tsg101 tumor susceptibility genes
6764_g_at 308.3 A
homologous to mouse and human Tsg101 tumor susceptibility genes
6765_at -101.5 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 -168.5 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 503.7 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 450.4 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 183.7 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 -39.8 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 121.9 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
6772_at -139.7 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 691.4 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 749.2 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 4098.8 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 33.8 A
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 1939.2 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 2367.2 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 234.2 A
non-annotated SAGE orf Found reverse in NC_001135 between 204772 and 204939 with 100% identity. See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251

6731_at 349.8 A
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 43186.0 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 63350.7 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 -68.5 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 207.5 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

6736_r_at -193.2 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 -144.9 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 -1829.0 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 213.1 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 -171.6 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 341.9 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 309.4 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 64.3 A
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 -304.3 A
non-annotated SAGE orf Found forward in NC_001135 between 125368 and 125520 with 100% identity. See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251

6745_at 799.2 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 109.4 A
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 2212.3 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 -19.9 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 -59.2 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 -204.0 A
TY5-1
6751_at 72.4 A
snRNA
6752_i_at -159.5 A
Centromere
6753_at 1544.0 P
snRNA
6754_at 45.4 A
snRNA
6708_at 29.5 A
snRNA
6709_i_at 103.5 A
strong similarity to sugar transport proteins
6710_at 320.2 A
Hypothetical aryl-alcohol dehydrogenase
6711_at 239.9 P
strong similarity to hypothetical protein YPR079w
6712_at 518.1 P
hypothetical protein
6713_at 392.4 P
Protein similar to LIM-domain proteins and to rho\/rac GTPase-activating family of proteins
6714_at 485.0 P
hypothetical protein
6715_at -54.8 A
similarity to E.coli hypothetical protein and to chlorohydrolases
6716_at 1002.1 P
hypothetical protein
6717_at 3358.0 P
p-nitrophenyl phosphatase
6718_at 936.6 P
Two-component phosphorelay intermediate
6719_at 239.2 A
protein of unknown function
6720_at 393.0 P
hypothetical protein
6721_at 5567.6 P
3.6-kDa protein, probably membrane-located
6722_at 1113.5 P
hypothetical protein
6723_at 1023.7 P
phosphotyrosine-specific protein phosphatase
6724_at 9072.0 P
similarity to A.klebsiana glutamate dehydrogenase
6725_at 2119.3 P
Homothallic switching endonuclease

6726_at	1704.6	P	ADP-ribosylation factor GTPase-activating protein (ARF GAP)
6727_at	1684.8	P	similarity to Cdc11p, Cdc3p and human CDC10 protein
6728_at	465.9	P	Possible RNA binding protein. Homolog of Whi3.
6729_at	496.3	P	weak similarity to mucin
6730_at	-21.0	A	strong similarity to hypothetical protein YNL194c and similarity to YML052w
6686_at	-179.6	A	questionable ORF
6687_at	564.5	P	binds to single-stranded TG1-3 telomere G-tails
6688_at	2876.3	P	strong similarity to S.equisimilis hypothetical protein
6689_at	1355.5	P	strong similarity to S.equisimilis hypothetical protein
6690_at	257.0	A	weak similarity to hypothetical protein YNR061c
6691_at	606.8	P	Mitochondrial inner membrane protein involved in import of proteins of the ADP\/ATP carrier (AAC) family
6692_at	-220.3	A	similarity to Jun activation domain binding protein homologue of A. thaliana
6693_at	602.4	P	NAD-dependent glutamate dehydrogenase
6694_at	-120.7	A	strong similarity to putative protein kinase NPR1
6695_at	1186.4	P	has an RNA recognition domain in the N-terminal region
6696_at	3532.0	P	Integral membrane component of the endoplasmic reticulum
6697_at	-114.3	A	similarity to hypothetical protein YNL176c
6698_at	123.0	A	GABA-specific transport protein
6699_at	390.0	A	similarity to hypothetical S. pombe protein
6700_at	10004.7	P	HMG-like nuclear protein
6701_at	279.5	A	Nuclear-export-signal (NES)-containing protein
6702_at	163.1	A	weak similarity to transporter proteins
6703_at	170.8	A	phorphobilinogen deaminase (uroporphyrinogen synthase), the third step in heme biosynthesis
6704_at	-40.6	A	similarity to hypothetical protein YDR233c
6705_at	428.9	A	similarity to Skt5p
6706_at	278.6	A	Mitochondrial ribosomal protein MRPL11 (YmL11)
6707_at	2677.1	P	strong similarity to human D1075-like protein
6663_at	183.2	A	6-O-methylguanine-DNA methylase

6664_at -76.3 A
similarity to sugar transporter proteins
6665_at 2267.1 P
high copy suppressor of abf2 lacking the HMG1-like mitochondrial HM protein\; putative mitochondrial carrier protein
6666_at 505.7 A
Anti-silencing protein that causes depression of silent loci when overexpressed
6667_at 232.8 A
hypothetical protein
6668_at 5371.6 P
involved in protein transport from endoplasmic reticulum to Golgi
6669_at 257.4 A
glucose transporter
6670_at 995.2 P
similarity to N.crassa hypothetical 32 kDa protein
6671_at 32734.2 P
ADP-ribosylation factor
6672_s_at 28061.8 P
Ribosomal protein L35A
6673_at 1400.4 P
ubiquitin fusion degradation protein
6674_at 14.8 A
hypothetical protein
6675_at 764.7 P
hypothetical protein
6676_at 869.4 P
serine-threonine protein phosphatase 2A
6677_at -40.7 A
questionable ORF
6678_at 16.8 A
hypothetical protein
6679_at 24631.1 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 60416.1 P
Ribosomal protein L41A (YL41) (L47A)
6681_at 373.9 A
weak similarity to S.pombe hypothetical protein SPAC23H3
6682_at 47911.7 P
homocitrate synthase, highly homologous to YDL131W
6683_g_at 36903.8 P
homocitrate synthase, highly homologous to YDL131W
6684_at 226.6 A
ATPase inhibitor
6685_at 916.2 P
hypothetical protein
6641_at 368.9 P
PHO85 cyclin
6642_at 2078.6 P
D-Lactate Dehydrogenase (Cytochrome)
6643_at 260.7 A
similarity to hypothetical protein YCR059c
6644_at 37.8 A
hypothetical protein
6645_at 130.4 A

strong similarity to hypothetical protein YIL079c and weak similarity to cellular nucleic acid binding proteins
6646_at 3438.9 P
mitochondrial enzyme D-lactate ferricytochrome c oxidoreductase
6647_at 1914.4 P
hypothetical protein
6648_at -70.0 A
questionable ORF
6649_at 4916.8 P
Glutamate synthase (NADPH)
6650_at 334.5 A
zinc-finger transcription factor of the Zn(2)-Cys(6) binuclear cluster domain type
6651_at 246.0 A
protein of unknown function
6652_at 1175.9 P
Long-chain alcohol dehydrogenase (glutathione-dependent formaldehyde dehydrogenase)
6653_at 919.2 P
Asparagine-rich protein
6654_at 1921.5 P
weak similarity to Pyrococcus horikoshii hypothetical protein PHBJ019
6655_at 1331.5 P
nuclear protein that negatively regulates basal transcription
6656_at 1142.4 A
DNA ligase
6657_at -94.8 A
questionable ORF
6658_at -427.8 A
hypothetical protein
6659_at 2230.9 P
strong similarity to hypothetical protein YLR206w and to human KIAA0171 protein
6660_at 792.9 P
Putative RNA helicase of DEAD box family, required for Rap1p localization to telomeres
6661_at 416.6 P
MEK homolog
6662_at 841.1 P
questionable ORF
6618_at 3762.9 P
hypothetical protein
6619_at 279.4 A
weak similarity to Pas7p
6620_at 1092.1 P
G(sub)2-specific B-type cyclin
6621_at 107.8 A
MutS homolog involved in chromosome exchange
6622_at 2407.9 P
Something About Silencing 10
6623_at -4.5 A
questionable ORF
6624_at 114.3 A
questionable ORF
6625_at 1321.2 P
RNA polymerase III (C) subunit, homologus to human BN51 protein
6626_at 33.0 A
hypothetical protein
6627_at 1177.4 P
similarity to human mRNA clone RES4-25

6628_at	4328.0	P	Subunit of the regulatory particle of the proteasome
6629_at	230.1	A	weak similarity to Orc3p
6630_at	4942.1	P	alpha subunit of the coatamer complex\; gamma-alpha-COP
6631_at	2535.6	P	hypothetical protein
6632_at	7327.7	P	Cytoplasmic chaperonin subunit required for actin cytoskeleton assembly or function
6633_at	583.5	P	Cardiolipin synthase
6634_at	625.0	P	Biotin:apoprotein ligase
6635_at	6719.7	P	RNA polymerase II large subunit
6636_at	354.8	A	hypothetical protein
6637_at	187.1	A	suppressor of snf3 mutant
6638_at	16112.4	P	ADP-ribosylation factor 2
6639_at	1907.9	P	Rho GDP dissociation inhibitor with activity toward Rho1p
6640_at	633.2	P	serine-threonine protein phosphatase 2A
6595_at	864.0	P	hypothetical protein
6596_at	1439.6	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	21768.9	P	homocitrate synthase, highly homologous to YDL182W
6598_at	1767.2	P	ATPase stabilizing factor
6599_at	66034.6	P	Ribosomal protein P1B (L44) (YP1beta) (Ax)
6600_at	75266.9	P	Ribosomal protein P1B (L44) (YP1beta) (Ax)
6601_at	109.5	A	hypothetical protein
6602_at	2214.4	P	vacuolar H+\/Ca2+ exchanger
6603_at	551.0	P	G1 cyclin
6604_at	25837.5	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	9007.8	P	Yeast member of the Histidine Triad protein family (HIT)
6606_at	8632.9	P	Yeast member of the Histidine Triad protein family (HIT)
6607_at	1952.2	P	similarity to aldose reductases
6608_at	212.9	A	similarity to hypothetical protein YJL151c

6609_at 2720.6 P
Ubiquitin-specific protease
6610_at 762.9 P
hypothetical protein
6611_at 823.7 P
Mitochondrial protein that regulates mitochondrial iron accumulation iron accumulation
6612_at 412.1 A
similarity to bovine Graves disease carrier protein
6613_at -164.8 A
questionable ORF
6614_at 1193.7 P
similarity to hypothetical S. pombe protein
6615_at 1246.7 P
Protein with homology to mammalian Nup107p
6616_at 61.8 A
hypothetical protein
6617_at -405.9 A
weak similarity to Rhizobium nodulation protein nodG
6573_at 192.4 A
similarity to hypothetical protein YDR425w
6574_at 2061.2 P
similarity to C-terminus of human TRP-185 protein
6575_at 1423.0 P
Component of the exosome 3->5 exoribonuclease complex with Rrp4p, Rrp41p, Rrp43p and Dis3p (Rrp44p).
6576_at 1142.1 P
hypothetical protein
6577_at 263.1 A
strong similarity to thiamine-repressed protein Thi4p
6578_at 596.0 P
serine-threonine kinase, subunit of transcription factor TFIIK, a subcomplex of TFIIH
6579_at -135.8 A
cox1 pre-mRNA splicing factor
6580_at -145.0 A
Homeobox-domain containing protein which is a positive regulator of PHO5 and other genes
6581_at 277.7 A
protein of unknown function
6582_at 141.6 A
similarity to H.influenzae sialoglycoprotease (gcp)
6583_at 1712.7 P
UDP-N-acetylglucosamine pyrophosphorylase
6584_at 870.3 P
largest and catalytic subunit of DNA polymerase III (delta)
6585_at 232.3 A
protein kinase
6586_at 4154.9 P
similarity to E.coli arsenical pump-driving ATPase
6587_at 1475.4 P
weak similarity to myosin heavy chain proteins
6588_at 464.7 A
hypothetical protein
6589_at 6103.8 P
Subunit of the regulatory particle of the proteasome
6590_at 246.2 A
questionable ORF
6591_at 5869.1 P

dolichyl phosphate-D-mannose:protein O-D-mannosyltransferase
6592_at 113.4 A
questionable ORF
6593_at 605.4 P
dolichyl phosphate-D-mannose:protein O-D-mannosyltransferase
6594_at 1372.9 P
Signal recognition particle subunit
6550_at 316.2 A
weak similarity to mouse FAF1 protein
6551_at 1682.0 P
beta subunit of farnesyltransferase
6552_at 1019.4 P
hypothetical protein
6553_at 851.9 P
Suppressor of thermosensitive mutations in the DNA polymerase delta gene
6554_at -373.3 A
Living Under Cap-binding complex expression
6555_at 6742.8 P
similarity to hypothetical Synechocystis protein
6556_at -250.8 A
strong similarity to NADH dehydrogenase (ubiquinone)
6557_at 12221.1 P
suppressor of the cold-sensitive snRNP biogenesis mutant brr1-1
6558_i_at 43027.1 P
Ribosomal protein S16B (rp61R)
6559_f_at 43085.4 P
Ribosomal protein S16B (rp61R)
6560_at 17954.9 P
Ribosomal protein L13A
6561_at 58584.9 P
Acidic ribosomal protein P1A (YP1alpha) (A1)
6562_at 924.5 P
positive regulatory factor with thiamin pyrophosphate-binding motif for thiamin metabolism
6563_at 449.9 P
MDS1 related protein kinase
6564_at 68.7 A
MDS1 related protein kinase
6565_at 1855.1 P
malate dehydrogenase
6566_at 434.5 P
Required for the vacuolar morphogenesis in yeast
6567_at 495.6 P
hypothetical protein
6568_f_at 67631.8 P
Ribosomal protein L31A (L34A) (YL28)
6569_at 88599.2 P
Ribosomal protein L31A (L34A) (YL28)
6570_at 698.6 A
weak similarity to spindle pole body protein NUF1
6571_at 670.4 P
weak similarity to Cyprinus carpio calcium channel protein
6572_at 3048.1 P
weak similarity to hypothetical protein YMR040w
6527_at 417.0 A
questionable ORF
6528_at 3379.0 P

Bromodomain protein, homolog of Bdf1
6529_at 138.4 A
translational activator of cytochrome b
6530_at 117.3 A
questionable ORF
6531_at 1306.6 P
Subunit VIIa of cytochrome c oxidase
6532_at 6191.9 P
Mitochondrial form of NADP-specific isocitrate dehydrogenase
6533_at 677.6 P
40 kDa farnesylated protein associated with peroxisomes
6534_at 2007.0 P
ubiquitin-conjugating enzyme
6535_at 1216.7 P
weak similarity to human estrogen-responsive finger protein
6536_at 282.0 A
questionable ORF
6537_f_at 48159.2 P
Ribosomal protein S29B (S36B) (YS29)
6538_at 4263.9 P
similarity to C.elegans hypothetical protein
6539_at 202.2 A
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 1075.6 A
Integrin analogue gene
6541_at 241.7 A
hypothetical protein
6542_at 2060.3 P
transcription factor
6543_at 37011.3 P
mannose-1-phosphate guanyltransferase, GDP-mannose pyrophosphorylase
6544_at 485.1 P
hypothetical protein
6545_at 958.2 P
hypothetical protein
6546_at 2465.2 P
putative 1-acyl-sn-gylcerol-3-phosphate acyl transferase
6547_at 1850.0 P
Protein homologous to human La (SS-B) autoantigen
6548_at 563.4 A
questionable ORF
6549_at 310.7 A
KRE9 homolog
6504_at 862.6 P
SIT4 suppress mutations in DBF2
6505_at 2452.4 P
hypothetical protein
6506_at 1271.6 P
homologous to Yml37p, component of the 37 S subunit of mitochondrial ribosomes
6507_at 440.9 P
FAD synthetase
6508_at 278.8 A
Necessary for the stability and\/or processing of some large mitochondrial transcripts
6509_at 373.3 P

snRNA-associated protein
6510_at 847.8 P
regulator of silent mating loci
6511_at 275.6 A
questionable ORF
6512_at 1775.4 P
N-terminal acetyltransferase
6513_at 4903.9 P
questionable ORF
6514_at 1478.6 P
similarity to mucin proteins
6515_at 150.0 A
strong similarity to glucan 1,4-alpha-glucosidase
6516_at 744.1 P
strong similarity to RIB2 protein
6517_at 856.6 P
G-protein coupled receptor
6518_at -297.0 A
questionable ORF
6519_at 886.2 P
similarity to H.influenzae hypothetical protein HI0174
6520_at 111.8 A
questionable ORF
6521_at 1369.1 P
DEAD box protein 10
6522_at 715.1 P
RNA splicing factor
6523_at 7194.0 P
actin-related protein
6524_at 232.7 A
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 564.1 P
hypothetical protein
6526_at 198.4 A
questionable ORF
6482_at 911.4 P
ser/thr protein kinase of the DEAD/DEAH box family
6483_at 413.9 A
strong similarity to acid phosphatase
6484_at -7.2 A
questionable ORF
6485_at 3175.3 P
glycerol-3-phosphate dehydrogenase
6486_at 485.5 P
Similar to GPM1 (phosphoglycerate mutase)
6487_at 3981.9 P
involved in ubiquitin degradation pathway
6488_at 1032.0 P
similarity to Osh1p
6489_at 308.8 A
p24 protein involved in membrane trafficking
6490_at 750.7 P
serine\/threonine protein kinase

6491_at	-13.3	A	questionable ORF
6492_at	4840.5	P	similarity to rat synaptic glycoprotein SC2
6493_at	14215.8	P	nucleolar protein, homologous to mammalian fibrillarin
6494_at	1105.8	A	Protein involved in hexose metabolism
6495_at	4671.6	P	strong similarity to hypothetical protein YBR016w and YDR210w
6496_at	57.5	A	questionable ORF
6497_at	962.1	P	similarity to hypothetical protein YBR014c and glutaredoxins
6498_at	494.8	P	questionable ORF
6499_at	848.6	P	subunit of the anaphase promoting complex (APC)
6500_at	3751.2	P	Probable 26S protease subunit and member of CDC48\/PAS1\/SEC18 family of ATPases
6501_at	561.4	P	serine-threonine protein phosphatase
6502_at	592.0	P	Stoichiometric member of mediator complex
6503_at	2111.1	P	ATP synthase delta subunit
6459_at	385.1	A	Mitotic omosome Determinant\; similar to S. pombe RAD21\; may function in chromosome morphogenesis from S phase through mitosis
6460_at	933.8	P	HMG1-box containing protein
6461_at	267.4	A	similarity to hypothetical protein YFR048w, YDR282c and S.pombe hypothetical protein SPAC12G12.14
6462_at	1339.8	P	neutral trehalase (alpha,alpha-trehalase)
6463_at	12599.3	P	Yeast Ran Binder #1\; suppressor of FUS1\; homolog of mouse HTF9a and human RanBP1
6464_at	199.9	A	strong similarity to hypothetical protein YBR005w
6465_at	685.3	P	RecA homolog (similar to DMC1, RAD51, and RAD55), interacts with Rad 55p by two-hybrid analysis
6466_at	398.8	A	required for sorting of Mod5p
6467_at	455.7	A	gene dosage suppressors of the conditional growth defect of several temperature-sensitive A kinase mutants
6468_at	1037.9	P	n-(5 -phosphoribosyl)-anthranilate isomerase
6469_at	393.3	A	questionable ORF
6470_at	40.3	A	galactokinase
6471_at	-175.6	A	hypothetical protein
6472_at	13443.7	P	ABC transporter

6473_i_at 34396.4 P
Ribosomal protein L4B (L2B) (rp2) (YL2)
6474_at 487.5 P
similarity to human hypothetical KIAA0186 protein
6475_at 38.4 A
weak similarity to chicken neurofilament triplet M protein
6476_at -40.3 A
hypothetical protein
6477_at 334.3 A
hypothetical protein
6478_at 770.5 P
Shows homology to basic leucine zipper family of transcription factors
6479_at -12.9 A
strong similarity to hypothetical protein YBR042c
6480_at 1308.3 P
glycine cleavage T protein (T subunit of glycine decarboxylase complex
6481_at 87.7 A
weak similarity to uridine kinases and phosphoribulokinases
6436_at 737.8 P
DEAD-box protein, putative RNA helicase
6437_at -31.3 A
cik1 suppressor
6438_at 15048.7 P
seryl-tRNA synthetase
6439_at 36.7 A
hypothetical protein
6440_at 821.7 P
strong similarity to DNA-binding protein Reb1p
6441_at 1139.8 P
Loss Upsets Vacuole
6442_at 655.0 P
regulatory subunit for protein phosphatase Glc7p
6443_at 282.8 A
hypothetical protein
6444_at 318.6 A
Protein involved in the same pathway as Rad26p, has beta-transducin (WD-40) repeats
6445_at 515.0 A
hypothetical protein
6446_at 7670.2 P
strong similarity to S.pombe obr1
6447_at 13577.3 P
strong similarity to putative heat shock protein YRO2
6448_at 1262.4 P
Transcriptional activator of lysine pathway genes with 2-aminoadipate semialdehyde as co-inducer\; saccharopine reductase synthesis
6449_at 470.7 M
identified by SAGE expression analysis
6450_at 6369.4 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 1374.7 P
similarity to enoyl CoA hydratase
6452_at 24057.1 P
lysyl-tRNA synthetase
6453_at 2376.8 P

P-type ATPase involved in Na+ efflux
6454_g_at 5041.5 P
P-type ATPase involved in Na+ efflux
6455_s_at 2646.3 P
plasma membrane protein\; putative Na+ pump\; P-type ATPase
6456_at 444.4 P
weak similarity to bacterial ribosomal S10 proteins
6457_at -94.1 A
hypothetical protein
6458_at 224.9 A
Suppressor of SNf
6413_at 1107.4 P
Coproporphyrinogen III oxidase
6414_at 1889.4 P
strong similarity to S.acidocaldarius transcription elongation factor tfs
6415_at 1854.8 P
Valine transporter
6416_at 4270.1 P
uroporphyrinogen decarboxylase
6417_at 185.2 A
questionable ORF
6418_at 654.1 A
similarity to C.elegans K06H7.3 protein
6419_at 150570.5 P
triosephosphate isomerase
6420_at 1528.8 P
similarity to hypothetical A. thaliana protein BAC F7G19
6421_at 237.6 A
cyclin-like kinase required for late nuclear division
6422_at 127.1 A
questionable ORF
6423_at 352.7 A
ubiquitin-conjugating enzyme, E2
6424_at 4494.6 P
strong similarity to SPS2 protein
6425_at 1022.4 P
hypothetical protein
6426_at 261.2 A
weak similarity to L.lactis mleR protein
6427_at 187.7 A
TriGlyceride Lipase
6428_at 328.0 A
ubiquitin-conjugating enzyme
6429_at 2432.4 P
similarity to mouse putative CCAAT binding factor CBF1 and CBF2
6430_at 1206.9 P
similarity to E.coli modF and photorepair protein phrA
6431_at 4689.6 P
Probable component of serine palmitoyltransferase, which catalyzes the first step in biosynthesis of long-chain sphingolipids
6432_at 1241.8 P
weak similarity to glia maturation factor beta
6433_at 35105.4 P
Ribosomal protein S13 (S27a) (YS15)
6434_at 78.6 A
hypothetical protein

6435_at	560.9	A	similarity to hypothetical protein YER139c
6391_at	137.4	A	similarity to YNL099c
6392_at	1000.8	P	involved in genome stability
6393_at	79.8	A	ubiquitin isopeptidase
6394_at	-5.4	A	hypothetical protein
6395_at	2248.0	P	similarity to O.aries arylalkylamine N-acetyltransferase
6396_at	2078.9	P	inositolphosphotransferase 1
6397_at	630.5	P	component of SWI\/SNF global transcription activator complex
6398_at	1439.2	P	Trehalose-6-phosphate phosphatase
6399_at	421.3	A	protein phosphatase type 2A
6400_at	417.1	A	RecA homolog (related to DMC1, RAD51, RAD57), interacts with Rad51p and Rad57p by two-hybrid analysis
6401_at	31003.1	P	putative cell surface glycoprotein
6402_at	75.3	A	Preferential Use of Neither donor locus during mating type switching.
6403_at	1006.4	P	cytochrome c oxidase-specific assembly factor
6404_at	387.1	A	vacuolar protein sorting
6405_at	1721.8	P	Asparagine and serine-rich protein
6406_at	221.8	A	Involved in telemere length regulation, may be functional in telemere metabolism during late S phase
6407_at	2344.0	P	similarity to hypothetical S.pombe protein
6408_at	1105.3	P	similarity to hypothetical C.elegans protein
6409_at	691.3	P	coordinates regulation of alpha-factor receptor signalling and induction of morphogenesis during conjugation
6410_at	11910.9	P	endoplasmic reticulum protein that is part of the Sec61 trimeric complex and the Ssh1 trimeric complex
6411_at	1520.5	P	involved in processing rRNA precursor species to mature rRNAs
6412_at	11.4	M	involved in 3 splice site choices and 2nd step of splicing
6368_at	406.0	P	weak similarity to Streptococcus transposase
6369_at	781.8	P	weak similarity to YRO2 protein
6370_at	3568.6	P	strong similarity to human RNase L inhibitor and M.jannaschii ABC transporter protein
6371_at	2317.2	P	ubiquitin-conjugating enzyme

6372_at 1280.9 P
similarity to P.falciparum ATPase 2
6373_g_at 4828.9 P
similarity to P.falciparum ATPase 2
6374_at 2375.3 P
questionable ORF
6375_at 227.1 A
hypothetical protein
6376_at 733.3 P
putative zinc finger protein
6377_at 1445.4 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 2149.7 P
similarity to Legionella glutaredoxin-like protein
6379_at 7183.1 P
Homolog of mammalian 14-3-3 proteins
6380_at 1263.0 P
similarity to Dictyostelium development-specific membrane protein
6381_at 2034.6 P
weak similarity to proliferation-associated protein
6382_at 8.5 A
hypothetical protein
6383_at 652.0 P
Protein of the pheromone pathway
6384_at 343.3 A
hypothetical protein
6385_at 665.5 A
similarity to mouse hypothetical protein
6386_at 73.7 A
Actin-related protein
6387_at 240.7 A
strong similarity to Emp70 protein
6388_at -103.3 A
Probably has role late in meiosis following DNA replication
6389_at 427.5 A
similarity to Mpa43p
6390_at 446.7 P
DNA replication fork blocking protein
6346_at 286.3 A
strong similarity to alanine transaminase
6347_at -55.7 A
questionable ORF
6348_at 382.0 A
42-kDa nuclear protein
6349_at 37.3 A
questionable ORF
6350_at 554.4 P
similarity to bacterial ribosomal L34 proteins
6351_at 686.9 P
similarity to bacterial ribosomal L1 proteins
6352_at 479.1 P
similarity to mouse ligatin, a trafficking receptor for phosphoglycoproteins
6353_at 83.2 A
subunit of the anaphase promoting complex (APC)
6354_at 1835.9 P

similarity to B.subtilis tetracyclin resistance

6355_at 1409.6 P

N2,N2-dimethylguanosine-specific tRNA methyltransferase

6356_at 524.0 P

weak similarity to YNC2beta protein

6357_at 867.5 P

Serine\/threonine protein kinase

6358_at 30.1 A

helix-loop-helix protein

6359_at -179.5 A

hypothetical protein

6360_at -109.0 A

ExtraCellular Mutant

6361_at 11.0 A

similarity to hypothetical protein YLR246w and YOL003c

6362_at 7207.3 P

pentafunctional arom polypeptide (contains: 3-dehydroquinate synthase, 3-dehydroquinate dehydratase (3-dehydroquinase), shikimate 5-dehydrogenase, shikimate kinase, and epsp synthase)

6363_at 1048.6 P

weak similarity to Sec27p, YMR131c and human retinoblastoma-binding protein

6364_at 5871.4 P

fibrim homolog (actin-filament bundling protein)

6365_at 215.1 A

weak similarity to sea urchin myosin heavy chain

6366_at 20.8 A

similarity to hypothetical protein YJL149w

6367_at -27.4 A

strong similarity to hypothetical protein YLR108c

6323_at 47115.4 P

questionable ORF

6324_g_at 26197.9 P

questionable ORF

6325_at 1706.0 P

Metal resistance protein with similarity to human cystic fibrosis protein CFTR and multidrug resistance proteins

6326_at 60.6 A

questionable ORF

6327_at 1281.5 P

Reduced growth phenotype

6328_at 212.7 A

Hyperrecombination protein that suppresses intrachromosomal excision recombination

6329_at 3131.3 P

ubiquitin-like protein

6330_at 1911.3 P

ubiquitin-like protein

6331_at 1673.7 P

weak similarity H.influenzae protoporphyrinogen oxidase (hemK) homolog

6332_at 678.9 P

hypothetical protein

6333_at 169.8 A

Member of beta-transducin-related (WD-40) protein family

6334_at 1591.0 P

mating-type regulation protein

6335_at 5648.2 P

aspartyl protease related to Yap3p

6336_at 269.7 A

TFIID subunit
6337_at 411.6 P
transcriptional activator
6338_at 615.9 P
Ethanolamine Kinase
6339_at 1798.5 P
dihydrolipoyl transsuccinylase component of alpha-ketoglutarate dehydrogenase complex in mitochondria
6340_at -107.0 A
questionable ORF
6341_at 1367.6 P
Protein with variable number of tandem repeats of a 64 amino-acid polypeptide, potential Ca2+-binding site, and pleckstrin homology domain
6342_at 230.4 A
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 2208.2 P
weak similarity to C.elegans hypothetical protein CET26E3
6344_at 2172.8 P
hypothetical protein
6345_at 102432.5 P
questionable ORF
6300_g_at 52810.0 P
questionable ORF
6301_at 33620.6 P
cyclophilin peptidyl-prolyl cis-trans isomerase
6302_at 3610.8 P
RNA polymerase I subunit A14
6303_at 1992.7 A
questionable ORF
6304_at 8102.4 P
aspartic beta semi-aldehyde dehydrogenase
6305_at 710.3 P
Leucine permease transcriptional regulator
6306_at 165.1 A
Ssy1p controls expression of several transporter genes, including BAP2, TAT1, PTR2 and YDR046c
6307_at 1047.7 P
protein phosphatase Two C-Interacting protein
6308_at 536.1 P
Nap1p-binding protein
6309_at 1909.1 A
weak similarity to S.pombe hypothetical protein
6310_at 929.8 P
Hydrophilic protein involved at the late stage of secretion
6311_at 1512.0 P
weak similarity to hypothetical C.elegans protein
6312_at 1112.3 P
107 kDa component of the Exocyst complex\; required for exocytosis.
6313_at 1908.6 P
TFIID subunit
6314_at 3085.4 P
Cell cycle protein necessary for passage through START
6315_at 653.5 A
Binds Sin3p in two-hybrid assay
6316_at 6740.6 P
Guanine nucleotide exchange protein for ARF
6317_at 1202.5 P

Similar to HSP26\; expression is regulated by stress conditions
6318_at 4304.0 P
putative translation factor
6319_at 426.1 A
Regulator of arginine-responsive genes with ARG80 and ARG81
6320_at 5182.4 P
Non-histone protein
6321_at 307.4 A
similarity to S.pombe hypothetical protein SPAC2F7.15
6322_at 717.0 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 3814.1 P
ubiquitin-conjugating enzyme
6279_at 2397.3 P
succinate dehydrogenase membrane anchor subunit
6280_at 269.1 A
hypothetical protein
6281_at -199.5 A
hypothetical protein
6282_at 710.9 P
Sister chromatid cohesion protein
6283_at 336.1 A
Involved in silencing at telomeres, HML and HMR
6284_at 1267.5 P
Protein that affects bud emergence, intrachromosomal recombination, and nuclear division
6285_at 129.2 A
weak similarity to thioredoxin
6286_at 413.2 A
Aip Three Complex\; interacts with AIP3, localized to the nucleus
6287_at 307.8 A
strong similarity to Msf1p
6288_at 399.5 P
hypothetical protein
6289_at 386.5 A
questionable ORF
6290_at 3314.2 P
Cytoplasmic chaperonin of the Cct ring complex (previously called TCP1 or TRiC), distantly related to Tcp1p and to Hsp60
6291_at 940.2 P
Hydrophilic suppressor of ypt1 involved in vesicle trafficking between ER and Golgi
6292_at 3070.7 P
strong similarity to TATA-binding protein-interacting protein 49 - rat
6293_at 352.8 A
Homolog of SIR2
6294_at 480.3 A
nucleoporin
6295_at 261.4 A
questionable ORF
6296_at 2587.1 P
Mitochondrial RNA helicase of the DEAD box family
6297_at 521.7 A
RNA-binding protein involved in cleavage step of mRNA 3 -end formation, prior to polyadenylation
6298_at 1212.2 P
similarity to C.elegans hypothetical protein T05G5.5

6299_at 726.1 P
cytochrome b translational activator
6255_at 913.6 P
hypothetical protein

6256_at 222.8 A
questionable ORF
6257_at 742.5 P
similarity to hypothetical protein YLR238w
6258_at 999.8 P
component of spindle pole
6259_at 315.1 A
hypothetical protein
6260_at 133.5 A
questionable ORF
6261_at 1039.7 P
Involved in ubiquinone biosynthesis
6262_at 520.5 P
similarity to A.eutrophus cation efflux system membrane protein czcD, rat zinc transport protein ZnT-1 and Cot1p
6263_at 534.5 P
EST1-like bcy1 Suppressor
6264_at 456.9 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 1826.1 P
Phosphatidylinositol 4-phosphate kinase
6266_at 1354.5 P
questionable ORF
6267_at 5385.8 P
strong similarity to hypothetical protein YBR016w
6268_at 2723.5 P
Translation initiation factor eIF-2B epsilon subunit
6269_at 9384.4 P
chaperonin subunit alpha
6270_at 71.0 A
regulatory protein involved in control of sterol uptake
6271_at 5223.2 P
similarity to hypothetical protein YNL281w
6272_at 185.0 A
hypothetical protein
6273_at 107.4 A
positive transcriptional regulator of ADH2 and peroxisomal protein genes
6274_at 405.2 A
cell cycle arrest protein
6275_at 88.3 A
Septin-related protein expressed during sporulation
6276_at 100.0 A
hypothetical protein
6277_at 175.2 A
questionable ORF
6232_at 391.3 A
weak similarity to the beta subunit of an ER luminal alpha-glucosidase from mouse
6233_at 883.5 P
strong similarity to hypothetical protein YLR225c

6234_at	169.7	A	similarity to Ifh1p
6235_at	10259.6	P	Histone H2B (HTB1 and HTB2 code for nearly identical proteins)
6236_i_at	33666.9	P	Histone H2A (HTA1 and HTA2 code for nearly identical proteins)
6237_at	23144.2	P	cytosolic adenylate kinase
6238_at	279.3	A	regulator of silent mating loci
6239_at	575.8	P	Component of pre-mRNA cleavage and polyadenylation factor I, interacts with Rna14p and Rna15p
6240_at	908.1	P	hypothetical protein
6241_at	-44.8	A	questionable ORF
6242_at	163.2	A	hypothetical protein
6243_at	3255.2	P	5-aminolevulinate synthase
6244_at	19391.8	P	similarity to hypothetical protein YDL204w
6245_at	12414.7	P	homoaconitase
6246_at	533.8	A	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	310.7	A	similarity to hypothetical A. thaliana protein
6248_at	85.3	A	Mitochondrial ribosomal protein MRPL7 (YmL7)
6249_at	6179.7	P	encodes a subunit of yeast coatomer
6250_at	1372.5	P	hypothetical protein
6251_at	74.6	A	Snurp = Small nuclear ribonucleoprotein particle of MW 56 kDa. Associated with the U1 snRNP\; no counterpart in mammalian U1 snRNP. Serine-rich.
6252_at	-242.8	A	questionable ORF
6253_at	473.3	P	putative amidase
6254_at	266.9	A	Required for the first step of splicing in vitro
6209_at	453.6	P	69-kDa protein containing tetratricopeptide repeat (TPR)
6210_at	1762.3	P	galactosyltransferase
6211_at	974.2	P	involved in targeting and fusion of ER to golgi transport vesicles
6212_at	35.5	A	strong similarity to Sks1p
6213_at	1285.5	P	strong similarity to E.coli thermoresistant gluconokinase
6214_at	79.7	A	weak similarity to cytochrome b

6215_at 88.9 A
hypothetical protein
6216_at 1661.4 P
coiled-coil protein multicopy suppressor of loss of PP2A
6217_at 154.1 A
Negative effect on expression of several genes transcribed by RNA polymerase II\; BTF3 homolog
6218_at -2.4 A
zinc finger DNA binding factor, transcriptional regulator of sulfur amino acid metabolism, highly homologous to Met31p
6219_at 164.4 A
Protein necessary for stability of ARS-CEN plasmids\; suggested to be required for kinetochore function
6220_at 396.0 A
weak similarity to hypothetical S.pombe hypothetical protein SPBC29A3
6221_at -111.2 A
catalase A
6222_at 387.9 A
Transcription regulator
6223_at 1922.3 P
Mitochondrial heat shock protein 78 kDa
6224_at 121.8 A
bZIP protein
6225_at 512.9 A
hypothetical protein
6226_at 2043.0 P
Exo-1,3-b-glucanase
6227_at 856.8 P
hypothetical protein
6228_at 286.4 A
DNA-damage inducible gene
6229_at 1299.7 P
Ankyrin repeat-containing protein
6230_at 190.2 A
C3HC4 zinc-binding integral peroxisomal membrane protein
6231_at 879.9 P
similarity to hypothetical C.elegans protein
6187_at 1604.6 P
weak similarity to human TAFII100 and other WD-40 repeat containing proteins
6188_at 221.3 A
mitochondrial tryptophanyl-tRNA synthetase
6189_at 14.9 A
questionable ORF
6190_at 1147.7 P
Copper-transporting P-type ATPase with similarity to human Menkes and Wilsons genes
6191_at 617.5 P
questionable ORF
6192_at 798.2 P
Cytoplasmic glyoxylase-II
6193_at -0.9 A
weak similarity to YOR042w
6194_at -52.0 A
hypothetical protein
6195_at 370.0 A
weak similarity to YOR042w
6196_at 21919.5 P
strong similarity to Hordeum vulgare blt101 protein
6197_at 211.6 A

Protein is 61\% identical to Msn3p
6198_at -28.3 A
hypothetical protein
6199_at 126.8 A
hypothetical protein
6200_at 1266.6 P
Putative 3 ->5 exoribonuclease\; component of exosome complex of 3 ->5 exonucleases
6201_at 1075.3 P
hypothetical protein
6202_at 289.5 A
similarity to hypothetical protein YDL001w, YFR048w and S.pombe hypothetical protein SPAC12G12.14
6203_at 507.6 P
eukaryotic initiation factor 2 alpha (eIF2-alpha) kinase
6204_at 1233.9 P
Diacylglycerol Pyrophosphate Phosphatase
6205_at 427.5 A
Synaptonemal complex protein, component of the central element
6206_at 447.8 A
hypothetical protein
6207_at 642.6 P
similarity to inositolmonophosphatases
6208_at 99.6 A
hypothetical protein
6163_at 315.7 A
hypothetical protein
6164_at -1.9 A
questionable ORF
6165_at 1027.0 P
similarity to B.subtilis helicases
6166_at 1406.1 P
signal recognition particle receptor - alpha subunit
6167_at 1968.3 P
putative protein phosphatase
6168_at 4007.6 P
dihydrosphingosine phosphate lyase (also known as sphingosine phosphate lyase)
6169_at 214.5 A
weak similarity to Uso1p, YPR179c and fruit fly tropomyosin
6170_at 925.3 P
hypothetical protein
6171_at 1678.7 P
Syringomycin response protein 2
6172_at 1493.6 P
ATP synthase subunit 5\; oligomycin sensitivity-conferring protein
6173_at 1153.0 P
involved in protein transport step at the Brefeldin A blocks
6174_at 1848.1 P
gamma-glutamyl kinase
6175_at 1633.0 P
Component of pre-mRNA cleavage factor II (CFII)\; 150-kDa protein associated with polyadenylation factor 1 (PF I)
6176_at 911.0 M
weak similarity to human GPI-anchor biosynthesis protein
6177_at 872.2 P
similarity to transcriptional regulator proteins
6178_at 3395.9 P
Cyclophilin D, Peptidyl-prolyl cis-trans isomerase D

6179_at 668.1 P
Yeast member of the Histidine Triad protein family (HIT)
6180_i_at 276.5 A
Yeast member of the Histidine Triad protein family (HIT)
6181_r_at -196.6 A
Yeast member of the Histidine Triad protein family (HIT)
6182_f_at -614.6 A
Yeast member of the Histidine Triad protein family (HIT)
6183_at 475.0 P
weak similarity to S.pombe hypothetical protein SPAC6F6
6184_at 1787.4 P
similarity to Pmt1p, Pmt2p, Pmt3p and Pmt5p
6185_at 625.2 P
RNA polymerase II holoenzyme component
6186_at 3766.4 P
GTPase-interacting component 2
6140_at 2526.4 P
Suppresor of mar1-1 (sir2) mutation
6141_at 452.4 A
Component of transcription initiation factor IIb, 75 kDa subunit
6142_i_at 9895.8 P
high copy suppressor of G beta subunit temperature sensitive mutation
6143_f_at 10112.9 P
high copy suppressor of G beta subunit temperature sensitive mutation
6144_at 111.3 A
Phosphatidylinositol(3)-phosphate binding
6145_at 139.3 A
weak similarity to hypothetical S.pombe protein
6146_at 35.7 A
hypothetical protein
6147_at 856.4 P
hypothetical protein
6148_at 280.4 A
hypothetical protein
6149_at 306.4 A
Involved in minichromosome maintenance
6150_at 777.5 P
hypothetical protein
6151_at 529.8 P
similarity to hypothetical S. pombe protein and weak similarity to bovine auxilin
6152_at 10671.8 P
Asparaginase I, intracellular isozyme
6153_at 850.6 P
Mitochondrial ribosomal protein MRPL35 (YmL35)
6154_at 3398.7 A
subunit e of mitochondrial F1F0-ATPase
6155_at 68.3 A
cytosolic and peripheral membrane protein with three zinc fingers\; cysteine rich regions of amino acids are essential for function
6156_at 2176.6 P
weak similarity to beta transducin from S. pombe and other WD-40 repeat containing proteins
6157_at 1122.8 P
weak similarity to S.pombe hypothetical protein SPAC1B9
6158_at 253.3 A
strong similarity to YHR080c, similarity to YFL042c and YLR072w
6159_at 356.8 A

questionable ORF
6160_at 3343.8 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. SculCdc4 complexes transfer ubiquitin to phosphorylated Sic1p, and substrate recognition is thought to involve the Cdc4p and Skp1p subunits. Following the SculCdc4-mediated monoubiquitination of Sic1p, a polyubiquitin chain is added, andubiquitinated Sic1p is then degraded by the 26S proteosome.
6161_at 795.7 P
48-kDa peroxisomal integral membrane protein
6162_at 563.5 A
similarity to hypothetical S. pombe protein
6117_at 927.6 P
Protein involved in the attachment of glycosylphosphatidylinositol (GPI) anchors to proteins
6118_at 312.5 A
similarity to E.coli hypothetical protein and weak similarity to RNA helicase MSS116 / YDR194c
6119_at 563.6 P
similarity to hypothetical S. pombe protein
6120_at 597.7 P
similarity to nuclear Sth1p, Snf2p and related proteins
6121_at 4095.2 P
Multicopy suppressor of snf1 mutation
6122_at 503.6 P
weak similarity to B.subtilis hypothetical protein X
6123_at 669.3 P
Mitochondrial ribosomal protein MRPS28 (E. coli S15)
6124_at 441.6 A
similarity to Erc1p
6125_at 1175.0 P
weak similarity to hypothetical protein YOR004w
6126_at 357.8 A
questionable ORF
6127_at 27091.2 P
strong similarity to arginine-tRNA ligase
6128_f_at 14471.3 P
Hexose transporter
6129_f_at 12311.4 P
Hexose transporter
6130_at -501.6 A
hypothetical protein
6131_at 47118.7 P
High-affinity glucose transporter
6132_at 674.5 P
similarity to hypothetical S.pombe protein
6133_at 912.2 P
37 kDa mitochondrial ribosomal protein
6134_at 1490.5 P
similarity to hypothetical protein YHR097c
6135_at 2348.0 P
GPI-anchored aspartic protease
6136_at 189.2 A
protein of unknown function
6137_at 1064.4 P
required for bud growth
6138_at 268.3 A
weak similarity to hypothetical proteins YOL092w, YBR147w and YMR010w

6139_at	8948.9	P	Thioredoxin reductase
6095_at	650.5	A	anthranilate phosphoribosyl transferase
6096_at	329.8	A	questionable ORF
6097_at	559.5	A	component of the spindle pole body that interacts with Spc42p, calmodulin, and a 35 kDa protein
6098_at	1274.9	P	hypothetical protein
6099_at	505.8	A	strong similarity to hypothetical protein YHR108w and weak similarity to signal transducing adaptor from mouse and man
6100_at	603.6	A	hypothetical protein
6101_at	-393.2	A	questionable ORF
6102_at	887.6	P	hypothetical protein
6103_at	495.8	A	91 kDa tau91 subunit of transcription factor IIIC (TFIIIC)
6104_at	182.0	A	Establishes Silent omatin
6105_at	2422.8	P	Homolog of DSS1\; similar to hypothetical protein from S. pombe
6106_at	449.2	P	Member of the beta transducin family
6107_at	2496.9	P	weak similarity to Streptococcus M protein
6108_at	137.3	A	similarity to YOL106w and YER181c
6109_at	1209.9	P	hypothetical protein
6110_at	2393.6	P	homologous to the aldo-keto reductase protein family
6111_at	218.6	A	DNA repair protein
6112_at	730.5	P	hypothetical protein
6113_at	213.7	A	similarity to chitinases
6114_at	1084.0	P	similarity to hypothetical S. pombe protein
6115_at	2149.5	P	strong similarity to human BDR-1 protein and other calcium binding proteins
6116_at	-44.2	A	similarity to hypothetical A. thaliana protein BAC F21M12
6072_at	429.0	P	Mitochondrial protein of the CDC48\/PAS1\/SEC18 ATPase family, required for expression of functional Rieske iron-sulfur protein
6073_at	810.7	P	adrenodoxin oxidoreductase homolog
6074_at	740.1	P	ATP synthase subunit f
6075_at	826.6	P	Sm-like protein

6076_at	321.8	A	Contains a Rho-GAP domain and two LIM domains. Has strong similarity to Rga1p. Has some similarity to all known Rho-GAPs.
6077_at	5196.8	P	similarity to Pdc6p, Thi3p and to pyruvate decarboxylases
6078_at	3866.8	P	Nuclear RNA-binding RNA annealing protein
6079_at	3456.8	P	Nuclear RNA-binding RNA annealing protein
6080_at	81004.4	P	Ribosomal protein P2B (YP2beta) (L45)
6081_at	-37.4	A	weak similarity to S.pombe paramyosin
6082_at	1480.9	P	strong similarity to Y.lipolytica GPR1 gene
6083_at	177.8	A	MMS and UV Sensitive\; Mus81p and Rad54p are found together in a complex from whole-cell extracts
6084_at	343.4	P	similarity to Itr1p and Itr2p and E.coli araE
6085_at	5140.9	P	involved in endocytosis
6086_at	396.0	A	GTPase activating protein (GAP) for RHO1
6087_at	766.4	P	Protein with homology to mammalian ubiquitin activating (E1) enzyme
6088_at	478.4	P	strong similarity to hypothetical protein YOR013w
6089_at	960.3	P	transcription factor, member of the histone acetyltransferase SAGA complex
6090_at	125.1	A	mRNA (identified by a library screen) that causes growth arrest when overexpressed
6091_at	1393.7	P	probable 26S protease subunit and member of the CDC48\/PAS1\/SEC18 family of ATPases
6092_at	2122.1	P	Sxm1p
6093_at	-16.4	A	hypothetical protein
6094_at	1113.6	P	repressor of class II transcription
6049_at	2338.2	P	similarity to human KIAA0007 gene
6050_at	4218.1	P	Hypoxanthine Phosphoribosyltransferase
6051_at	964.8	P	similarity to C. fasciculata inosine-uridine preferring nucleoside hydrolase (EC 3.2.2.1)
6052_at	-34.1	A	Cytochrome P450 56, Dit2p catalyzes oxidation of N-formyl tyrosine to N,N-bisformyl dityrosine in vitro
6053_at	-371.2	A	questionable ORF
6054_at	-153.4	A	first enzyme in dityrosine synthesis in the outer layer of the spore wall pathway converting L-tyrosine to N-formyl-L-tyrosine, expressed late (10-16 hr) in sporulation
6055_at	2800.9	P	dissociable subunit of RNA polymerase II
6056_at	424.1	P	263-amino acid mitochondrial ribosomal large subunit protein\; similar to L23 family of ribosomal proteins

6057_at	313.2	A	probable multidrug resistance transporter
6058_at	1279.8	P	weak similarity to Myo1p
6059_at	2282.2	P	glycinamide ribotide transformylase
6060_at	241.3	A	similarity to Nfi1p
6061_at	1376.2	P	farnesyl cysteine-carboxyl methyltransferase
6062_at	877.1	P	weak similarity to Der1p
6063_at	180.6	A	weak similarity to NADH dehydrogenase
6064_at	1011.2	P	questionable ORF
6065_at	231.6	A	Protein required for retention of luminal ER proteins
6066_at	1062.6	P	strong similarity to bacterial leucyl aminopeptidase
6067_at	861.0	P	SYnthetic lethal with cdcForty
6068_at	1134.5	P	questionable ORF
6069_i_at	37376.1	P	Ribosomal protein L12B (L15B) (YL23)
6070_s_at	33643.8	P	Ribosomal protein L12B (L15B) (YL23)
6071_at	317.7	P	similar to E. coli DinB and S. cerevisiae REV1
6026_at	1113.1	P	Type 1 membrane protein with EF hand motif
6027_at	222.0	A	hypothetical protein
6028_at	593.6	M	SNF1 protein kinase substrate
6029_at	1101.4	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	4359.5	P	putative light chain of dynein
6031_at	263.5	A	similarity to hypothetical protein YDL113c
6032_at	547.1	P	questionable ORF
6033_at	1869.5	P	Subunit of the regulatory particle of the proteasome
6034_at	723.0	P	hypothetical protein
6035_at	7172.7	P	Translation initiation factor 3 p33 subunit
6036_at	1416.6	P	similarity to C.perfringens hypothetical hypA protein
6037_at	360.1	A	questionable ORF
6038_at	4552.6	P	

nuclear shuttling protein with an RNA recognition motif
6039_g_at	21426.0	P
nuclear shuttling protein with an RNA recognition motif
6040_i_at	22052.7	P
questionable ORF
6041_at	1377.6	P
similarity to S.pombe hypothetical protein
6042_at	423.9	A
similarity to YOL141w and hypothetical C.elegans protein
6043_at	153.0	A
serine-threonine phosphatase Z
6044_at	-154.9	A
hypothetical protein
6045_at	319.2	A
strong similarity to hypothetical protein YML018c
6046_at	296.5	A
Loss of rDNA silencing
6047_at	790.3	P
Pachytene CHeckpoint
6048_at	880.1	P
Adenine phosphoribosyltransferase
6003_at	-25.8	A
questionable ORF
6004_at	720.6	P
RNA polymerase II holoenzyme component
6005_at	882.9	P
similarity to hypothetical protein YGL144c and YDL109c
6006_at	114.0	A
questionable ORF
6007_at	94.3	A
ExtraCellular Mutant
6008_at	437.3	P
transcription factor, member of ADA and SAGA, two transcriptional adaptor\/HAT (histone acetyltransferase)complexes
6009_at	824.6	P
hypothetical protein
6010_at	521.1	P
strong similarity to Yox1p
6011_at	1917.3	P
similarity to human sphingomyelin phosphodiesterase
6012_at	158.6	A
strong similarity to thiol-specific antioxidant proteins
6013_at	10409.9	P
guanylate kinase
6014_at	37.3	A
questionable ORF
6015_at	1401.4	P
Na+\/H+ exchanger
6016_at	2398.5	P
hect-domain-containing protein, required for G2\/M transition\; similar to RSP5\; contains motifs typical of protein kinases
6017_at	225.8	A
similarity to hypothetical protein YML034w and YML033w
6018_at	117.6	A
weak similarity to YNL326c
6019_at	258.8	A

TFIIH subunit Tfb3 , contains ring finger motif\; similar to mammalian CAK subunit
6020_r_at 1161.4 A
a-factor mating pheromone precursor
6021_f_at 13.4 A
a-factor mating pheromone precursor
6022_at 951.3 P
Mitochondrial ribosomal protein MRPL28 (YmL28)
6023_at 1169.1 P
Nuclear-localized protein containing zinc finger motifs
6024_at 861.5 P
negative regulator of prp genes
6025_at 3088.9 P
Protein arginine methyltransferase
5980_at 1132.4 P
similarity to ser/thr protein kinase
5981_at 15.0 A
questionable ORF
5982_at 624.8 A
tSNARE that affects a Late Golgi compartment
5983_at 623.1 A
hypothetical protein
5984_at 161.6 A
similarity to chromosome segregation protein Cse1p
5985_at 15019.3 P
Ribosomal protein L27B
5986_at 829.2 P
similarity to P.falciparum 41-2 protein antigen
5987_at 392.5 P
essential splicing factor
5988_at 593.4 P
similarity to C-terminal region of YOR019w
5989_at -171.1 A
hypothetical protein
5990_at 3119.6 P
hypothetical protein
5991_at 1057.6 P
protein serine\/threonine kinase
5992_at 391.6 A
RNAse MRP protein component
5993_at 354.3 A
weak similarity to YHR150w
5994_at 234.1 A
MAP kinase-associated protein
5995_at 1198.8 P
repressible alkaline phosphatase
5996_at 335.9 A
hypothetical protein
5997_at 7231.2 P
alpha-1,2-mannosyltransferase
5998_at 493.1 A
May interact with actin as a component or controller of the assembly or stability of the actin cytoskeleton
5999_at 398.5 A
similarity to trichohyalin
6000_at 792.0 P
weak similarity to Snf7p
6001_at 2519.0 P

3,4-dihydroxy-2-butanone 4-phosphate synthase
6002_at 592.2 P
Protein required in the absence of Cin8p
5958_at 131.0 A
hypothetical protein
5959_at 547.4 P
Ser\/Thr protein kinase
5960_at -22.1 A
questionable ORF
5961_at 4304.2 P
strong similarity to hypothetical protein YOL002c
5962_at 248.3 A
hypothetical protein
5963_at 792.3 P
hypothetical protein
5964_at 102.4 A
Vacuolar sorting protein
5965_at 2215.0 P
similarity to hypothetical human and C.elegans proteins
5966_at 7935.8 P
myo-inositol transporter
5967_at 1177.3 P
membrane glycoprotein, sorted by HDEL retrieval system
5968_at 722.1 P
weak similarity to hypothetical C.elegans protein, M.genitalium peptide chain release factor 1 and YJL149w
5969_at 32840.7 P
60S ribosomal protein L37B (L43) (YL35)
5970_at 19.4 A
similarity to hypothetical protein YLR183c
5971_at 9571.6 P
S-adenosylmethionine synthetase
5972_at 258.2 A
Lipid phosphate phosphatase
5973_at 836.7 P
similarity to hypothetical T.brucei protein
5974_at 402.8 A
high copy suppressor of ts mutations in DNA polymerase alpha
5975_at 567.0 P
similarity to FET3, YFL041w and F.floriforme diphenol oxidase
5976_at 2287.8 P
putative serine\/threonine kinase
5977_at 7441.7 P
high-affinity glutamine permease
5978_at 155.2 A
questionable ORF
5979_at 3748.0 P
may be involved in function and\/or structure of the eukaryotic kinetochore
5935_at 527.4 P
weak similarity to C. elegans protein F25H9.7 and to the human complement 3 precursor
5936_at 945.5 P
questionable ORF
5937_at 2143.5 P
Glutaredoxin (thioltransferase) (glutathione reductase)
5938_at 260.1 A
strong similarity to hypothetical protein YCL036w

5939_at 231.9 A
regulates the copper-dependent mineralization of copper sulfide complexes on the cell surface in cells cultured in medium containing copper salts
5940_at 1643.4 P
strong similarity to glucokinase
5941_at 707.9 P
weak similarity to hypothetical S.pombe protein
5942_at 1005.1 P
Protein disulfide isomerase homolog
5943_at 1843.7 P
FKBP (FK506 binding protein) 13\; peptidylprolyl cis-trans isomerase activity
5944_at 502.1 P
weak similarity to transcription factors of the zinc finger class
5945_at 558.9 P
questionable ORF
5946_at -488.8 A
Middle\/late gene of meiosis
5947_at 59.3 A
serine\/threonine kinase homologous to Ste20p\; expressed in middle\/late meiosis
5948_at 246.0 A
similarity to hypothetical human protein and YIL044c
5949_at -280.5 A
hypothetical protein
5950_at 397.6 A
questionable ORF
5951_at 1121.8 P
weak similarity to Plasmodium yoelii rhoptry protein
5952_at 190.2 A
similarity to Lre1p
5953_at 3118.1 P
ubiquinol-cytochrome c oxidoreductase subunit 7 (14 kDa)
5954_at 657.1 A
5 ,5 -P-1,P-4-tetraphosphate phosphorylase II
5955_at 1921.4 P
similarity to hypothetical A. thaliana and C. elegans proteins
5956_at 109.5 A
weak similarity Plasmodium repeat organellar protein
5957_at 3084.9 P
strong similarity to hypothetical proteins YPL280w, YOR391c and YMR322c
5913_at 390.1 A
similarity to YOR383c,Sta1p and pig mucin
5914_at 235.8 A
hypothetical protein
5915_at -182.9 A
sugar transporter-like protein
5916_at 111.8 A
questionable ORF
5917_at 1280.0 P
Phenylacrylic acid decarboxylase
5918_at 1454.5 P
similarity to E.coli hypothetical 55.3 kDa protein in rfah-rfe intergenic region
5919_at 102.9 A
hypothetical protein
5920_at 149.7 A
similarity to dihydroflavonol-4-reductases
5921_at 3313.4 P

hypothetical protein identified by SAGE
5922_s_at 3043.9 P
homing endonuclease with protein splicing activity
5923_at 1794.8 P
identified by SAGE
5924_at 7110.1 P
identified by SAGE
5925_at 189554.7 P
identified by SAGE
5926_g_at 248477.9 P
identified by SAGE
5927_at 2244.0 P
Involved in pre-tRNA splicing and in uptake of branched-chain amino acids
5928_at 147.3 A
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 474.8 A
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 444.9 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 1311.5 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 703.6 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 -364.7 A
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 929.5 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 235175.5 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 28.1 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 149.9 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 681.8 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 418.4 P
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 7.9 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 18.8 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	276.5	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	265.1	A	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	-7.6	A	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	244.0	A	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	127.6	A	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	13433.9	P	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	932.6	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	3625.7	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	-87.9	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	47.3	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	4025.4	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	41.5	A	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	700.1	A	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	162.6	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	18928.5	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	-49.7	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	6502.4	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	332.3	A	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 374.8 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 349.3 A
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 157.5 A
non-annotated SAGE orf Found reverse in NC_001136 between 971521 and 971670 with 100% identity. See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251
5866_at 422.5 A
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 171.9 A
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 359.2 A
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 -3.9 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 276.1 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 -295.8 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 279.4 A
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 493.9 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 403.5 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 -194.0 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 2469.3 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 762.2 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 2257.1 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
5879_at 3888.1 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 2516.7 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 325.7 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 954.7 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 -182.0 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
5884_r_at -138.4 A
non-annotated SAGE orf Found forward in NC_001136 between 871688 and 871912 with 100% identity. See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251
5885_at 1033.2 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 -112.5 A
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 244.6 A
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 136.7 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 -149.2 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 -2.8 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 334.5 A
non-annotated SAGE orf Found reverse in NC_001136 between 1204280 and 1204438 with 100% identity. See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251
5846_at 800.4 A
non-annotated SAGE orf Found forward in NC_001136 between 1480287 and 1480421 with 100% identity. See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251
5847_at 70.1 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 13.7 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	846.8	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	19.5	A
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	33.6	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	384.7	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	6.4	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	132.3	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	-187.2	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	86.2	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
5857_g_at	-174.2	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	31.4	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	-587.1	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	66.5	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	1045.8	P
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	644.3	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	-127.6	A
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	499.6	A
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	42.2	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	1557.2	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 392.8 A
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 78.6 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 224.7 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 1.2 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 -99.7 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 -172.2 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 -33.2 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 -203.8 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 3706.7 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 283.5 A
non-annotated SAGE orf Found reverse in NC_001136 between 423540 and 423701 with 100% identity. See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251
5830_at 341.2 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 556.6 A
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 -194.7 A
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 256.0 A
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 104.5 A
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 -280.5 A
non-annotated SAGE orf Found reverse in NC_001136 between 541283 and 541441 with 100% identity. See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251
5836_at 17.1 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	-148.5	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	718.4	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	1466.6	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	1478.8	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	1291.0	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	571.2	P
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	1281.7	P
non-annotated SAGE orf Found forward in NC_001136 between 945505 and 945678 with 100% identity. See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251
5795_at	-26.0	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	284.9	A
non-annotated SAGE orf Found forward in NC_001136 between 979658 and 979807 with 100% identity. See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251
5797_at	45.0	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	307.1	A
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	823.6	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	2806.9	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	-112.3	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	-233.6	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	558.3	A
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	1282.3	P	snRNA
5805_i_at	258.2	A	Centromere
5806_i_at	224.5	A	snRNA
5807_at	2251.2	P	snRNA
5808_i_at	-188.6	A	questionable ORF
5809_i_at	2.7	A	similarity to subtelomeric encoded proteins
5810_s_at	638.4	A	similarity to subtelomeric encoded proteins
5811_at	-174.4	A	similarity to YJR108w
5812_at	20.6	A	hypothetical protein
5813_at	6045.1	P	strong similarity to Aip2p
5814_at	113.8	A	hypothetical protein
5815_at	-34.6	A	weak similarity to YKL083w
5816_at	1266.0	P	Histone and other Protein Acetyltransferase\; Has sequence homology to known HATs and NATs
5769_at	580.0	A	probably multidrug resistance protein
5770_at	134.2	A	similarity to YBL089w
5771_at	1796.6	P	arginine permease
5772_at	273.2	A	Non-membrane-embedded, PEST sequence-containing protein
5773_at	343.4	A	Kinesin-related protein involved in establishment and maintenance of mitotic spindle
5774_at	2764.5	P	vacuolar protease B
5775_at	1957.9	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	254.9	A	hypothetical protein
5777_at	14911.4	P	Phosphoacetylglucosamine Mutase
5778_at	-22.3	A	hypothetical protein
5779_at	1427.9	P	subunit of a cytoplasmic histone acetyltransferase
5780_at	2553.8	P	DNA polymerase V that has motifs typical of DNA polymerase family
5781_i_at	29236.2	P	Ribosomal protein L12A (L15A) (YL23)
5782_at	541.6	P	glucose-repressible protein

5783_at	1549.7	P	ATPase family gene
5784_at	1748.8	P	Vacuolar H-ATPase D subunit of the V1 catalytic sector
5785_at	553.5	P	Mitochondrial ribosomal protein L2 of the large subunit
5786_f_at	304.1	A	member of the seripauperin protein\/gene family (see Gene_class PAU)
5787_at	89.2	A	hypothetical protein
5788_at	4323.2	P	strong similarity to Osm1p
5789_at	4310.4	P	Threonine Aldolase
5790_at	248.7	A	weak similarity to cytochrome c oxidase III of T.brucei kinetoplast
5791_at	1024.0	P	hypothetical protein
5747_at	2225.3	P	weak similarity to Mad1p
5748_at	5209.8	P	Guanosine diphosphatase of Golgi membrane
5749_at	-254.5	A	strong similarity to Utr1p
5750_at	17984.1	P	weak similarity to Bacillus 1,3-1,4-beta-glucanase
5751_at	100.1	A	iso-2-cytochrome c
5752_at	1506.6	P	similarity to K.oxytoca enolase-phosphatase E-1
5753_at	4964.0	P	ubiquitin-like protein
5754_at	3770.4	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	-93.4	A	protein of unknown function
5756_at	105086.7	P	Translation initiation factor eIF-5A
5757_at	21530.1	P	weak similarity to Sauroleishmania mitochondrial hypothetical ORF-5 protein
5758_at	1583.5	P	Member of complex that acts at ARS s to initiate replication
5759_at	7008.6	P	P-type ATPase
5760_at	171.8	A	ExtraCellular Mutant
5761_at	185.9	A	similarity to hypothetical protein YNR027w
5762_at	-53.2	A	hypothetical protein
5763_at	35008.0	P	Vacuolar ATP synthase 17-kDa proteolipid C subunit of VO sector\; dicyclohexylcarbodiimide binding subunit
5764_at	22668.2	P	strong similarity to high mobility group-like protein Nhp2p

5765_at 326.2 A
hypothetical protein
5766_at 2156.1 P
Rieske iron-sulfur protein of the mitochondrial cytochrome bc1 complex
5767_at 313.4 P
hypothetical protein
5768_at 410.6 M
ARF GTP\/GDP exchange factor
5724_at -28.7 A
orotidine-5 -phosphate decarboxylase
5725_at 359.5 A
similarity to O.formigenes oxalyl-CoA decarboxylase
5726_at 120.6 A
Protein involved in DNA repair
5727_at 907.1 P
weak similarity to Rad50p
5728_i_at 66593.1 P
Proteolipid associated with plasma membrane H(+)-ATPase (Pma1p)
5729_f_at 22674.2 P
Proteolipid associated with plasma membrane H(+)-ATPase (Pma1p)
5730_at 2908.8 P
hypothetical protein
5731_at 735.4 P
similarity to human nucleotide pyrophosphatase
5732_at 2266.7 P
weak similarity to Spa2p
5733_at 242.0 A
hypothetical protein
5734_at 1564.1 P
An armadillo repeat-containing protein localized on the vacuolar membrane
5735_at 340.6 A
1,4-glucan-6-(1,4-glucano)-transferase
5736_at -279.8 A
hypothetical protein
5737_at 27717.4 P
transcriptional activator of amino acid biosynthetic genes
5738_at -191.1 A
hypothetical protein
5739_at 2543.5 P
similarity to S.pombe pac2 protein
5740_at 754.8 A
similarity to peroxisomal membrane and mitochondrial carrier proteins
5741_at 422.9 A
hypothetical protein
5742_at 340.8 A
Shows sequence similarity to GOG5, a gene involved in vanadate resistance
5743_at 2026.1 P
Putative homolog of subunit 2 of bovine prefoldin, a chaperone comprised of six subunits
5744_at 8388.3 P
oligosaccharyl transferase glycoprotein complex, beta subunit
5745_at 5162.7 P
hypothetical protein
5746_at 1616.7 P
Alpha-1,3-mannosyltransferase
5701_at 1732.1 P
weak similarity to chicken microfibril-associated protein

5702_at	11447.9	P	mannose-6-phosphate isomerase
5703_at	4514.9	P	similarity to hypothetical E.coli and C.elegans proteins
5704_at	480.5	A	similarity to Gda1p
5705_at	6041.1	P	similarity to P.polycephalum myosin-related protein mlpA
5706_at	511.6	P	Required for viability in the absence of the kinesin-related mitotic motor Cin8p\; required for normal microtubule stability
5707_at	4224.6	P	putattive ORF identified by SAGE
5708_at	1829.3	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	5851.1	P	May coordinate the Ran-dependent (GSP1\/GSP2) association and disassociation reactions of nuclear import\; human homologue complements yeast mutants
5710_at	1429.7	P	similarity to L.pneumophila dlpA protein
5711_at	9604.4	P	Cold-shock induced protein of the Srp1p\/Tip1p family of serine-alanine-rich proteins
5712_at	3647.1	P	22.6 kDa proteasome subunit
5713_at	465.4	P	helicase-like protein
5714_at	756.9	P	protoporphyrinogen oxidase
5715_at	11.7	A	Acyl-CoA synthetase (fatty acid activator 2)
5716_at	932.8	P	BInding to Microtubules
5717_at	2745.0	P	ATP-dependent metalloprotease
5718_at	-432.4	A	component of spindle pole
5719_at	1372.6	P	putative neutral sphingomyelinase
5720_at	6499.8	P	homologous to Sbh1p
5721_at	2668.8	P	nucleotide binding regulatory protein
5722_at	4249.3	P	component of the regulatory module of the 26S proteasome, homologous to human p58 subunit
5723_at	338.5	A	subunit of RNA polymerase II holoenzyme\/mediator complex
5678_at	7853.4	P	delta 1-pyrroline-5-carboxylate reductase
5679_at	532.7	P	similarity to carnitine O-acetyltransferase Yat1p
5680_at	8773.5	P	gamma subunit of translational initiation factor eIF-2
5681_at	2119.8	P	phosphatidylserine synthase
5682_at	893.8	P	

glucose repression protein
5683_at 269.5 A
similarity to Mig1p
5684_at 725.6 A
Associated with U1 snRNP as part of the Sm-core that is common to all spliceosomal snRNPs
5685_at 1950.4 P
similarity to mouse nucleolin
5686_at 2571.4 P
ras-like GTPase, highly homologous to YPT32
5687_at 106.5 A
Putative participant in 3 mRNA processing
5688_at 508.8 A
weak similarity to Nmd2p, Kex1p and hamster nucleolin
5689_at 697.3 P
hypothetical protein
5690_at 1424.9 P
hypothetical protein
5691_at 11037.2 P
strong similarity to members of the ABC transporter family
5692_at 11.0 A
strong similarity to hypothetical protein YGL224c
5693_at -6.7 A
hypothetical protein
5694_at 360.5 P
Homologous to VRG4
5695_at 158.7 A
positive nitrogen regulatory protein
5696_at 571.4 P
weak similarity to DNA repair protein Rad2p and Dsh1p
5697_at 129.8 M
responsible for the reduction of methionine sulfoxide
5698_at 27455.5 P
putative S-adenosyl-L-homocysteine hydrolase
5699_at 8963.6 P
hypothetical protein
5700_at 84.8 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.
5655_n_at -88.7 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 489.3 A
weak similarity to transcription factor Sko1p
5657_at 275.2 A
hypothetical protein
5658_at 558.2 P
member of the AAA ATPase family of proteins
5659_at 2921.8 P

Homologous to E. coli DnaJ\; contains leucine zipper-like motif
5660_at 194.9 A
putative ORF identified by SAGE
5661_at 3132.8 P
strong similarity to hypothetical S.pombe protein YER049W
5662_at 1011.1 P
hypothetical protein
5663_at 206.6 A
similarity to C.elegans hypothetical protein
5664_at 4515.4 P
Aspartate kinase (L-aspartate 4-P-transferase) (EC 2.7.2.4)
5665_at 499.8 P
strong similarity to mitochondrial phosphate carrier protein
5666_at 55.8 A
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 7431.0 P
ATP phosphoribosyltransferase
5668_at 6310.0 P
purine-cytosine permease
5669_g_at 5365.9 P
purine-cytosine permease
5670_i_at 51602.5 P
Ribosomal protein L34A
5671_s_at 102141.0 P
Ribosomal protein L34A
5672_at 7723.2 P
Inhibitor of cell Growth\; heat shock inducible
5673_at 922.0 P
cytochrome c oxidase assembly factor
5674_at 255.2 A
PHO85 cyclin
5675_at 759.1 P
purine-cytosine permease
5676_at -282.2 A
purine-cytosine permease
5677_at 665.9 P
Protein homologous to beta-keto-acyl synthase
5633_at 1792.4 P
DL-glycerol-3-phosphatase
5634_at 1905.6 P
Suppressor of the Transcriptional (T) defect of Hpr1 (H) by Overexpression (O)
5635_at 2044.4 P
similarity to hypothetical protein YIL056w
5636_at 283.9 A
isocitrate lyase
5637_at 350.9 P
strong similarity to cell division control protein Cdc4p
5638_g_at 805.6 P
strong similarity to cell division control protein Cdc4p
5639_at 221.9 A
hypothetical protein
5640_at 276.6 P
strong similarity to hypothetical protein YIL057c
5641_at 1119.8 P

putative zinc finger protein
5642_at 3448.9 P
N-acetyl-gamma-glutamyl-phosphate reductase and acetylglutamate kinase
5643_at 4519.9 P
ribonucleotide reductase
5644_at 1361.6 P
hypothetical protein
5645_at 26961.0 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 1214.5 P
aldehyde dehydrogenase (NAD+)
5647_s_at 27835.4 P
40S ribosomal protein S24A
5648_at 739.2 P
Protein tyrosine phosphatase
5649_at 611.7 P
similarity to killer toxin Khr1p
5650_at 399.9 P
hypothetical protein
5651_at 250.5 A
similarity to E.coli X-Pro aminopeptidase II
5652_at 874.0 P
hypothetical protein
5653_at 1175.4 P
hypothetical protein
5654_at 229.4 A
strong similarity to phosphoglycerate dehydrogenases
5610_at 934.1 P
similarity to M.sexta steroid regulated MNG10 protein
5611_at 4410.1 P
hypothetical protein
5612_at 477.7 A
questionable ORF
5613_at 53.6 A
weak similarity to myosins
5614_at 6765.9 P
threonine deaminase
5615_at 958.2 P
similarity to E.coli prolyl-tRNA synthetase
5616_at 4298.9 P
homologous to Sbh2p
5617_at 1341.3 P
Derepression Of Telomeric silencing
5618_at 4422.8 P
Protein phosphatase type 2C
5619_at 5129.3 P
anthranilate synthase Component I
5620_at 7617.9 P
vitamin B12-(cobalamin)-independent isozyme of methionine synthase (also called N5-methyltetrahydrofolate homocysteine methyltransferase or 5-methyltetrahydropteroyl triglutamate homocysteine methyltransferase)
5621_at 1132.0 P
hypothetical protein
5622_at 882.5 P
weak similarity to S.epidermidis PepB protein

5623_at	588.8	P	similarity to hypothetical protein YBL059w
5624_at	45.8	A	similarity to hypothetical protein YBL059w
5625_at	8212.3	P	20S proteasome subunit (beta3)
5626_at	2359.2	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	-59.9	A	sporulation-specific homolog of csd4
5628_at	-10.7	A	weak similarity to ribosomal S3 proteins
5629_at	-98.6	A	ubiquitin carboxyl-terminal hydrolase
5630_at	1183.2	P	ribose-phosphate pyrophosphokinase 2
5631_at	832.5	P	ubiquitin-conjugating enzyme
5632_at	467.5	P	Protein involved in targeting of plasma membrane [H+]ATPase
5588_at	567.6	A	member of 70 kDa heat shock protein family
5589_at	325.7	A	hypothetical protein
5590_at	3251.6	P	Nucleoporin similar to Nup157p and to mammalian Nup155p
5591_at	67.3	A	hypothetical protein
5592_at	1516.8	P	homologous to S. pombe RAE1 gene\; 2-hybrid analysis demonstrates an interaction with Srp1p and Rip1p\; copurifies with Nup116p
5593_at	322.2	A	putative transcriptional activator of FLO1
5594_at	-191.3	A	putative transcriptional activator of FLO1
5595_at	5029.0	P	Karyopherin beta 4
5596_at	-41.7	A	transcription factor
5597_at	2068.1	P	U6 snRNA associated protein
5598_at	953.8	P	similarity to Emp70p
5599_at	1202.6	P	Protein which binds Bem1p and contains a proline-rich sequence, an SH3 domain, and a pleckstrin homology domain
5600_at	1003.7	P	sporulation-specific protein
5601_at	-280.1	A	zinc-finger protein
5602_at	1018.7	P	Transmembrane osmosensor
5603_at	865.5	P	weak similarity to E.herbicola tyrosine permease

5604_at 167.2 A
questionable ORF
5605_at 8429.7 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 96.4 A
hypothetical protein
5607_at 1746.5 P
Zinc-finger-containing protein with similarity to Gcs1p and Sps18p
5608_at 257.1 A
plasma membrane-bound casein kinase I homolog
5609_at 397.6 P
weak similarity to Dictyostelium WD40 repeat protein 2
5565_at 1489.9 P
Rsp5p encodes a hect (homologous to E6-AP C terminus) and encodes a ubiquitin-protein ligase (E3 enzyme)
5566_at 3227.3 P
weak similarity to E.coli colicin N
5567_at 1106.9 P
Lethal with conditional pap1 allele
5568_at 342.7 A
hypothetical protein
5569_at 278.9 A
DNA polymerase alpha suppressing protein kinase
5570_at 851.4 P
similarity to Msn2p and weak similarity to Msn4p
5571_at 13114.2 P
Ribosomal protein S26B
5572_at 1518.3 P
Paralog of MDS3
5573_at 298.1 P
protein phosphatase type I
5574_at 3274.0 P
protein phosphatase type I
5575_at 270.2 A
weak similarity to S.pombe SPBC13G1 and C.elegans F26F2.d hypothetical proteins
5576_at 114.9 A
hypothetical protein
5577_at 3127.7 P
GDP dissociation inhibitor
5578_at 250.3 A
weak similarity to Mycoplasma hominis P120 protein
5579_at 105.7 A
similarity to hypothetical protein YDR066c
5580_at 524.4 P
hypothetical protein
5581_at 3165.9 P
cytochrome oxidase assembly factor
5582_at 56.2 A
3-methyladenine DNA glycosylase
5583_at 1033.9 P
DNA Damage Inducible
5584_at 619.9 P
Putative Ubiquitin-specific protease
5585_at 2494.0 P
Iron permease

5586_at 1921.4 P
Sm-like protein
5587_at 199.6 A
weak similarity to mouse NAD(P)H dehydrogenase (quinone)
5542_at 3643.0 P
TATA-binding protein (tfIId)
5543_at 491.7 A
Protein with coiled-coil domain
5544_at 357.8 A
strong similarity to putative cell surface glycoprotein Sed1p
5545_at 1804.2 P
Ubiquitin-specific protease
5546_at 3427.7 P
weak similarity to E.coli hypothetical protein f470
5547_at 12058.9 A
translational activator of cytochrome c oxidase subunit III
5548_at 3376.1 P
Required for correct assembly of the cytochrome c oxidase and the ATP synthase complex
5549_at 2155.5 P
Rho-type GTPase activating protein (GAP)
5550_at 3020.0 P
similarity to hypothetical C. elegans protein C27H6.5
5551_at 372.3 A
hypothetical protein
5552_at 394.4 M
weak similarity to Afr1p
5553_at 2426.8 P
Transcriptional regulator which functions in modulating the activity of the general transcription machinery in vivo
5554_at 637.0 P
non-specific DNA binding protein (sin1)
5555_at 160.0 A
Nucleotide excision repair protein
5556_at 803.5 P
weak similarity to E.coli cation transport protein
5557_at 624.3 P
transcriptional regulator
5558_at 16109.7 P
Poly(A) binding protein, cytoplasmic and nuclear
5559_at 1521.5 P
similarity to ATPase P.falciparum ATPase 2
5560_at 750.5 P
Serine\/threonine protein kinase
5561_at 412.0 A
tRNA nucleotidyltransferase (tRNA CCA-pyrophosphorylase)
5562_at 53.2 A
Repressor of PHR1 transcription\; binds to PHR1 URS
5563_at 501.7 P
Adenylate kinase (mitochondrial GTP:AMP phosphotransferase)
5564_at 780.3 P
DNA repair helicase component of transcription factor b
5520_at 1247.5 P
putative ATP-dependent RNA helicase
5521_at 510.1 P
checkpoint protein
5522_at 389.6 A

similarity to Legionella glutaredoxin-like protein
5523_at 421.0 A
similarity to hypothetical protein YHR209w
5524_at 944.6 P
DNA Helicase I
5525_at 14348.1 P
Ribosomal protein L23B (L17aB) (YL32)
5526_at 10772.9 P
alpha subunit of pyruvate dehydrogenase (E1 alpha)
5527_at -2.2 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 113.3 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 291.7 A
Meiosis-specific protein required for spore formation
5530_at 264.5 A
questionable ORF
5531_at 436.0 A
hypothetical protein
5532_at 745.3 P
similarity to human 5,10-methenyltetrahydrofolate synthetase
5533_at -109.0 A
similarity to multidrug resistance proteins Pdr3p and Pdr1p
5534_at 142.2 A
strong similarity to Rtm1p
5535_at 566.6 A
weak similarity to hypothetical protein YMR316w
5536_at 373.9 A
similarity to killer toxin KHS precursor
5537_at 236.8 A
hypothetical protein
5538_at 1864.1 P
Translocase in inner membrane of mitochondria involved in mitochondrial protein import
5539_at 256.5 A
hypothetical protein
5540_at -72.1 A
hypothetical protein identified by SAGE
5541_at 498.1 A
questionable ORF
5497_at 470.2 P
questionable ORF
5498_at 108.4 A
questionable ORF
5499_at 261.4 A
questionable ORF
5500_at 553.1 P
questionable ORF
5501_at -78.2 A
questionable ORF
5502_at 68.2 A
questionable ORF
5503_at 99.2 A

questionable ORF
5504_at	-84.2	A
questionable ORF
5505_at	-54.2	A
hypothetical protein
5506_s_at	493.9	A
ubiquitin-conjugating enzyme\; ubiquitin-protein ligase
5507_at	1029.0	P
non-annotated SAGE orf Found forward in NC_001137 between 67199 and 67363 with 100% identity.
See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251
5508_at	-982.8	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	78.8	A
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	-50.2	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	1417.4	A
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	291.4	A
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	165.1	A
non-annotated SAGE orf Found reverse in NC_001137 between 90086 and 90226 with 100% identity.
See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251
5514_at	4182.6	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	-67.9	A
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	5417.2	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	17725.6	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	100.4	A
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	83.3	A
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	1287.1	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	28.1	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	808.3	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	3125.1	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 3480.2 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 337.5 A
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 44.2 A
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 629.9 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
5481_at -20.4 A
non-annotated SAGE orf Found reverse in NC_001137 between 84843 and 84983 with 100% identity.
See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251
5482_at 336.7 A
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 2300.2 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 115.6 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 -516.8 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 173.3 A
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 134.0 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 88.8 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 498.4 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 -124.7 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 74.2 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 -107.6 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 113.8 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 -136.3 A
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 12.7 A
non-annotated SAGE orf Found forward in NC_001137 between 194842 and 194988 with 100% identity.
See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251
5496_g_at -20.3 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
5449_at 51.3 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
5450_g_at 94.0 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 -97.0 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 -21.5 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 78.8 A
non-annotated SAGE orf Found forward in NC_001137 between 284585 and 284719 with 100% identity.
See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251
5454_at -131.3 A
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 739.7 A
non-annotated SAGE orf Found reverse in NC_001137 between 311731 and 311907 with 100% identity.
See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251
5456_at -160.1 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 55.7 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 -173.7 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 -173.8 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 2157.2 A
non-annotated SAGE orf Found reverse in NC_001137 between 467935 and 468081 with 100% identity.
See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251
5461_at 508.8 A
non-annotated SAGE orf Found reverse in NC_001137 between 504589 and 504738 with 100% identity.
See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251
5462_at 134.6 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 215.0 A
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 1129.7 A
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 4459.5 P
non-annotated SAGE orf Found reverse in NC_001137 between 52351 and 52515 with 100% identity.

See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251
5466_i_at -156.8 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 6742.7 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 -74.0 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 -88.3 A
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 1128.2 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 10977.1 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 -205.8 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 -88.1 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 49.2 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 219.6 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 98.3 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 155.7 A
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 1216.6 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 165.5 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
5443_g_at -440.0 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 125.3 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 2818.1 P
non-annotated SAGE orf Found reverse in NC_001137 between 441063 and 441299 with 100% identity.
See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251
5446_r_at 13.9 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 1639.9 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	553.6	A
snRNA		
5412_at	111.5	A
snRNA		
5413_at	1247.2	P
RNase P RNA		
5414_i_at	-9.4	A
Centromere		
5415_r_at	24.0	A
Centromere		
5416_at	183.3	A
snRNA R14		
5417_at	2635.2	P
snRNA U4		
5418_at	526.2	A
snRNA		
5419_at	1133.2	P
small cytoplasmic RNA		
5420_s_at	3672.2	A
weak similarity to hypothetical E.coli protein		
5421_i_at	-271.5	A
similarity to mouse period clock protein		
5422_s_at	657.2	P
similarity to mouse period clock protein		
5423_s_at	507.3	P
strong similarity to aryl-alcohol dehydrogenases		
5424_at	110.8	A
Hypothetical aryl-alcohol dehydrogenase (AAD)		
5425_at	60.2	A
Amino acid permease		
5426_at	208.8	A
similarity to channel proteins		
5427_at	18.7	A
dihydroxyacetone kinase		
5428_at	34.9	A
strong similarity to Mal63p, YPR196w and Mal13p		
5429_at	-155.3	A
putative pseudogene		
5430_at	291.3	M
ALuminium Resistance 2		
5431_at	476.8	A
weak similarity to Npl6p		
5432_at	1511.8	P
47 kDa type I transmembrane protein localized to the Golgi		
5433_at	1000.0	P
similarity to S.pombe hypothetical protein SPAC2F7.18c		
5434_at	335.9	A
weak similarity to middle part of C.elegans myosin heavy chain A		
5435_at	11655.2	P
phosphomannomutase		
5389_at	613.1	P
weak similarity to human dystrophin		
5390_at	1413.6	P
multicopper oxidase, type 1 integral membrane protein		

5391_at	-8.1	A	similarity to yeast glucose transport proteins
5392_at	84781.9	P	Actin
5393_at	8574.2	P	Ras-like GTP-binding protein\; most similar to mammalian Rab1A protein
5394_at	12246.6	P	beta-tubulin
5395_at	2118.4	P	mitochondrial RNA polymerase II
5396_at	4975.0	P	Ribosomal protein L22B (L1c) (rp4) (YL31)
5397_at	228.6	A	similarity to hypothetical S. pombe protein and to C.elegans F35D11 protein
5398_at	615.0	P	Trehalose-associated protein kinase related to S. pombe cek1+
5399_at	10.2	A	questionable ORF
5400_at	128.7	A	similarity to several transaminases
5401_at	914.7	P	Cyclin-dependent kinase-activating kinase
5402_at	593.9	M	ABC ATPase
5403_at	499.5	P	weak similarity to P.falciparum Pfmdr2 protein
5404_at	-141.8	A	alpha-factor pheromone receptor\; seven-transmembrane domain protein
5405_at	665.0	P	Negatively regulates COPII vesicle formation
5406_at	438.9	A	Probable chromatin protein because of homology to Drosophila Enahncer of Polycomb
5407_at	847.6	P	similarity to repeat structures in a Plasmodium falciparum protein (MESA) that binds human erythrocyte protein 4.1.
5408_at	6775.0	P	Phenylalanyl-tRNA synthetase, beta subunit, cytoplasmic
5409_at	294.6	A	transcriptional activator with GATA-1-type Zn finger DNA-binding motif
5410_f_at	917.1	P	member of the seripauperin protein\/gene family (see Gene_class PAU)
5411_at	-58.9	A	hypothetical protein
5367_at	9367.8	P	dihydrolipoamide dehydrogenase precursor (mature protein is the E3 component of alpha-ketoacid dehydrogenase complexes)
5368_at	810.6	P	snRNP G protein (the homologue of the human Sm-G)
5369_at	1533.1	P	similarity to hypothetical S. pombe protein and to hypothetical C.elegans B0024.12 protein
5370_at	1677.0	P	DnaJ homolog involved in mitochondrial biogenesis and protein folding
5371_at	-142.5	A	weak similarity to YDR504c
5372_at	450.6	A	12 kDa heat shock protein

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5373_at        728.5          P
weak similarity to Dictyostelium protein kinase
5374_at        -121.7         A
questionable ORF
5375_at        -46.7          A
hypothetical protein
5376_at        -129.1         A
High-affinity hexose transporter
5377_at        1244.8         P
Involved in ammonia regulation of GAP1 activity
5378_at        8963.8         P
questionable ORF
5379_at        631.2          P
beta subunit of large (heterotrimeric) G-proteins (beta-transducin)
5380_at        1495.0         P
omosome segregation protein
5381_at        784.2          P
weak similarity to Mms19p
5382_at        1624.1         P
hypothetical protein
5383_at        2050.9         P
Ras-like small GTP-binding protein
5384_at        8562.7         P
strong similarity to hypothetical protein YPL019c
5385_at        98.7           A
meiosis specific protein, E.coli MutS protein, localizes to discrete sites on meiotic chromosomes
5386_at        1661.9         P
ATP-dependent RNA helicase
5387_at        791.6          P
Depressed growth-rate protein
5388_at        2072.8         P
weak similarity to rabbit triadin Spp41p
5344_at        848.6          P
96 kDa nucleoporin-interacting component
5345_at        688.5          A
hypothetical protein
5346_at        5812.9         P
Similar to S. pombe PAD1 gene product
5347_at        313.0          P
similarity to hypothetical A. thaliana proteins
5348_at        3596.8         P
similarity to X-Pro dipeptidases
5349_at        315.0          A
weak similarity to YER176w
5350_at        -39.6          A
weak similarity to human centromere protein E
5351_at        3714.8         P
Member of ATP-binding cassette (ABC) family of proteins
5352_at        3480.3         P
encodes putative deubiquitinating enzyme
5353_at        1012.5         P
ochre suppressor tyr-tRNA
5354_at        -324.2         A
similarity to hypothetical protein YOL019w
5355_at        848.1          P
similarity to YOL017w
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5356_at	437.6	P	Calmodulin-dependent protein kinase
5357_at	211.2	A	Glycogen synthase (UDP-gluocse--starch glucosyltransferase)
5358_at	1073.3	P	similarity to mammalian neurofilament proteins and to Dictyostelium protein kinase
5359_at	720.0	P	hypothetical protein
5360_at	2800.3	P	similarity to human glutaminyl-peptide cyclotransferase
5361_at	2096.9	P	type II PI(4)P5-kinase (PIP4,5 kinase) similar to human PIP5K-II
5362_at	803.9	P	hypothetical protein
5363_at	1057.3	P	similarity to hypothetical protein YPL100w
5364_at	424.7	P	similarity to Rod1p
5365_at	78.3	A	poly(A) binding protein\; related to PES4 protein homolog YHR015w
5366_s_at	2126.5	P	similarity to Acanthamoeba myosin heavy chain IC and weak similarity to other myosin class I heavy chains
5322_at	340.3	A	Histidinolphosphatase
5323_at	-159.3	A	hypothetical protein
5324_at	-145.7	A	hypothetical protein
5325_at	2141.1	P	soluble tyrosine-specific protein phosphatase
5326_at	255.9	A	Regulator of expression of the PTR2, GAP1, and BAP2 genes\; involved in the the control of peptide transport
5327_at	821.4	P	subunit of assimilatory sulfite reductase
5328_at	1358.1	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	117410.0	P	Ribosomal protein L2A (L5A) (rp8) (YL6)
5330_at	54.5	A	weak similarity to S.pombe polyadenylate-binding protein, YPR112c and Sbp1p
5331_at	26465.1	P	Ribosomal protein L29 (YL43)
5332_at	6796.8	P	ubiquinol-cytochrome c oxidoreductase subunit 6 (17 kDa)
5333_at	173.4	A	myc-type helix-loop-helix transcription factor
5334_at	220.1	A	hypothetical protein
5335_at	1333.2	P	cell division control protein
5336_at	2361.6	P	Rsc8 is the eighth largest subunit of RSC, a fifteen-protein chromatin remodeling complex and related to the Swi\/snf Complex.

5337_at 149.8 A
strong similarity to mouse lymphocyte specific helicase
5338_at 639.3 P
similarity to hypothetical protein YGL228w
5339_at 430.3 A
155 kDa SIT4 protein phosphatase-associated protein
5340_at 627.4 P
weak similarity to dnaJ-like heat shock proteins
5341_at 497.9 P
hypothetical protein
5342_at 445.7 A
hypothetical protein
5343_at 13772.6 P
similarity to hypothetical protein YBR281c
5299_at 375.6 P
similarity to mitochondrial citrate transport proteins
5300_at 31.6 A
hypothetical protein
5301_at 2814.3 P
strong similarity to human quinolinate phosphoribosyltransferase
5302_at 210.4 A
similarity to hypothetical S.pombe protein SPAC12G12.14 and to YDL001w and YDR282c
5303_at 1653.5 P
mitochondrial ribosomal protein (precursor)
5304_at 5495.9 P
proteasome subunit necessary for peptidyl glutamyl peptide hydrolyzing activity
5305_at 2828.5 P
Coatomer (COPI) complex delta subunit
5306_at 1828.1 P
cytoplasmic 32 - 34 kDa protein
5307_at 797.3 P
Hexokinase I (PI) (also called Hexokinase A)
5308_at -209.4 A
hypothetical protein
5309_at -159.4 A
questionable ORF
5310_at 662.4 P
strong similarity to beta-cystathionases
5311_at -56.8 A
weak similarity to Cha4p
5312_s_at 372.5 P
hypothetical protein
5313_s_at 1536.3 P
Mob1p-like protein
5314_at 170.9 A
hypothetical protein
5315_at 279.5 A
questionable ORF
5316_at 1076.6 P
questionable ORF
5317_s_at 326.3 A
similarity to hypothetical protein YLR072w
5318_s_at 2872.0 P
bZIP (basic-leucine zipper) protein
5319_at 3522.2 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 4.7 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 85.7 A
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 1133.9 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 -41.2 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 -218.4 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 5983.7 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 422.7 A
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 205.7 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 -207.6 A
non-annotated SAGE orf Found reverse in NC_001138 between 5806 and 6033 with 100% identity. See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251
5281_f_at -92.9 A
non-annotated SAGE orf Found reverse in NC_001138 between 5806 and 6033 with 100% identity. See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251
5282_at -55.3 A
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 -58.0 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 535.1 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 502.5 M
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 -169.1 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 1794.6 A
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 -20.1 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 486.1 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 -48.5 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 360.0 A

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 683.2 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 100.6 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 14.0 A

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

5295_f_at 282.4 P

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

5296_i_at -289.1 A

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

5297_at 144.8 A

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

5298_at -98.5 A

similarity to hypothetical protein YER187w

5251_f_at 896.6 P

strong similarity to members of the Srp1/Tip1 family

5252_at 47.1 A

GPI-anchored aspartic protease

5253_g_at 101.6 A

GPI-anchored aspartic protease

5254_i_at -239.6 A

strong similarity to hypothetical protein YOR387c

5255_s_at -70.4 A

strong similarity to hypothetical protein YOR387c

5256_at 388.0 A

similarity to Mnn1p

5257_at 1101.1 P

alcohol dehydrogenase isoenzyme IV

5258_at 1212.0 P

high-affinity zinc transport protein

5259_at 359.2 A

putative transcription factor, has five zinc fingers

5260_at 18840.0 P

Hexokinase II (PII) (also called Hexokinase B)

5261_at 1176.9 P

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

5262_at 120.3 A

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

5263_at -137.2 A

hypothetical protein

5264_at -118.8 A

Required for ZIPpering up meiotic chromosomes during chromosome synapsis

5265_at 1559.7 P

3 ,5 -Cyclic-nucleotide phosphodiesterase, low affinity

5266_at 827.3 P

similarity to hypothetical protein YHR036w

5267_at 797.5 P

weak similarity to C.elegans dom-3 protein
5268_at 28209.4 P
strong similarity to glutamine--tRNA ligase
5269_at 438.2 P
Nuclear protein
5270_at 497.8 P
tRNA-specific adenosine deaminase 1 (TAD1)\; Tad1p\/scADAT1
5271_at 2995.0 P
weak similarity to Drosophila ANK protein
5272_at 1412.5 P
similarity to Cse1p
5273_at 73.6 A
Doc1p and Cdc26p are associated with the anaphase-promoting complex and are involved in the degradation of Clb2p
5229_at 265.4 A
questionable ORF
5230_at 3097.1 P
Protein required for accurate mitotic chromosome segregation
5231_at -62.3 A
transcriptional activator protein of CYC1
5232_at 718.3 P
strong similarity to gidA E.coli protein
5233_at -437.8 A
questionable ORF
5234_at 18884.6 P
glycinamide ribotide synthetase and aminoimidazole ribotide synthetase
5235_at 604.4 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 25.1 A
weak similarity to P.falciparum dihydropteroate synthase
5237_at 909.8 A
weak similarity to P.falciparum dihydropteroate synthase
5238_at 1863.2 P
hypothetical protein
5239_at 213.0 A
hypothetical protein
5240_at 693.9 P
SAP4 is related to SAP155, SAP185, and SAP190, all of which associate with the SIT4 protein phosphatase
5241_at 3449.9 P
mRNA (identified by a library screen) that causes growth arrest when overexpressed
5242_at 263.7 A
TOR inhibitor
5243_at 5087.3 P
9.5-kDa zeta subunit of oligosaccharyltransferase complex
5244_at 1207.9 P
similarity to N.crassa cytochrome-c oxidase chain V
5245_at 6535.0 P
May regulate Golgi function and glycosylation in Golgi
5246_at 741.0 P
strong similarity to hypothetical protein YER037w
5247_at 313.1 P
weak similarity to Clostridium regulatory protein
5248_at -468.9 A
hypothetical protein

5249_at 2068.6 P
Ngg1p-interacting factor 3
5250_at 4259.0 P
weak similarity to V.alginolyticus bolA protein
5206_at 747.2 P
hypothetical protein
5207_at 57.3 A
questionable ORF
5208_at 243.2 A
questionable ORF
5209_at 593.8 P
Kinesin-related protein
5210_at 262.3 P
Cyclin-like protein that interacts with Pho85p in affinity chromatography
5211_at 304.4 A
questionable ORF
5212_at 1660.6 P
antiviral protein, mRNA is induced early in meiosis
5213_at -97.1 A
hydrophilic protein, heptad repeat motif
5214_at 515.2 A
similarity to M.jannaschii hypothetical proteins MJ1157 and MJ1478
5215_at 1337.0 P
ras-like GTPase, highly homologous to YPT31
5216_at 1462.5 P
Protein containing zinc fingers very similar to zinc fingers in Mig1p
5217_at 147.6 A
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 6020.7 P
transcription factor
5219_at 3384.5 P
presumed vesicle coat protein
5220_at -19.5 A
fatty-acyl coenzyme A oxidase
5221_at 658.9 P
questionable ORF
5222_at 839.8 P
carboxypeptidase B-like processing protease
5223_at 8873.7 P
aromatic amino acid aminotransferase
5224_at 915.3 P
Member of the MCM\/P1 family of proteins involved in DNA replication
5225_at 8923.6 P
type I transmemebrane protein, component of COPII-coated, ER-derived transport vesicles
5226_at 744.3 P
questionable ORF
5227_at 3171.4 P
weak similarity to Yip1p
5228_at 607.1 P
Mck1 Dosage Suppressor 3\; negative regulator of early meiotic gene expression
5183_at 1901.7 P
hypothetical protein
5184_at 3148.7 P
translational activator of GCN4 through activation of GCN2 in response to starvation
5185_at 99.8 A

Protein with similarity to Hda1p, Rpd3p, Hos1p, and Hos3p
5186_at 877.0 P
questionable ORF
5187_at 23.4 A
IME4 appears to activate IME1 in response to cell-type and nutritional signals and thereby regulate meiosis
5188_at 4180.9 P
subunit VIa of cytochrome c oxidase, may specifically interact with ATP
5189_at 263.8 A
Protein phosphatase 2A regulatory subunit B
5190_i_at 71734.9 P
Ribosomal protein S26A
5191_f_at 87756.7 P
Ribosomal protein S26A
5192_at 66.1 A
hypothetical protein
5193_at 1976.8 P
subunit IV of cytochrome c oxidase
5194_at 2495.8 P
similarity to hypothetical protein Fcy21p and weak similarity to FCY2 protein
5195_at 1195.2 P
weak similarity to dehydrogenases
5196_at 527.2 A
strong similarity to Emericella nidulans cystathionine beta-lyase
5197_at -204.1 A
hypothetical protein
5198_at 402.0 A
questionable ORF
5199_at 1973.7 P
Glycine-threonine-serine repeat protein
5200_at 358.6 A
Protein kinase
5201_at 598.9 P
ser/thr protein kinase
5202_at -29.7 A
questionable ORF
5203_at 2686.6 P
multicopy suppressor of POP2
5204_at 559.7 A
weak similarity to Oryctolagus calcium channel BIII
5205_at 107.2 A
involved in meiotic recombination and chromosome metabolism
5161_at 428.0 A
weak similarity to C.elegans hypothetical protein R08D7.1
5162_at 6245.9 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 2236.6 P
nuclear pore complex protein with GLFG repetitive sequence motif
5164_at 2057.1 P
Contains domains found in the DEAD protein family of ATP-dependent RNA helicases\; high-copy suppressor of kem1 null mutant
5165_at 23.2 A
hypothetical protein
5166_at 492.5 P

Protein involved in translation initiation
5167_at 362.8 A
questionable ORF
5168_at 1870.3 P
Ca++-Pump, ATPase
5169_at 890.0 P
Activator of transcription
5170_at 503.9 A
questionable ORF
5171_at 547.2 P
similarity to S.pombe hypothetical protein SPAC31A2.10
5172_at 610.0 P
Required for X-ray damage repair, mitotic recombination, and full meiotic recombination. mRNA increases in meiosis.
5173_at 661.5 P
Involved in sterol uptake
5174_at 2432.4 P
hypothetical protein
5175_at 287.4 A
similarity to hypothetical protein YLR047c and Fre2p
5176_at 1164.5 P
hypothetical protein
5177_at -113.7 A
Serine\/threonine protein kinase
5178_at 3323.5 P
similarity to V.vinifera dihydroflavonol 4-reductase
5179_at 207.0 A
vacuolar alpha mannosidase
5180_at 293.2 A
polypeptide subunit of a yeast type 1 protein geranylgeranyltransferase
5181_at 792.7 P
aminoadipate-semialdehyde dehydrogenase small subunit (alpha-aminoadipate reductase)
5182_at 523.6 A
questionable ORF
5137_at 675.5 P
Peroxisomal peripheral membrane protein (peroxin) involved in import of peroxisomal matrix proteins
5138_at 608.5 P
negative regulator of URS2 of the HO promoter
5139_at 1030.0 P
Shows similarity to the Snf2p family of DNA-dependent ATPases
5140_at 273.4 A
questionable ORF
5141_at 15912.4 P
Chorismate synthase
5142_i_at 23693.1 P
Ribosomal protein L9A (L8A) (rp24) (YL11)
5143_at -148.3 A
hypothetical protein
5144_at 133.4 A
transport protein that interacts with Sec20p\; required for protein transport from the endoplasmic reticulum to the golgi apparatus
5145_at 304.6 A
strong similarity to hypothetical protein YDL109c
5146_at 249.7 A
Mitochondrial polypeptide chain release factor
5147_at 576.7 P

Most likely an alpha 1,2 mannosyltransferase utilized for the addition of the third mannose onto the GPI core structure.
5148_at 675.3 P
similarity to human human E6-associated protein
5149_at 642.3 P
weak similarity to Lactobacillus putative histidine protein kinase SppK
5150_at 257.9 A
strong similarity to hypothetical protein YPL221w
5151_at 68.5 A
hypothetical protein
5152_at 5173.4 P
encodes beta -subunit of yeast coatomer
5153_at 276.7 A
weak similarity to E.coli ftsJ protein
5154_at 508.9 P
PHO85 cyclin
5155_at 662.5 P
similarity to hypothetical protein YPL216w
5156_at 118.7 A
questionable ORF
5157_at 267.6 A
weak similarity to S.pombe hypothetical protein C3H1.12C
5158_at 2026.1 P
mRNA guanylyltransferase (mRNA capping enzyme), alpha subunit
5159_at 467.0 A
hypothetical protein
5160_at 495.7 A
weak similarity to rat cysteine string protein
5115_at 436.6 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 1658.2 P
required for inositol prototrophy
5117_at 1003.8 P
putative methylenetetrahydrofolate reductase (mthfr)
5118_at 107.8 A
similarity to S.pombe hypothetical protein
5119_at 103382.1 P
Ribosomal protein S2 (S4) (rp12) (YS5)
5120_at 1396.3 P
nuclear polyadenylated RNA binding protein
5121_at 684.1 P
hypothetical protein
5122_at 5701.4 P
pre-mRNA processing factor involved in disassembly of spliceosomes after the release of mature mRNA
5123_at 687.9 P
multicopy suppressor of a cytochrome b mRNA translation defect, essential for the electron transfer in the bc1 complex
5124_at -193.7 A
questionable ORF
5125_at 77.0 A
hypothetical protein
5126_at 715.2 P
beta-transducin homolog
5127_at 340.9 A
associates with Snf1p

5128_at	924.8	P	weak similarity to H.influenzae permease
5129_at	662.1	M	weak similarity to YOR165w
5130_at	2062.9	P	TATA-binding protein-associated-factor
5131_at	1647.2	P	hypothetical protein
5132_at	847.2	P	hypothetical protein
5133_at	95.2	A	questionable ORF
5134_at	429.3	A	weak similarity to hypotetical S.pombe protein
5135_at	1068.6	P	strong similarity to hypothetical protein YBR238c
5136_at	3499.2	P	light chain for myosin Myo2p
5092_at	9485.7	P	Associated with tRNA and amino acyl-tRNA synthetases\; has affinity for quadruplex nucleic acids
5093_at	249.7	A	similarity to glucose transport proteins
5094_at	66710.2	P	Ribosomal protein L28 (L29) (rp44) (YL24)
5095_at	6268.7	P	questionable ORF
5096_at	810.8	P	strong similarity to hypothetical protein YBR242w
5097_at	1606.8	P	nuclear pore protein, homologous to sec13
5098_at	1513.2	P	similarity to putative human GTP-binding protein MMR1
5099_at	-51.7	A	hypothetical protein
5100_at	3736.2	P	pheromone response pathway suppressor
5101_at	248.2	A	similarity to copper homeostasis protein Cup9p
5102_at	408.5	P	cytosolic and peripheral membrane protein
5103_at	541.1	A	135-kDa protein that is subunit of poly(A) ribonuclease
5104_at	1142.3	P	component of spindle pole
5105_at	2015.2	P	Nuclear pore complex protein with GLFG motif
5106_at	859.6	P	35 kDa nucleotide binding protein
5107_at	598.1	A	Ligase Interacting Factor 1\; physically interacts with DNA ligase 4 protein (Lig4p)
5108_at	21960.9	P	alpha mating factor
5109_at	1356.4	P	questionable ORF
5110_at	1908.7	P	Similar to ubiquitin conjugating protein family

5111_at 397.2 A
Coiled-coil protein involved in spindle-assembly checkpoint
5112_at 364.2 P
weak similarity to Staphylococcus aureus nuclease (SNase)
5113_at 1026.8 P
strong similarity to hypothetical protein YPL189w
5114_at 463.5 P
suppressor of GTPase mutant
5069_at 1417.8 P
strong similarity to hypothetical protein YPL191c
5070_at 104.0 A
hypothetical protein
5071_at 898.1 P
strong similarity to C.elegans R07E5.13 protein
5072_at 476.3 P
hypothetical protein
5073_at 2863.3 P
ATP-dependent RNA helicase CA3 of the DEAD\/DEAH box family
5074_at 5480.1 P
Transporter (permease) for choline and nitrogen mustard\; share homology with UGA4
5075_i_at 24890.1 P
Ribosomal protein L7A (L6A) (rp11) (YL8)
5076_f_at 17081.3 P
Ribosomal protein L7A (L6A) (rp11) (YL8)
5077_at -100.0 A
Mitotic Membrane Component
5078_at -25.7 A
questionable ORF
5079_at 1248.2 P
heat shock transcription factor
5080_at 229.0 A
questionable ORF
5081_at 500.2 P
Putative transcription factor that binds the consensus site PyPuCACCCPu
5082_at 1353.7 P
RNA polymerase II subunit
5083_at -248.4 A
questionable ORF
5084_at 1138.1 P
probable ribosomal protein L12
5085_at 1356.3 P
weak similarity to H.influenzae hypothetical protein
5086_at 959.1 P
hypothetical protein
5087_at 495.1 P
glycosyltransferase
5088_at 446.6 P
similarity to YLR276c and YKR024c
5089_at 502.6 P
pseudouridine synthase 2
5090_at 2700.5 P
pyruvate carboxylase
5091_at 220.0 A
Death Upon Overexpression
5047_at 578.2 A
strong similarity to hypothetical protein YBR216c

5048_at 20.5 A
similarity to rat branched-chain alpha-ketoacid dehydrogenase kinase
5049_at 1579.0 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 241.7 A
hypothetical protein
5051_at 850.8 P
homologue of pombe SDS23\; localizes to spindle pole body
5052_at 18161.7 P
delta-9-fatty acid desaturase
5053_at 971.6 P
strong similarity to D.melagonaster cni protein
5054_at 466.7 A
strong similarity to hypothetical proteins YAR031w, YGL051w, YAR028w, YAR033w and YCR007c
5055_at 195.5 A
questionable ORF
5056_at -1.0 A
strong similarity to YAR033w protein
5057_at 836.4 P
hypothetical protein
5058_at 890.3 P
mRNA cap-binding protein (eIF-4F), 130K subunit
5059_at 9440.0 P
ATPase
5060_at 748.0 P
similarity to hypothetical S. pombe protein
5061_at 116.4 A
hypothetical protein
5062_at 569.2 P
hypothetical protein
5063_at 366.3 A
component of the cleavage and polyadenylation factor CF I involved in pre-mRNA 3 -end processing
5064_at 883.7 P
RNA polymerase II elongation factor
5065_at 945.6 P
questionable ORF
5066_at 351.2 A
weak similarity to YJL109c
5067_at 2306.3 P
delta-aminolevulinate dehydratase (porphobilinogen synthase)
5068_at 1242.4 P
similarity to V. vinifera dihydroflavonol reductase
5024_at 913.8 P
membrane-bound mannosyltransferase
5025_at 2972.7 P
similarity to E.coli hypothetical 23K protein
5026_at 1009.9 P
Mtf1 Two Hybrid Clone 2
5027_at 185.2 A
C2H2 zinc finger protein which resembles the mammalian Egr and Wilms tumour proteins
5028_at -108.6 A
questionable ORF
5029_at 44.6 A

Meiosis-specific gene required for the pairing of homologous chromosomes
5030_at 169.5 A
adhesion subunit of a-agglutinin
5031_at 61640.8 P
Ribosomal protein L24A (rp29) (YL21) (L30A)
5032_at 73047.3 P
Large ribosomal subunit protein L30 (L32) (rp73) (YL38)
5033_at 1420.8 P
weak similarity to human chromatin assembly factor I p150 chain
5034_at 1158.8 P
glucanase gene family member
5035_at 3686.1 P
glucosidase I
5036_at 27157.9 P
tryptophan synthetase
5037_at 502.7 P
Probable transcription factor, polyglutamine domain protein
5038_at 524.7 P
questionable ORF
5039_at 2059.7 P
weak similarity to Vsp27p
5040_at 6101.6 P
required for protein glycosylation
5041_at 957.2 P
DNA damage-responsive protein
5042_at 3187.5 P
hypothetical protein
5043_at 2565.0 P
beta (38kDa) subunit of casein kinase II (CKII)
5044_at 571.5 P
Homolog of E. coli Hsc20 co-chaperone protein
5045_at 341.7 A
arginyl-tRNA-protein transferase
5046_at 979.1 P
pleiotropic drug resistance regulatory protein
5002_at 336.6 P
hypothetical protein
5003_at 2823.9 P
similarity to Drosophila pumilio protein and Mpt5p protein
5004_at 1456.0 P
zinc-finger transcription factor of the Zn(2)-Cys(6) binuclear cluster domain type
5005_at 5802.8 P
Sterol C-24 reductase
5006_at 2490.9 P
Proteasome subunit YC7alphaVY8 (protease yscE subunit 7)
5007_at 367.1 M
similarity to hypothetical S. pombe protein
5008_at 13274.9 P
isopropylmalate isomerase
5009_at 52337.5 P
plasma membrane H+-ATPase
5010_at 74.8 A
questionable ORF
5011_at 1762.9 P
putative vacuolar Ca2+ ATPase
5012_at -28.4 A

			weak similarity to Xenopus kinesin-related protein Eg5
5013_at	576.3	P	weak similarity to Tup1p
5014_at	374.6	P	protein required for Clb2 and Ase1 degradation
5015_at	718.9	P	p24 protein involved in membrane trafficking
5016_at	3122.3	P	putative 3-beta-hydroxysteroid dehydrogenase
5017_at	1222.2	P	similarity to C.elegans hypothetical M142.5 protein
5018_at	680.7	P	similarity to C.elegans hypothetical M142.5 protein
5019_at	456.4	A	similarity to hypothetical S. pombe protein
5020_at	453.6	P	similarity to D.melanogaster lin19 protein
5021_at	845.2	P	strong similarity to hypothetical protein YLR324w
5022_at	1234.6	P	transcription initiation factor TFIIF middle subunit
5023_at	35.0	A	RNA splicing factor associated with U5 snRNP
4979_at	2745.1	P	choline phosphate cytidylyltransferase (also called phosphoethanolamine cytidylyltransferase or phosphocholine cytidylyltransferase)
4980_at	1832.6	P	ATPase stabilizing factor
4981_at	1294.7	P	Putative t-SNARE of the plasma membrane
4982_at	188.6	A	strong similarity to hypothetical protein YLR328w
4983_g_at	1014.4	P	strong similarity to hypothetical protein YLR328w
4984_at	477.9	A	questionable ORF
4985_at	1207.7	P	similarity to E.nidulans cysteine synthase
4986_at	212.1	A	Associated with U1 snRNP (no counterpart in mammalian U1 snRNP. Contains few SR-, RE- and RD-dipeptides.
4987_at	4436.0	P	putative integral membrane protein
4988_at	164.2	A	similarity to hypothetical protein YGR031w
4989_at	329.6	A	weak similarity to M.jannaschii hypothetical protein MJ1317
4990_at	1405.7	P	hypothetical protein
4991_at	-20.0	A	questionable ORF
4992_at	1031.5	P	gamma-aminobutyrate (GABA) transaminase (4-aminobutyrate aminotransferase)
4993_at	6074.6	P	Vacuolar H-ATPase 14 kDa subunit (subunit F) of the catalytic (V1) sector
4994_at	656.6	P	

similarity to M.leprae yfcA protein
4995_at -20.5 A
questionable ORF
4996_at 240.6 A
acts in concert with Mid2p to transduce cell wall stress signals
4997_at 448.5 P
weak similarity to Methanobacterium thermoautotrophicum hypothetical protein MTH972
4998_at 139.9 A
questionable ORF
4999_at 1324.7 P
hypothetical protein
5000_i_at 11274.6 P
Ribosomal protein S25A (S31A) (rp45) (YS23)
5001_f_at 66637.1 P
Ribosomal protein S25A (S31A) (rp45) (YS23)
4956_at 974.0 P
40 kDa putative membrane-spanning ATPase
4957_at 912.9 P
integral subunit of RNase P and apparent subunit of RNase MRP
4958_at 704.3 P
similarity to hypothetical protein YGR015c and weak similarity H.influenzae dihydrolipoamide acetyltransferase
4959_at 2248.4 P
catalytic component of 1,3-beta-D-glucan synthase
4960_at 1174.9 P
hypothetical protein
4961_at 2354.6 P
hypothetical protein
4962_at 141.9 A
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 15156.0 P
Acyl-CoA-binding protein (ACBP)\/Diazepam binding inhibitor (DBI)\/endozepine (EP)
4964_at 1703.7 P
strong similarity to hypothetical protein YLR350w
4965_at -131.8 A
questionable ORF
4966_at 268.5 A
MAP protein kinase homolog involved in pheromone signal transduction
4967_at 585.7 A
Among a group of genes whose products are necessary for bud-site selection\; likely involvement in positioning the proximal pole signal
4968_at 54.7 A
hypothetical protein
4969_at 263.5 A
strong similarity to transaldolase
4970_at 828.3 P
zinc finger protein\; negative regulator of meiosis\; directly repressed by a1-a2 regulator
4971_at 218.0 A
questionable ORF
4972_at 65.3 A
hypothetical protein
4973_at 624.0 P
transcription factor tau (TFIIIC) subunit 131
4974_at 905.3 P
ubiquitin fusion degradation protein

4975_at 3460.0 P
Protein that suppresses ts allele of CDC4 when overexpressed
4976_at 4.1 A
questionable ORF
4977_at -26.6 A
questionable ORF
4978_at -67.2 A
similarity to ser/thr protein kinases
4934_at -194.9 A
hypothetical protein
4935_at 1805.6 P
similarity to C.elegans E04D5.1 protein
4936_at 3207.0 P
high affinity methionine permease
4937_at 901.9 A
Member of RSC complex
4938_at 332.3 A
Required for amino acid permease transport from the Golgi to the cell surface
4939_at 316.9 A
similarity to mouse calcium-binding protein
4940_at 231.9 A a
sporulation-specific homologue of the yeast CDC3\/10\/11\/12 family of bud neck microfilament genes and is regulated by ABFI
4941_at 30390.8 P
C-4 sterol methyl oxidase
4942_at 12469.7 P 5
-phosphoribosylformyl glycinamidine synthetase
4943_at 722.5 P
Cytochrome OXidase gene 18
4944_at 1375.2 P
Zn-finger protein, transcriptional regulator
4945_at 505.3 P
questionable ORF
4946_at 408.5 A
similarity to P.putida phthalate transporter
4947_at 56.8 A
similarity to hypothetical protein YBR105c
4948_at 420.1 A
weak similarity to transcription factors
4949_at 118.4 A
weak similarity to Rod1p
4950_at -65.4 A
questionable ORF
4951_at 374.0 A
GDP-GTP Exchange Protein (GEP) for the Rho1p Small GTP-binding Protein
4952_at 471.6 P
similarity to hypothetical protein YLR373c
4953_at 180.9 A
factor stimulating decay of mRNAs containing premature stop codons\; acts with Nmd2p and Nam7p
4954_at 339.2 P
questionable ORF
4955_at 417.6 A
Homolog of human core snRNP protein D1, involved in snRNA maturation
4911_at 220.4 A
RNA splicing factor
4912_at 990.3 P

Mitochondrial ribosomal protein MRPL25 (YmL25)
4913_at 1106.8 P
peroxisome associated protein containing a PTS1 signal
4914_at 2241.2 P
Polypeptide 3 of a Yeast Non-native Actin Binding Complex, homolog of a component of the bovine NABC complex
4915_at 2868.5 P
hypothetical protein
4916_at 1712.5 P
Twinfilin A, an actin monomer sequestering protein
4917_at 345.5 A
weak similarity to mammalian myosin heavy chain
4918_at 3208.6 P
20 kDa mitochondrial outer membrane protein import receptor
4919_at 1702.0 P
translation initiation factor eIF2B, 71 kDa (delta) subunit\; translational repressor of GCN4 protein
4920_at 577.7 P
35 kDa mitochondrial ribosomal small subunit protein
4921_i_at 74066.4 P
60S ribosomal protein L11B (L16B) (rp39B) (YL22)
4922_at 4519.1 P
strong similarity to hypothetical protein YPL004c
4923_at -279.2 A
Third, minor isozyme of pyruvate decarboxylase
4924_at 56.6 A
cytoplasmic catalase T
4925_at 182.9 A
weak similarity to rat tropomyosin
4926_at 2376.7 P
hypothetical protein
4927_at 174.7 A
pre-mRNA splicing protein
4928_at 944.3 P
Serine\/threonine protein kinase
4929_at 605.8 P
similarity to hypothetical S.pombe protein
4930_at 12803.7 P
mitochondrial and cytoplasmic valyl-tRNA synthetase
4931_at 2654.2 P
Putative 3 ->5 exoribonuclease\; component of exosome complex of 3 ->5 exonucleases
4932_at 548.1 A
similarity to bovine Graves disease carrier protein
4933_at 2079.9 P
transcriptional activator of the SKN7 mediated two-component regulatory system
4888_at 904.3 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 290.1 A
involved in controlling telomere length
4890_at 646.8 P
Mac1-dependent regulator
4891_at 535.4 P
weak similarity to B.subtilis YqgP
4892_at 696.1 P
hypothetical protein

4893_at 1424.1 P
similarity to zebrafish essential for embryonic development gene pescadillo
4894_at 846.8 P
subunit of RNA polymerase II holoenzyme\/mediator complex
4895_at 1879.8 P
Protein involved in vacuolar H-ATPase assembly or function
4896_at 7016.1 P
hypothetical protein
4897_at -161.3 A
questionable ORF
4898_at 487.5 A
G(sub)2-specific B-type cyclin
4899_at 17.9 A
B-type cyclin
4900_at 339.6 A
weak similarity to YLR099c and YDR125c
4901_at 230.1 A
weak similarity to mosquito carboxylesterase
4902_at 226.9 A
mitochondrial protein with homology to the mammalian SURF-1 gene
4903_at 629.1 P
Duo1 And Mps1 interacting
4904_at 70.1 A
questionable ORF
4905_g_at 462.1 A
questionable ORF
4906_at -638.8 A
questionable ORF
4907_at 604.9 M
transcriptional regulator, interacts with histones, primarily histone H3, possesses nucleosome assembly activity
4908_at 286.8 A
hypothetical protein
4909_f_at 22718.1 P
Ribosomal protein S23A (S28A) (rp37) (YS14)
4910_at 873.4 P
Contains GLFG repeats in N-terminal half and heptad repeats in C-terminal half
4865_at 468.3 P
required for ER to golgi vesicle docking
4866_at 935.5 P
ammonia permease
4867_at 344.0 P
hypothetical protein
4868_at 1347.0 P
serine\/threonine phosphatase
4869_at 15993.2 P
asparagine synthetase
4870_at 2196.6 P
similarity to S.pombe hypothetical protein SPAC24H6.11c
4871_at -295.1 A
weak similarity to hypothetical protein YPR156c
4872_at 197.8 A
weak similarity to mouse T10 protein
4873_at 2150.1 P
hypothetical protein
4874_at 532.8 P

SYnthetic lethal with cdcForty
4875_at 403.9 P
weak similarity to myosin heavy chain proteins
4876_at 339.5 A
strong similarity to Nce2p
4877_at 1179.4 P
mitochondrial protein, prohibitin homolog\; similar to S. cerevisiae Phb2p
4878_at -174.0 A
Member of ubiquitin-conjugating protein family
4879_at 753.6 A
hypothetical protein
4880_at 3267.7 P
proteasome component Y13
4881_at 1712.2 P
weak similarity to chicken growth factor receptor-binding protein GRB2 homolog
4882_g_at 1561.3 P
weak similarity to chicken growth factor receptor-binding protein GRB2 homolog
4883_at 489.9 P
questionable ORF
4884_i_at 8882.7 P
similarity to multidrug resistance proteins
4885_at 9.4 A
questionable ORF
4886_at 599.5 P
110 kDa subunit of the centromere binding factor CBF3
4887_at 165.2 A
strong similarity to hypothetical protein YPR157w
4842_at 1020.4 P
similarity to hypothetical protein YPR158w
4843_at 769.0 P
encodes a predicted type II membrane protein highly homologous to Kre6p
4844_at 178.2 A
component of the biosynthetic pathway producing the thiazole precursor of thiamine
4845_at 1097.2 P
similarity to C.elegans hypothetical protein
4846_at 1349.8 P
hypothetical protein
4847_at 666.1 P N
alpha-acetyltransferase that acts on methionine termini
4848_at 86318.7 P
Ribosomal protein L24B (rp29) (YL21) (L30B)
4849_at 718.2 P
hypothetical protein
4850_at -9.8 A
hypothetical protein
4851_i_at 2353.0 P
questionable ORF
4852_s_at 1789.1 P
questionable ORF
4853_at 245.7 A
GTP-binding protein of the ras superfamily involved in bud site selection
4854_at 35.0 A
hypothetical protein
4855_at 237.7 A
strong similarity to hypothetical proteins YKR076w and YMR251w
4856_at 11763.4 P

Cystathionine beta-synthase
4857_at 417.4 A
hypothetical protein
4858_at 3774.7 P
Phosphatidyl-ethanolamine N-methyltransferase
4859_at -521.9 A
involved in mRNA transport
4860_at 6216.6 P
nuclear localization sequence binding protein
4861_at 429.7 A
questionable ORF
4862_at 2609.8 P
hypothetical protein
4863_at 3056.1 P
mRNA cap-binding protein (eIF-4F), 150K subunit , highly homologous to Tif4632p, homologs of mammalian p220
4864_at 787.3 P
GTP-binding protein
4819_at 49.8 A
questionable ORF
4820_at 456.5 P
hypothetical protein
4821_at 903.9 P
Involved in biosynthetic pathway for cell wall beta-glucans
4822_at 2827.3 P
Clathrin light chain
4823_at 150.2 A
hypothetical protein
4824_at 738.1 P
similarity to Rib2p
4825_at 671.3 P
phosphatidylserine decarboxylase located in vacuole or Golgi
4826_at 394.7 A
mitochondrial methionyl-tRNA synthetase
4827_at 1190.9 P
Golgi membrane protein
4828_at 1796.3 P
strong similarity to human GTP-binding protein
4829_at 365.9 A
Essential for the expression and activity of ubiquinol-cytochrome c reductase
4830_at 16207.3 P
Squalene monooxygenase
4831_at 169.3 A
questionable ORF
4832_at 1828.3 P
Alcohol acetyltransferase
4833_at 3064.2 P
Poly(A)-binding protein binding protein
4834_at 454.4 A
hypothetical protein
4835_at 17812.1 P
Ribonucleotide Reductase
4836_at 3934.9 P
similarity to YHR004c-a
4837_at 2422.5 P
questionable ORF

4838_at	3130.9	P	7.3 kDa subunit 9 of the ubiquinol cytochrome c oxidoreductase complex
4839_at	1803.6	P	Ubiquitin-protein ligase
4840_at	7334.0	P	tyrosyl-tRNA synthetase, cytoplasmic
4841_at	1212.2	P	Transcription factor TFIIF large subunit
4797_at	2286.1	P	HMG1\/2 homolog
4798_at	-380.3	A	Serine\/threonine protein kinase required for cell cycle arrest in response to loss of microtubule function
4799_at	8793.8	P	similarity to Aspergillus fumigatus rAsp
4800_at	55.7	A	questionable ORF
4801_at	3420.5	P	histidine permease
4802_i_at	99032.7	P	Glyceraldehyde-3-phosphate dehydrogenase 3
4803_at	1773.0	P	Protein X component of mitochondrial pyruvate dehydrogenase complex
4804_at	456.3	A	xylulokinase
4805_at	1589.5	P	homolog of RNAse PH
4806_at	835.3	P	weak similarity to Tetrahymena acidic repetitive protein arp1
4807_at	460.1	P	involved in nitrosoguanidine resistance
4808_at	2650.9	P	hypothetical protein
4809_at	1211.3	P	dolichyl phosphate-D-mannose:protein O-D-mannosyltransferase
4810_at	1418.7	P	weak similarity to rape guanine nucleotide regulatory protein
4811_at	331.3	P	strong similarity to translation elongation factor eEF1 alpha chain Cam1p
4812_at	588.0	A	phosphorylcholine transferase\; or cholinephosphate cytidylyltransferase
4813_at	469.2	P	weak similarity to X.laevis protein-tyrosin-phosphatase cdc homolog 2 and to hypothetical protein YPR200c
4814_at	18252.2	P	encodes the cytoplasmic trifunctional enzyme C1-tetrahydrofolate synthase
4815_at	270.4	A	similarity to S.pombe hypothetical protein D89234
4816_at	743.4	P	similarity to Xenopus transcription factor Oct-1.17
4817_at	203.9	A	electron-transferring flavoprotein, beta chain
4818_at	1458.5	P	phosphoserine phosphatase
4774_at	13306.1	P	thioredoxin
4775_at	4499.8	P	

similarity to M.jannaschii GTP-binding protein and to M.capricolum hypothetical protein SGC3
4776_at 1734.2 P
zinc finger protein
4777_at 66.8 A
weak similarity to S.pombe hypothetical protein SPAC18B11.03c
4778_at 474.6 P
involved in 7-aminocholesterol resistance
4779_f_at 17978.4 P
Ribosomal protein S0A
4780_at 29749.4 P
Ribosomal protein S0A
4781_at 590.5 P
strong similarity to hypothetical S. pombe protein
4782_at 443.6 P
Participates in synthesis of N-acetylglucoaminylphosphatidylinositol, the first intermediate in synthesis of glycosylphosphatidylinositol (GPI) anchors
4783_at 949.2 P
putative calcium channel
4784_at 167.3 A
omosome region maintenance protein
4785_at 519.5 P
questionable ORF
4786_at 1328.4 P
Mitochondrial ribosomal protein MRPL9 (YmL9) (E. coli L3) (human MRL3)
4787_at -330.3 A
similarity to hypothetical protein YHR149c
4788_at -152.0 A
translational activator of cytochrome c oxidase subunit III
4789_at 616.7 P
weak similarity to hypothetical protein YFR021w
4790_at 481.0 P
strong similarity to drug resistance protein SGE1
4791_at 369.2 A
weak similarity to human p55CDC and Cdc20p
4792_at -68.8 A
hypothetical protein
4793_at 1412.6 P
De-repression of ITR1 Expression
4794_at 1195.4 P
questionable ORF
4795_at 2086.8 P
57 kDa nuclear protein
4796_at 248.8 A
questionable ORF
4751_at 2946.0 P
mitochondrial protein, prohibitin homolog\; homolog of mammalian BAP37 and S. cerevisiae Phb1p
4752_at 964.7 P
possible homolog of human 26S proteasome regulatory subunit p28
4753_at 4170.9 P
Positive regulatory protein of phosphate pathway
4754_at 22480.7 P
Flavohemoglobin
4755_at 1493.5 P
hypothetical protein
4756_at 111.1 A
questionable ORF

4757_at	339.8	A	weak similarity to YOR019w
4758_at	377.2	A	protein containing kelch repeats, similar to YHR158c and YPL263c
4759_at	348.7	A	weak similarity to hypothetical protein YHR160c
4760_at	36824.4	P	phosphofructokinase alpha subunit
4761_at	1010.5	P	Yeast Assembly Polypeptide, member of AP180 protein family, binds Pan1p and clathrin
4762_at	166.8	A	questionable ORF
4763_at	226.0	A	strong similarity to hypothetical protein YHR162w
4764_at	2454.9	P	Succinate-CoA Ligase (ADP-Forming)
4765_at	2337.3	P	similarity to hypothetical S.pombe protein
4766_at	1063.9	P	RNA polymerase III transcription factor with homology to TFIIB
4767_at	11.5	A	hypothetical protein
4768_at	85.5	A	similar to SOL3
4769_at	56.2	A	Mga1p shows similarity to heat shock transcription factor
4770_at	1192.5	P	weak similarity to human cleavage stimulation factor 64K chain
4771_at	525.7	A	hypothetical protein
4772_at	394.4	A	histone acetyltransferase
4773_at	7144.1	P	Proteasome subunit
4729_i_at	90555.2	P	enolase I
4730_s_at	238347.9	P	enolase I
4731_at	1657.9	P	COQ6 monooxygenase
4732_at	107.6	A	6-phosphogluconate dehydrogenase
4733_at	1281.3	P	similarity to C.elegans C16C10.1
4734_at	423.9	A	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	271.1	A	questionable ORF
4736_at	7249.7	P	similarity to allantoate transport protein
4737_at	2742.3	P	putative beta adaptin component of the membrane-associate clathrin assembly complex
4738_at	653.5	P	ser/thr protein kinase

4739_at	536.1	P	weak similarity to E.coli lipase like enzyme
4740_at	15529.1	P	methionyl tRNA synthetase
4741_at	160.7	A	questionable ORF
4742_at	943.7	P	hypothetical protein
4743_at	2706.5	P	GTP-cyclohydrolase I
4744_at	836.3	P	weak similarity to S.pombe hypothetical protein SPAC17A5
4745_at	-224.0	A	questionable ORF
4746_at	1362.2	P	Member of CDC48\/PAS1\/SEC18 family of ATPases
4747_at	510.0	A	strong similarity to S.pombe RNA helicase
4748_at	578.4	P	similarity to hypothetical S.pombe protein SPAC12G12.02
4749_at	-118.4	A	similarity to hypothetical protein YMR295c
4750_at	1695.0	P	Component of the TAFII complex required for activated transcription
4705_at	1441.9	P	hypothetical protein
4706_at	1398.3	P	ribonuclease H
4707_at	1155.1	P	similarity to hypothetical S.pombe protein
4708_at	212.3	A	similarity to C.elegans LET-858
4709_at	56470.2	P	glucanase gene family member
4710_at	3040.0	P	weak similarity to Cbf5p
4711_at	14463.3	P	ABC transporter
4712_at	19473.7	P	Cell wall endo-beta-1,3-glucanase
4713_at	830.3	P	similarity to hypothetical protein YMR310c
4714_at	2204.5	P	similarity to mouse Surf-4 protein
4715_at	24986.2	P	Zuotin, putative Z-DNA binding protein
4716_at	993.1	P	Biotin synthase
4717_at	150.4	A	strong similarity to maltase
4718_at	178.2	A	maltose pathway regulatory protein
4719_at	259.6	A	alpha-glucoside transporter
4720_at	52.0	A	hypothetical protein

4721_at -14.9 A
hypothetical protein
4722_s_at -46.8 A
strong similarity to hypothetical protein YBR300c
4723_f_at -508.8 A
strong similarity to members of the Srp1p/Tip1p family
4724_i_at 478.2 A
hypothetical protein
4725_f_at 365.4 P
hypothetical protein
4726_at 130.7 A
identified by SAGE
4727_s_at 634.2 P
Protein essential for mitochondrial biogenesis and cell viability
4728_at 23.7 A
non-annotated SAGE orf Found reverse in NC_001139 between 110655 and 110840 with 100% identity. See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251
4681_at 7222.0 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 1765.8 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 650.5 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 208.9 A
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 1274.9 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 192.7 A
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 588.0 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 -13.8 A
non-annotated SAGE orf Found forward in NC_001139 between 323656 and 323817 with 100% identity. See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251
4689_at 128.7 A
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 505.9 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 4120.1 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 599.7 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 -202.2 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 28.4 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 276.8 A
non-annotated SAGE orf Found forward in NC_001139 between 299797 and 299946 with 100% identity.
See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251
4696_at 3577.9 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 507.9 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 257.8 A
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 700.0 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 179.4 A
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 3098.9 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 4393.6 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 420.3 A
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 77.5 A
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 238.5 A
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 1429.9 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 76.4 A
non-annotated SAGE orf Found forward in NC_001139 between 783944 and 784078 with 100% identity.
See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251
4661_r_at 50.7 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 27959.9 P
non-annotated SAGE orf Found forward in NC_001139 between 827159 and 827320 with 100% identity.
See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251
4663_at 739.4 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 -87.5 A
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 -76.5 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 6954.9 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 148.5 A
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 33.0 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 26.4 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 1644.1 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 225.9 A
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 -64.7 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 262.4 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 2.3 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 -44.1 A
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 209.5 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 164.5 A
non-annotated SAGE orf Found forward in NC_001139 between 773986 and 774189 with 100% identity. See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251
4678_at -190.7 A
non-annotated SAGE orf Found forward in NC_001139 between 1069513 and 1069650 with 100% identity. See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251
4679_at 268.9 A
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 -184.8 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 -149.8 A
non-annotated SAGE orf Found reverse in NC_001139 between 74536 and 74757 with 100% identity. See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251
4632_g_at 5.5 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 37.3 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 -403.9 A
non-annotated SAGE orf Found reverse in NC_001139 between 93374 and 93667 with 100% identity.
See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251
4635_g_at -81.5 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 -226.7 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 -122.5 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 114.1 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 777.2 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 20.4 A
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 452.9 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 -247.8 A
non-annotated SAGE orf Found reverse in NC_001139 between 401513 and 401656 with 100% identity.
See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251
4643_f_at -151.8 A
non-annotated SAGE orf Found reverse in NC_001139 between 401513 and 401656 with 100% identity.
See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251
4644_i_at 265.7 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 1.5 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 169.7 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 96.4 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 24.5 A
non-annotated SAGE orf Found reverse in NC_001139 between 701262 and 701477 with 100% identity.
See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251
4649_r_at 83.4 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
4650_f_at 288.0 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
4651_at 827.9 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 1161.7 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 375.3 A
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 404.1 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 439.6 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 808.4 P
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 213.2 A
non-annotated SAGE orf Found reverse in NC_001139 between 823398 and 823550 with 100% identity.
See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251
4608_g_at 75.4 A
non-annotated SAGE orf Found reverse in NC_001139 between 823398 and 823550 with 100% identity.
See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251
4609_at 149.1 A
non-annotated SAGE orf Found reverse in NC_001139 between 919562 and 919735 with 100% identity.
See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251
4610_at 43.2 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 123.1 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 -108.4 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 110.0 A
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 904.3 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 1996.3 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 633.0 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 806.6 A
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 1780.8 P
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 307.3 A
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 137.7 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 509.9 P
non-annotated SAGE orf Found forward in NC_001139 between 274428 and 274583 with 100% identity.
See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251
4622_at 798.2 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 9933.2 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 392.1 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 23430.8 P
non-annotated SAGE orf Found reverse in NC_001139 between 533928 and 534068 with 100% identity.
See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251
4626_at 501.0 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 513.1 A
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 430.9 A
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 217.8 A
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 634.7 P
non-annotated SAGE orf Found forward in NC_001139 between 733406 and 733621 with 100% identity.
See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251
4585_at 626.1 A
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 211.0 A
non-annotated SAGE orf Found forward in NC_001139 between 787843 and 788070 with 100% identity.
See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251
4587_at -111.4 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 186.3 A
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 194.4 A
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 480.2 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 727.4 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 -67.3 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 138.9 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 93.0 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 74.2 A
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 -88.6 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 143.1 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
4598_g_at -96.2 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 168.6 A
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 1296.5 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 5135.1 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 1138.1 P
non-annotated SAGE orf Found reverse in NC_001139 between 1058818 and 1058976 with 100% identity. See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251
4603_at 255.2 A
snRNA
4604_i_at 308.1 A
snRNA
4605_s_at 417.1 A
snRNA
4606_at 258.5 A
snRNA
4607_at 161.0 A
snRNA
4561_s_at 259.0 A
snRNA
4562_at -98.5 A
similarity to C.carbonum toxin pump
4563_f_at 1719.3 P
strong similarity to members of the Srp1p/Tip1p family
4564_at -3.2 A
similarity to subtelomeric encoded proteins

4565_at	76.1	A	ExtraCellular Mutant
4566_at	264.2	A	similarity to subtelomeric encoded proteins
4567_at	173.2	A	weak similarity to Drosophila hypothetical protein 6
4568_at	264.6	A	similarity to C.carbonum toxin pump
4569_at	948.6	P	weak similarity to YPL208w
4570_at	249.4	A	Cytochrome B pre-mRNA processing protein
4571_at	-2.0	A	hypothetical protein
4572_at	386.7	A	very low affinity methionine permease
4573_at	148.9	A	ABC transporter
4574_at	20402.6	P	Single-strand nucleic acid binding protein
4575_i_at	36620.4	P	Ribosomal protein L8A (rp6) (YL5) (L4A)
4576_at	470.7	A	glyerol kinase (converts glycerol to glycerol-3-phosphate
4577_at	1564.3	P	SNARE protein with a C-terminal membrane anchor
4578_at	1187.4	P	ExtraCellular Mutant
4579_at	1821.7	P	hypothetical protein
4580_at	541.0	P	Putative integral membrane protein containing novel cysteine motif. Similarity to SLG1 (WSC1), WSC2 and WSC3
4581_at	3237.8	P	Meiotic regulatory protein\; Cys-His zinc fingers
4582_at	713.5	P	hypothetical protein
4583_at	2091.4	P	transcriptional regulator
4584_at	236.4	A	RNA binding domain (N-term) with asparagine rich region?
4539_at	725.1	P	hypothetical protein
4540_at	-119.7	A	Encodes one of the earliest meiosis-specific recombination functions.
4541_at	635.2	P	weak similarity to Pseudomonas gamma-butyrobetaine hydroxylase
4542_at	2398.5	P	negative regulator of phospholipid biosynthesis
4543_at	625.6	P	Similiar to clathrin coat proteins
4544_at	-153.5	A	Dimerization cofactor of homeodomian protein NF1-alpha
4545_at	777.9	P	Probable transmembrane protein PTM1
4546_at	548.7	P	

Urea transporter
4547_at 21311.6 P
Ribosomal protein S20
4548_at -88.5 A
GTP-binding protein and glycogen phosphorylase (weak)
4549_at 782.8 P
similarity to C.elegans hypothetical protein F21D5.2
4550_at -68.4 A
UDP Glucose pyrophosphorylase
4551_at 5662.6 P
ribose-phosphate pyrophosphokinase 3
4552_at 59.4 A
similarity to C.elegans hypothetical protein
4553_at 493.4 P
bZip DNA binding proteins
4554_at 1192.4 P
Potential formate transporter nirC
4555_at 1232.5 P
serine\/threonine protein kinase
4556_at -82.3 A
hypothetical protein
4557_at 50.9 A
hypothetical protein
4558_at 252.0 A
mitochondrial ribosomal protein, homologous to E. coli ribosomal protein S2, component of the 37 S subunit of mitochondrial ribosomes
4559_at 415.7 A
YKL008c
4560_at 1084.6 P
SH3 domain
4515_i_at 10863.0 P
Ribosomal protein L14B
4516_f_at 21268.5 P
Ribosomal protein L14B
4517_at 766.0 P
60kD chaperonin (weak)
4518_at 1877.9 P
8.5 kDa subunit of the ubiqunol-cytochrome c oxidoreductase complex
4519_at 717.3 A
Mitochondrial carrier protein\/Grave s disease carrier protein
4520_at 1301.9 P
thiF, moeB, ubiquitin activating enzyme (all weak)
4521_at 254.2 A
similarity to YLL010c, YLR019w
4522_at 1975.5 P
alpha subunit of G protein coupled to mating factor receptors
4523_at 4083.6 P
May act cooperatively with Mrs5p in mitochondrial protein import or other related essential mitochondrial processes
4524_at 767.4 P
Zinc finger (Cys(2)-His(2))
4525_at 28008.4 P
cytochrome P450 lanosterol 14a-demethylase
4526_at 5265.3 P
Manganese-containing superoxide dismutase
4527_at 2385.4 P

similarity to S.pombe hypothetical protein
4528_i_at	46642.4	P
Ribosomal protein L27A
4529_f_at	32858.9	P
Ribosomal protein L27A
4530_at	317.4	A
Seryl-tRNA synthetase
4531_at	1111.2	P
Vacuolar protein sorting
4532_at	978.3	P
subunit of the major N alpha-acetyltransferase, complexes with the catalytic subunit of N-a-acetyltransferase (Nat1)
4533_at	-54.2	A
Encodes a 33.4 kDa basic protein that localizes to the nucleus. Thought to be a meiosis-specific negative regulator of M-phase during meiosis I, coordinating sister-chromatid\/centromere cohesion with nuclear division. Spo13p has transcriptional activation activity in one-hybrid analysis.
4534_at	194.2	A
PolyA-binding protein
4535_at	559.4	P
SH3 domain in C-terminus
4536_at	589.2	A
strong similarity to S.douglasii YSD83
4537_at	2706.5	P
argininosuccinate lyase
4538_at	10116.6	P
Asparaginyl-tRNA synthetase
4493_at	17832.6	P
Aminoacyl tRNA-synthetase
4494_at	66706.4	P
40S Ribosomal protein S27B (rp61) (YS20)
4495_at	18.3	A
ExtraCellular Mutant
4496_at	129.0	A
RAS-related protein
4497_at	425.9	P
Class II Myosin
4498_at	878.5	P
53 kDa subunit of the mitochondrial processing protease
4499_at	18870.6	P
homoserine kinase
4500_at	9447.1	P
proteolipid protein of the proton ATPase
4501_at	7481.8	P
Subunit of 26S Proteasome (PA700 subunit)
4502_at	2396.0	P
Dipeptidyl aminopeptidase B (DPAP B)
4503_at	946.6	P
Thymidylate synthase (putative\; weak)
4504_at	3851.3	P
putative protein kinase
4505_at	268.8	P
Pif1p, mitochondrial DNA repair and recombination protein
4506_at	652.7	P
ethionine resistance protein
4507_at	496.1	P
Pro1p (Gamma-glutamyl kinase)

4508_at	261.8	A	hypothetical protein
4509_at	97.3	A	Sec23p (weak)
4510_at	445.6	A	similarity to hypothetical protein YGL247w
4511_at	1051.8	P	delta-1-pyrroline-5-carboxylate dehydrogenase
4512_at	283.0	A	Killed in Mutagen, sensitive to Diepoxybutane and\/or Mitomycin C
4513_at	3483.5	P	Aldehyde dehydrogenases
4514_at	11270.0	P	13-kDa vacuolar H-ATPase subunit
4469_at	968.5	P	weak similarity to Hit1p
4470_at	1528.5	P	RNA polymerase II holoenzyme\/mediator subunit
4471_at	8382.2	P	NADP-cytochrome P450 reductase
4472_s_at	507.5	A	2-deoxyglucose-6-phosphate phosphatase
4473_i_at	838.2	P	2-deoxyglucose-6-phosphate phosphatase
4474_at	1640.1	P	hypothetical protein
4475_at	1894.9	P	Inositol monophosphatase
4476_at	3331.7	P	arginine\/alanine aminopeptidase
4477_at	-264.8	A	similarity to multidrug resistance proteins
4478_at	1291.9	P	similarity to S.pombe dihydrofolate reductase and YOR280c
4479_at	302.3	A	questionable ORF
4480_at	1153.8	P	localized to mitochondrial membrane
4481_at	2333.8	P	subunit VI of cytochrome c oxidase
4482_at	1354.9	P	weak similarity to P.yoelii rhoptry protein
4483_s_at	34675.2	P	copper-binding metallothionein
4484_s_at	2741.0	P	weak similarity to YOR262w
4485_at	3879.8	P	Peptidylprolyl isomerase (cyclophilin) ER or secreted
4486_at	410.9	A	RNA polymerase II transcriptional regulation mediator
4487_at	256.6	A	weak similarity to Ustilago hordei B east mating protein 2
4488_at	429.3	A	required for V-ATPase activity
4489_at	553.6	P	GTPase-interacting component 1

4490_at 1198.0 P
Protein subunit of nuclear ribonuclease P (RNase P)
4491_at 1954.5 P
weak similarity to translational activator CBS2
4492_at 14554.2 P
Hsp70 Protein
4446_at 1553.0 P
RRP3 is a DEAD box gene homologous to eIF-4a which encodes an RNA-dependent ATPase possessing helicase activity which is not specific for RNA
4447_at 1401.3 P
homologous to Ssf2p
4448_at 5.3 A
hypothetical protein
4449_at 9672.2 P
Deoxyhypusine synthase
4450_at 895.7 P
3->5 exoribonuclease\; Component of the exosome 3->5 exonuclease complex with Rrp41p, Rrp42p, Rrp43p and Dis3p (Rrp44p).
4451_at 642.5 P
strong similarity to N.crassa met-10+ protein
4452_at 929.5 P
G1\/S cyclin (weak)
4453_at 4480.5 P
2,3-oxidosqualene-lanosterol cyclase
4454_at 359.9 A
Oxysterol-binding protein
4455_at 1499.9 P
weak similarity to B.subtilis spore outgrowth factor B
4456_at 168.8 A
ribosomal protein of the small subunit, mitochondrial
4457_at 770.1 P
weak similarity to C.elegans hypothetical protein CEW09D10
4458_at 695.3 P
hypothetical protein
4459_at 330.9 A
Ire1p is a transmembrane protein that has both serine-threonine kinase and endoribonuclease activities
4460_i_at 10.3 A
Ire1p is a transmembrane protein that has both serine-threonine kinase and endoribonuclease activities
4461_r_at 19.0 A
Ire1p is a transmembrane protein that has both serine-threonine kinase and endoribonuclease activities
4462_at 794.8 A
similarity to hypothetical protein YDR326c, YFL042c and YLR072w
4463_at 491.2 P
weak similarity to human C1D protein
4464_at 1271.8 P
Ser\/Thr protein kinase
4465_at 1075.8 P
hypothetical protein
4466_at 1302.2 P
Transcription factor
4467_at 1116.0 P
weak similarity to fruit fly brahma transcriptional activator
4468_at 604.1 A
putative RNA binding protein, involved in meiosis-specific splicing of the REC107 transcripts in cooperation with the Mer1 protein
4423_at 525.3 P

hypothetical protein
4424_at 1184.9 P
similarity to hypothetical protein YNL075w
4425_at 18975.3 P
small nucleolar RNP proteins
4426_at 212.9 A
NuBbiN
4427_at 701.9 P
Arginyl-tRNA synthetase
4428_at 218.1 A
High-affinity glucose transporter
4429_at -94.4 A
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 7145.5 P
High-affinity hexose (glucose) transporter
4431_at 76.7 A
hypothetical protein
4432_at -38.2 A
hexose transporter
4433_at 1157.7 P
strong similarity to hypothetical protein YDR348c
4434_at 109.2 A
strong similarity to hypothetical protein YDR348c
4435_at 3702.6 P
binds to Sed5p and Sec23p by distinct domains
4436_at 1423.9 P
ATM\/Mec1\/TOR1+2-related
4437_at 1181.1 P
hypothetical protein
4438_at 776.2 P
Bad in glucose or big cells
4439_at 231.8 A
Bad in glucose or big cells
4440_at 785.4 P
Ser\/Thr protein kinase
4441_at 1081.6 P
functionally redundant and similar in structure to SBE2
4442_at 918.9 P
Aldo-keto reductase
4443_at 230.7 A
weak similarity to Mvp1p
4444_at 725.2 P
Thioredoxin reductase
4445_at 1313.3 P
Component of 10 nm filaments of mother-bud neck (septin)
4401_at 4155.4 P
strong similarity to hypothetical protein YDR358w
4402_at 198.8 A
hypothetical protein
4403_at 1224.1 P
p24 protein involved in membrane trafficking
4404_at 793.4 A
moeB, thiF, UBA1
4405_at 1748.8 P
Cystathionine gamma-synthase

4406_at 1471.1 P
Vacuolar aminopeptidase
4407_at 623.7 P
SH3 domain
4408_at 1598.9 P
strong similarity to hypothetical protein YNL116w
4409_at 210.3 A
hypothetical protein
4410_at 2301.2 P
71-kDa component of the protein translocase of the outer membrane of mitochondria
4411_at 152.2 A
50-kDa subunit of ORC
4412_at 912.2 P
trithorax
4413_at 840.4 P
mutS homolog involved in mitochondrial DNA repair
4414_at 1325.7 P
weak similarity to C.elegans hypothetical protein
4415_at 495.4 A
similarity to hypothetical C. elegans protein F45G2.a
4416_at 225.5 A
sn-1,2-diacylglycerol ethanolamine- and cholinephosphotranferase
4417_at 1247.4 P
sn-1,2-diacylglycerol ethanolamine- and cholinephosphotranferase
4418_at 30.7 A
meiosis-specific gene, mRNA is sporulation-specific
4419_at 63.7 A
questionable ORF
4420_at -103.8 A
hypothetical protein
4421_at 981.9 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 5898.9 P
UPRTase
4378_at 110.1 A
Centractin
4379_at 634.1 P
weak similarity to T.brucei H+-transporting ATP synthase
4380_at 247.1 A
Highly acidic C-terminus
4381_at 1914.4 P
Carboxypeptidase
4382_at 4601.6 P
similarity to hypothetical protein YNL156c
4383_at -63.7 A
hypothetical protein
4384_at 4464.4 P
membrane-bound casein kinase I homolog
4385_at 4589.7 P
17 kDa protein
4386_at 4257.0 P
aromatic amino acid aminotransferase II
4387_at 1251.3 P
hypothetical protein
4388_at -2.2 A

			sporulation-specific wall maturation protein
4389_at	47.1	A	hypothetical protein
4390_at	81.1	A	hypothetical protein
4391_at	2017.0	P	weak similarity to cytochrome-c oxidases
4392_at	9633.8	P	Ser-Thr rich protein
4393_at	1115.4	P	subunit of RNA polymerase II
4394_at	948.9	P	dCMP deaminase
4395_at	35.9	A	questionable ORF
4396_at	1838.2	P	similarity to pheromone-response G-protein Mdg1p
4397_at	239.8	A	Mitochondrial ribosomal protein MRPL6 (YmL6)
4398_at	658.7	P	ribosomal protein (weak similarity)
4399_at	529.9	P	similarity to hypothetical protein YGR221c
4400_at	-318.1	A	weak similarity to YDR479c
4356_at	773.5	P	hypothetical protein
4357_at	895.1	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	205.4	A	sporulation protein
4359_at	1255.4	P	Establishes Silent omatin
4360_at	699.7	P	Snf1-interacting protein Sip3p
4361_at	227.9	A	weak similarity to mouse kinesin KIF3B
4362_at	178.3	A	mRNA is induced early in meiosis
4363_at	883.3	P	protein containing kelch repeats, similar to YGR238c
4364_at	39.8	A	hypothetical protein
4365_at	159.2	A	weak similarity to hypothetical protein YGR239c
4366_at	1587.0	P	Yeast Assembly Polypeptide, member of AP180 protein family, binds Pan1p and clathrin
4367_at	7472.9	P	strong similarity to hypothetical protein YGR243w
4368_at	2815.7	P	shows similarity to glucose-6-phosphate dehydrogenase non-catalytic domains\; homologous to Sol2p and Sol1p
4369_at	623.7	P	DNA replication helicase

4370_at 1504.2 P
RNA splicing factor
4371_at 175.3 A
Cell division cycle protein
4372_at 384.9 P
hypothetical protein
4373_at 327.0 A
GTP-binding protein
4374_at 2147.9 P
DEAD-box protein
4375_at 3607.8 P
putative Upf1p-interacting protein
4376_at 330.6 A
autophagy
4377_at 93.2 A
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 125.3 A
hypothetical protein
4334_i_at 202996.9 P
enolase
4335_at 2054.1 P
Putative low-affinity copper transport protein
4336_at 438.6 P
Dimethylaniline monoxygenase
4337_at 184.8 A
weak similarity to Spombe pac2 protein
4338_at 156.1 A
Zinc finger (6-Cys)
4339_at 14131.6 P
NAPDH dehydrogenase (old yellow enzyme), isoform 2
4340_at 540.4 P
hypothetical protein
4341_at 1488.7 P
similarity to mouse TEG-261 protein
4342_at 628.0 P
hypothetical protein
4343_at 26284.6 P
Phosphogluconate Dehydrogenase (Decarboxylating)
4344_at 36.8 A
Involved in the control of meiotic nuclear divisions and spore formation
4345_at -188.5 A
hypothetical protein
4346_at 1292.0 P
similarity to C.elegans hypothetical protein C10C5.6
4347_at 141.9 A
confers sensitivity to killer toxin
4348_at 2308.0 P
similarity to hypothetical C. elegans proteins F17c11.7
4349_at -193.0 A
similarity to peptidyl-tRNA hydrolases
4350_at 10588.0 P
squalene synthetase
4351_at 911.9 P
protein of unknown function
4352_at 465.8 A

hypothetical protein
4353_at 11578.2 P
GAL4 enhancer protein, homolog of human alpha NAC subunit of the nascent-polypeptide-associated complex
4354_at 914.2 P
similarity to hypothetical protein YOR147w
4355_at 903.4 P
hypothetical protein
4310_at 1165.0 P
hypothetical protein
4311_at 1584.7 P
hypothetical protein
4312_at 340.1 A
strong similarity to hypothetical protein YHR199c
4313_at 2198.2 P
strong similarity to hypothetical protein YHR198c
4314_at 5837.6 P
homolog of the mammalian S5a protein, component of 26S proteasome
4315_at 2142.0 P
Cytosolic exopolyphosphatase
4316_at 317.5 A
similarity to S.pombe hypothetical protein SPAC17G6
4317_at 1449.8 P
similarity to alpha-mannosidases
4318_at 1636.9 P
cAMP-dependent protein kinase homolog, suppressor of cdc25ts
4319_at 1474.7 P
Protein with similarity to DNA-binding region of heat shock transcription factors
4320_at 580.9 A
weak similarity to YPL165c
4321_at 8558.8 P
branched-chain amino acid transaminase, highly similar to mammalian ECA39, which is regulated by the oncogene myc
4322_at 554.3 A
UDP-glucose-4-epimerase (GAL10, galE)
4323_f_at 18499.4 P
IMP dehydrogenase\; probable PUR5 gene
4324_s_at 1211.0 P
gene in Y repeat region
4325_at 84.0 A
questionable ORF
4326_at 438.8 A
questionable ORF
4327_at 34.9 A
questionable ORF
4328_at -98.4 A
questionable ORF
4329_at 508.6 A
questionable ORF
4330_at 4351.5 P
questionable ORF
4331_at 179.9 A
questionable ORF
4332_at 161.3 A
questionable ORF
4286_s_at 1960.4 P

Highly acidic C-terminus

4287_s_at 212.2 A

similarity to hypothetical protein YER175c

4288_at 689.4 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 -180.3 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 29.6 A

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

4291_i_at -229.5 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 -85.3 A

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 740.0 A

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 245.0 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 203.8 A

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 31.9 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 139.2 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 -137.2 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 199.9 A

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 474.3 M

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 7.6 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 284.1 A

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 1238.4 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 89.4 A

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 196.1 A

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 -431.9 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 -151.6 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 41.5 A

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 95.6 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 118.7 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 -53.0 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 123.5 A

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 45.0 A

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 -94.9 A

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 1617.0 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 148.8 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 -45.5 A

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

4269_f_at 142.9 A

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 226.1 A

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

4271_at 85.1 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 1688.0 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 292.2 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 477.9 M

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 126.6 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 101.3 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 -103.1 A
Centromere
4278_at 640.3 A
snRNA
4279_at 427.9 A
snRNA
4280_f_at -906.9 A
strong similarity to members of the Srp1p/Tip1p family
4281_i_at 196.1 A
High-affinity hexose transporter
4282_f_at 640.2 A
High-affinity hexose transporter
4283_at 161.9 A
L-serine dehydratase
4284_at -274.0 A
serine dehydratase
4285_at 135.1 A
similarity to allantoate permease Dal5p
4237_at 496.5 P
putative pseudogene
4238_at 247.6 P
Nit1 nitrilase
4239_at -1.8 A
questionable ORF
4240_at 595.8 P
hypothetical protein
4241_at 17.3 A
peroxisomal 3-oxoacyl CoA thiolase
4242_at 331.3 A
Bni1p-related protein, helps regulate reorganization of the actin cytoskeleton, potential target of Rho4p
4243_at 1247.1 P
similarity to hypothetical protein YKR100c
4244_at 1267.1 P
hypothetical protein
4245_at 185.8 A
Ubiquitin-specific protease
4246_at 427.2 A
glycerol-3-phosphate dehydrogenase, mitochondrial
4247_at 1743.9 P
transcription factor
4248_at 1567.1 P
Resistant to Rapamycin Deletion
4249_at 500.3 P
hypothetical protein
4250_at 385.2 A
similarity to mitochondrial aldehyde dehydrogenase Ald1p
4251_at 50.7 A
Protein required for S-phase (DNA synthesis) initiation or completion
4252_at 1450.1 P
similarity to Mlp1p and myosin heavy chains
4253_i_at 46360.2 P

Ribosomal protein L40A
4254_at 1437.7 P
histidine kinase osmosensor that regulates an osmosensing MAP kinase cascade and is similar to bacterial two-component regulators
4255_at 167.0 A
ExtraCellular Mutant
4256_at 1828.8 P
similarity to E.coli pantothenate synthetase
4257_at 154.0 A
Dmc1p interacting protein
4258_at 488.1 P
DNA helicase homolog\; homolog of human XPBC, ERCC3
4259_at 5924.9 P
molecular chaperone
4260_at -208.3 A
questionable ORF
4215_g_at 387.5 A
questionable ORF
4216_at 1217.0 P
localizes to the plasma membrane
4217_at 127.0 A
subunit of DNA polymerase-zeta (Pol-zeta), an enzyme whose sole function appears to be translesion synthesis
4218_at 444.3 A
Tropomyosin isoform 2
4219_at 1768.4 P
similarity to M.musculus aminopeptidase
4220_at 232.2 A
45-kDa mitochondrial outer membrane protein
4221_at 1248.8 P
similarity to Ymk1p
4222_at 330.1 P
mitochondrial inner membrane carrier protein for FAD
4223_at 53626.6 P
Ribosomal protein L16A (L21A) (rp22) (YL15)
4224_at -1.1 A
hypothetical protein
4225_at 619.7 P
similarity to Drosophila fork head protein
4226_at 554.4 P
similarity to Put3p and to hypothetical protein YJL206c
4227_at 1988.6 P
similarity to hypothetical human protein
4228_at 978.7 P
Involved in nucleotide excision repair and regulation of TFIIH
4229_at 1682.9 P
weak similarity to Smy2p
4230_at 1445.1 P
helicase related protein, snf2 homolog
4231_at 3694.9 P
alpha-ketoglutarate dehydrogenase
4232_at 1699.9 P
similarity to C.perfringens nanH protein
4233_at 7866.7 P
involved in cell cycle regulation and aging
4234_at 61.9 A

			hypothetical protein
4235_at	281.5	A	similarity to antibiotic resistance proteins
4236_at	21.9	A	similarity to antibiotic resistance proteins
4192_at	358.8	A	inhibitor of ras
4193_at	1544.7	P	ras homolog--GTP binding protein
4194_at	2645.8	P	hydrophobic transmembrane domain
4195_at	3210.4	P	histidinol-phosphate aminotransferase
4196_at	2544.2	P	159-kDa nucleoporin with coiled-coil domain and repeated motifs typical of nucleoporins
4197_at	1520.6	P	voltage dependent anion channel (YVDAC2)
4198_at	149.3	A	strong similarity to dual-specificity phosphatase Msg5p
4199_at	647.3	A	similarity to ankyrin and coiled-coil proteins
4200_at	168.7	A	Cytochrome-c oxidase chain Vb
4201_at	972.0	P	weak similarity to hypothetical C.elegans protein
4202_at	2901.3	P	The Sec23p-Sec24p complex is one of three cytoplamic COPII factors involved in ER to Golgi transport
4203_at	2275.1	P	similarity to hypothetical S. pombe protein
4204_at	98.9	A	6-Phosphofructose-2-kinase
4205_at	321.7	A	weak similarity to probable transcription factor Ask10p
4206_at	819.7	P	similarity to hypothetical S. pombe protein
4207_at	1156.9	P	weak similarity to Dph2 protein
4208_at	-72.7	A	strong similarity to YIL014c-a
4209_at	-10.2	A	DNA-binding transcriptional repressor
4210_at	81.9	A	similarity to mouse Gcap1 protein and fruit fly Bkm-like sex-determining region hypothetical protein CS314
4211_at	225.9	A	intracellular glucoamylase
4212_g_at	243.9	A	intracellular glucoamylase
4213_at	249.7	A	Formation of Mitochondrial Cytochromes 1
4214_at	148.8	A	hypothetical protein
4170_at	528.0	P	hypothetical protein
4171_at	26.1	A	probable serine\/threonine-protein kinase

4172_at	23754.2	P	Homo-isocitrate dehydrogenase
4173_at	197.2	A	weak similarity to S.pombe hypothetical protein SPBC16A3
4174_at	231.8	A	hypothetical protein
4175_at	1142.1	P	weak similarity to spt5p
4176_at	638.4	P	similarity to hypothetical S. pombe protein
4177_at	300.6	A	similarity to hypothetical protein YLR036c
4178_at	1848.9	P	weak similarity to A.thaliana aminoacid permease AAP4
4179_at	911.7	P	hypothetical protein
4180_at	42.4	A	hypothetical protein
4181_at	1014.5	P	Putative mannosyltransferase of the KRE2 family
4182_at	135.9	A	Functions are similar to those of SIN3 and RPD3
4183_at	1500.1	P	hypothetical protein
4184_s_at	1558.2	P	Ty3-2 orf C fragment
4185_at	389.3	M	strong similarity to hypothetical protein YDL175c
4186_at	14904.2	P	Threonyl-tRNA synthetase, cytoplasmic
4187_at	377.1	A	hypothetical protein
4188_at	1366.9	P	epsilon-COP coatomer subunit Sec28p
4189_at	7826.2	P	RPN2p is a component of the 26S proteosome
4190_at	963.2	P	strong similarity to E.coli phosphoglycerate dehydrogenase
4191_at	226.4	A	weak similarity to mouse polycystic kidney disease-related protein
4147_at	-34.5	A	Meiosis-specific protein involved in homologous chromosome synapsis and chiasmata formation
4148_at	77.1	A	hypothetical protein
4149_at	893.2	P	mitochondrial acidic matrix protein
4150_at	1567.7	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	1280.5	P	hypothetical protein
4152_at	990.2	P	similarity to C.elegans hypothetical protein
4153_at	750.9	P	weak similarity to fowlpox virus major core protein
4154_at	1530.8	P	

nuclear protein, interacts with Gsp1p and Crm1p
4155_at 3963.5 P
Arp Complex Subunit
4156_at 308.7 A
U1snRNP 70K protein homolog
4157_at 439.0 A
questionable ORF
4158_at 14.4 A
hypothetical protein
4159_at 291.4 A
hypothetical protein
4160_at 59.5 A
strong similarity to YER067w
4161_at 2180.4 P
similarity to YER064c
4162_at 121.9 A
hypothetical protein
4163_at 224.0 A
weak similarity to fruit fly NADH dehydrogenase
4164_at 31014.6 P
DL-glycerol-3-phosphatase
4165_i_at 54640.8 P
Ribosomal protein L34B
4166_at 10790.7 P
Maintenance of Mitochondrial DNA 1
4167_at 454.3 P
PHO85 cyclin
4168_at 1253.3 P
Protein required for filamentous growth, cell polarity, and cellular elongation
4169_at 1766.5 P
ATPase that leads to neomycin-resistant protein when overexpressed
4124_at 5755.4 P
plasma membrane protein
4125_at 333.4 P
Met30p contains five copies of WD40 motif and interacts with and regulates Met4p
4126_at 207.7 A
Protein with 30\%% identity to protein corresponding to YER054
4127_at 268.5 A
weak similarity to zinc finger protein Gcs1p
4128_at 8573.4 P
cytochrome b reductase
4129_at 266.0 A
similarity to rat branched-chain alpha-ketoacid dehydrogenase kinase
4130_at 5438.7 P
similarity to S.pombe hypothetical protein
4131_at 1061.7 P
weak similarity to T.brucei NADH dehydrogenase
4132_at 4755.3 P
hypothetical protein
4133_at 1719.3 P
General negative regulator of transcription\; may inhibit RNA polymerase II transcription machinery
4134_at 174.1 A
hypothetical protein
4135_at 702.5 P
weak similarity to human cAMP responce element-binding protein
4136_at 2055.6 P

alpha subunit of casein kinase II
4137_at 1771.2 P
beta subunit of capping protein
4138_at 2470.8 P
regulatory subunit of cAMP-dependent protein kinase
4139_at 480.5 A
hypothetical protein
4140_at 691.4 P
Suppressor of Mif Two
4141_at 2864.2 P
integral nuclear membrane protein
4142_at -31.5 A
strong similarity to hypothetical protein YPR071w
4143_at -265.1 A
putative pseudogene
4144_at 1654.0 P
hypothetical protein
4145_at 427.5 A
Irregular
4146_at -350.0 A
weak similarity to E.gracilis RNA polymerase subunit
4101_at 351.2 A
hypothetical protein
4102_at 644.1 P
similarity to mouse MHC H-2K/t-w5-linked ORF precursor
4103_at 3044.4 P
48.8 kDa protein involved in mitochondrial protein import
4104_at 2566.8 P
45 kDa subunit of RNA polymerase II
4105_at 612.5 P
phosphoribosyl-5-amino-1-phosphoribosyl-4-imidazolecarboxiamide isomerase
4106_at 403.3 P
weak similarity to S.pombe hypothetical protein SPAC3F10
4107_at 352.5 A
hypothetical protein
4108_at 838.2 P
18.3 kD integral membrane protein
4109_at -279.9 A
encodes a-cell barrier activity on alpha factor
4110_at -138.2 A
strong similarity to hypothetical protein YIL102c
4111_at 965.1 P
similarity to Mnn1p
4112_at 324.5 A
Putative member of the ABC family of membrane transporters
4113_at 77.5 A
hypothetical protein
4114_at 6246.8 P
strong similarity to members of the Srp1p/Tip1p family
4115_at 1378.2 P
Derepression Of Telomeric silencing
4116_at 955.3 P
181aa protein - 20.5 kD
4117_at 342.5 P
181aa protein - 20.5 kD
4118_at 1067.4 P

Acyl CoA synthase
4119_at 1933.8 P
hypothetical protein
4120_at 441.4 A
similarity to C.elegans hypothetical protein
4121_at 351.0 A
similarity to Flx1p
4122_at 2238.8 P
similarity to protein disulfide isomerases
4123_at 867.1 P
Synaptobrevin (t-SNARE) homolog present on ER vesicles recycling from Golgi
4079_at 818.9 P
strong similarity to Nbp35p and human nucleotide-binding protein
4080_at 449.0 A
phosphatidylinositol 4,5-bisphosphate 5-phosphatase
4081_at 397.8 A
similarity to S.pombe hypothetical protein, weak similarity to human ankyrin
4082_at 170.1 A
similarity to D.melanogaster RNA binding protein
4083_at 964.1 P
weak similarity to ATP-dependent RNA helicases
4084_at 1914.9 P
weak similarity to mammalian neurofilament triplet H proteins
4085_at 631.8 P
DnaJ-like protein required for Peroxisome biogenesis\; Djp1p is located in the cytosol
4086_at 172.9 A
similarity to RNA-binding proteins
4087_at 5550.4 P
polyA-specific ribonuclease
4088_at 472.0 P
hypothetical protein
4089_at 570.6 P
p48 polypeptide of DNA primase
4090_at 292.3 A
encodes YU2B, a component of yeast U2 snRNP
4091_at 961.9 P
hypothetical protein
4092_at 1278.7 P
restores protein transport when overexpressed and rRNA stability to a sec23 mutation
4093_at 5905.0 P
contains multiple WD repeats and interacts with Qsr1p in two hybrid
4094_at -165.4 A
strong similarity to YLR013w, similarity to YMR136w
4095_at 74.0 A
hypothetical protein
4096_at -31.2 A
an integral subunit of RNase P but not RNase MRP
4097_at 849.9 P
weak similarity to YOL036w
4098_at 55.5 A
Transcriptional activator of sulfur amino acid metabolism
4099_at 234.4 P
bZIP protein\; transcription factor
4100_at 934.5 P
cell surface flocculin with structure similar to serine\/threonine-rich GPI-anchored cell wall proteins
4056_at 35.6 A

hypothetical protein
4057_at 1140.8 P
mitochondrial RNA splicing
4058_at 1804.1 P
signal peptidase subunit
4059_at 898.2 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 207.4 A
G1 Factor needed for normal G1 phase
4061_at 540.0 P
hypothetical protein
4062_at 1653.1 P
nitrogen starvation-induced protein phosphatase
4063_at 78.1 A
allantoinase
4064_at 198.0 A
allantoin permease
4065_at 14.2 A
allantoicase
4066_at 385.2 A
involved in nitrogen-catabolite metabolism
4067_at 104.6 A
Malate synthase 2
4068_at -581.4 A
ureidoglycolate hydrolase
4069_at 855.4 P
may be involved in the remodeling chromatin structure
4070_at 2876.9 P
saccharopine dehydrogenase
4071_at 2165.5 P
similarity to human corticosteroid 11-beta-dehydrogenase
4072_at 1193.2 P
similarity to E.coli fabD
4073_at 4916.7 P
putative glutathione-peroxidase
4074_at 887.4 P
Glutathione transferase
4075_at 189.9 A
GPI-anchored aspartic protease
4076_f_at -15.7 A
similarity to members of the Srp1p/Tip1p family
4077_at 237.0 A
weak similarity to B.licheniformi hypothetical protein P20
4078_i_at 82.3 A
putative pseudogene
4032_f_at 456.6 A
putative pseudogene
4033_f_at 1667.0 P
putative pseudogene
4034_at -226.7 A
hypothetical protein
4035_at 21.5 A
questionable ORF
4036_at 55.5 A
questionable ORF

4037_at	-24.2	A	questionable ORF
4038_at	517.3	A	questionable ORF
4039_at	-191.1	A	questionable ORF
4040_at	91.3	A	questionable ORF
4041_at	95.9	A	hypothetical protein
4042_at	374.8	A	questionable ORF
4043_s_at	138.9	A	invertase (sucrose hydrolyzing enzyme)
4044_s_at	642.9	P	Mps One Binder
4045_s_at	-167.3	A	Ribonucleotide reductase (ribonucleoside-diphosphate reductase) large subunit
4046_at	169.7	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	-215.4	A	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	-85.6	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	316.4	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	465.3	A	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	206.5	A	non-annotated SAGE orf Found forward in NC_001141 between 173167 and 173406 with 100% identity. See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251
4052_i_at	-99.4	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	1047.7	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
4054_at	1660.7	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	-85.3	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	1609.4	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	-112.6	A	non-annotated SAGE orf Found reverse in NC_001141 between 139370 and 139600 with 100% identity. See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251
4011_at	151.4	A	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 443.8 A
non-annotated SAGE orf Found forward in NC_001141 between 169709 and 169858 with 100% identity.
See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251
4013_i_at -190.2 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 911.8 A
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 200.4 A
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 202.9 A
non-annotated SAGE orf Found forward in NC_001141 between 258506 and 258640 with 100% identity.
See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251
4017_at 271.5 A
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 232.3 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 817.1 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 375.9 A
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 -37.5 A
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 202.4 A
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 65.5 A
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 -55.5 A
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 470.6 A
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 -121.1 A
non-annotated SAGE orf Found forward in NC_001141 between 122286 and 122549 with 100% identity.
See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251
4027_at 139.5 A
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 -263.3 A
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 633.8 M
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 1554.0 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 484.0 P
snRNA
3983_at 132.5 A
cytochrome-c oxidase subunit II
3984_r_at -72.4 A
questionable ORF Found forward in NC_001224 between 74495 and 74804 with 99.677419% identity.
3985_i_at -788.4 A
questionable ORF Found forward in NC_001224 between 74495 and 74804 with 99.677419% identity.
3986_f_at -142.2 A
questionable ORF Found forward in NC_001224 between 74495 and 74804 with 99.677419% identity.
3987_at 69.3 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 -52.6 A
cytochrome-c oxidase chain III
3989_at -82.8 A
strong similarity to maturase-related hypothetical protein RF2
3990_i_at -146.2 A
similarity to hypothetical protein Sgc2p Found forward in NC_001224 between 75041 and 75472 with 64.392324% identity.
3991_r_at -145.7 A
similarity to hypothetical protein Sgc2p Found forward in NC_001224 between 75041 and 75472 with 64.392324% identity.
3992_f_at 1235.4 A
similarity to hypothetical protein Sgc2p Found forward in NC_001224 between 75041 and 75472 with 64.392324% identity.
3993_at -59.0 A
strong similarity to Yeast (S.uvarum) mitochondria RF2 gene and maturase-related hypothetical protein RF2
3994_at 658.9 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 35.2 A
RF2 protein Found forward in NC_001224 between 8526 and 8736 with 84.489796% identity.
3996_s_at 657.3 P
cytochrome-c oxidase subunit I Found forward in NC_001224 between 13818 and 13988 with 100% identity.
3997_at 764.0 P
questionable ORF Found reverse in NC_001224 between 13748 and 14122 with 100% identity.
3998_at 191.4 A
COX1 intron 1 protein Found forward in NC_001224 between 13818 and 16322 with 99.92016% identity.
3999_at -77.9 A
COX1 intron 2 protein Found forward in NC_001224 between 16473 and 18830 with 99.872774% identity.
4000_at -85.4 A
COX1 intron 3 protein Found forward in NC_001224 between 18992 and 19996 with 98.308458% identity.
4001_at 1159.0 P
cytochrome-c oxidase subunit I Found forward in NC_001224 between 20508 and 20984 with 99.790356% identity.
4002_at -10.2 A
DNA endonuclease I-SceII Found forward in NC_001224 between 20985 and 21935 with 99.684543% identity.
4003_s_at 1136.5 P

cytochrome-c oxidase subunit I Found forward in NC_001224 between 21995 and 22246 with 97.222222% identity.

4004_at 349.7 P

probable mRNA maturase aI5-alpha Found forward in NC_001224 between 21995 and 23167 with 99.40324% identity.

4005_at 8245.7 P

cytochrome-c oxidase subunit I Found forward in NC_001224 between 23612 and 23746 with 100% identity.

4006_at -73.5 A

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

4007_at 71.0 A

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

4008_at 171.4 A

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

3956_i_at 753.4 A

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

3957_r_at 540.2 A

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

3958_r_at 55.5 A

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

3959_at -94.8 A

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

3960_at -101.8 A

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

3961_i_at 103.3 A

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

3962_f_at 218.3 A

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

3963_at 33.0 A

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

3964_at -8.9 A

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

3965_i_at 350.5 A

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

3966_i_at -40.6 A

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

3967_r_at -281.5 A

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

3968_s_at 167.6 A

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

3969_at 17.5 A

mRNA maturase bI2 Found forward in NC_001224 between 37723 and 38579 with 99.883314% identity.
3970_s_at 265.8 A
ubiquinol--cytochrome-c reductase subunit (cytochrome B) Found forward in NC_001224 between 39141 and 39217 with 100% identity.
3971_at 101.9 A
mRNA maturase bI3 Found forward in NC_001224 between 39141 and 40265 with 98.577778% identity.
3972_s_at 115.6 A
ubiquinol--cytochrome-c reductase subunit (cytochrome B) Found forward in NC_001224 between 40841 and 41093 with 100% identity.
3973_at -114.3 A
mRNA maturase bI4 Found forward in NC_001224 between 40815 and 42251 with 99.860821% identity.
3974_at 306.6 A
ubiquinol--cytochrome-c reductase subunit (cytochrome B) Found forward in NC_001224 between 42508 and 42561 with 100% identity.
3975_at 315.1 A
ubiquinol--cytochrome-c reductase subunit (cytochrome B) Found forward in NC_001224 between 43297 and 43647 with 100% identity.
3976_at 24360.2 P
F1F0-ATPase complex, F0 subunit 9 Found forward in NC_001224 between 46723 and 46953 with 100% identity.
3977_i_at 424.3 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 -227.8 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 89.6 A
mitochondrial ribosomal protein Found forward in NC_001224 between 48901 and 50097 with 98.436214% identity.
3980_r_at -731.8 A
mitochondrial ribosomal protein Found forward in NC_001224 between 48901 and 50097 with 98.436214% identity.
3981_at 23.5 A
probable mRNA maturase in 21S rRNA intron Found forward in NC_001224 between 61193 and 61729 with 100% identity.
3982_at -231.4 A
kanamycin resistance casette
3932_at -178.8 A
MAL-activator 23 (MAL23) gene
3933_s_at 281.8 A
Required for the catabolism of melibiose and regulated by several GAL genes
3934_at 312.3 A
Protein that confers resistance to molasses
3935_at -268.2 A
Tropomyosin-related protein with transmembrane domain and basic C-terminal
3936_at 486.3 A
invertase (sucrose hydrolyzing enzyme)
3937_g_at 1449.2 P
invertase (sucrose hydrolyzing enzyme)
3938_at 1640.9 P
Protein involved in targeting of plasma membrane [H+]ATPase
3939_at 106.3 A
Probable aldehyde dehydrogenase (EC 1.2.1.-)
3940_at 106.5 A
Degradation in the Endoplasmic Reticulum
3941_at 541.9 P

			Ser\/Thr protein kinase
3942_at	2340.0	P	bZIP (basic-leucine zipper) protein
3943_i_at	6637.9	P	bZIP (basic-leucine zipper) protein
3944_f_at	844.3	P	bZIP (basic-leucine zipper) protein
3945_at	474.6	P	Protein essential for mitochondrial biogenesis and cell viability
3946_at	812.4	P	Protein essential for mitochondrial biogenesis and cell viability
3947_at	3151.4	P	strong similarity to holacid-halidohydrolase
3948_s_at	347.6	A	probable serine\/threonine-specific protein kinase (EC 2.7.1.-)
3949_i_at	1853.2	P	protein of unknown function
3950_at	967.1	P	Rho family GTPase
3951_at	2336.5	P	2 micron plasmid recombinase
3952_at	11281.1	P	2 micron plasmid rep1 protein
3953_at	4175.6	P	2 micron plasmid D protein
3954_at	6486.1	P	2 micron plasmid rep2 protein
3955_at	418.5	P	2 micron plasmid recombinase
3907_f_at	744.4	P	strong similarity to subtelomeric encoded proteins
3908_i_at	139.2	A	Ty1 LTR
3909_f_at	8.4	A	Ty1 LTR
3910_at	8.5	A	Ty1 LTR
3911_at	-57.2	A	Ty1 LTR
3912_f_at	28139.3	P	Ty1 LTR
3913_s_at	21517.9	P	Full length Ty1
3914_s_at	38684.5	P	Full length Ty1
3915_s_at	86419.4	P	Full length Ty1
3916_s_at	131689.2	P	Full length Ty1
3917_f_at	70265.7	P	Full length Ty1
3918_f_at	48535.5	P	Full length Ty1
3919_f_at	44583.4	P	Saccharomyces cerevisiae chromosome I, complete chromosome sequence. Found reverse in NC_001133 between 160593 and 164183 with 100% identity.

3920_f_at 105386.2 P
Saccharomyces cerevisiae chromosome I, complete chromosome sequence. Found reverse in NC_001133 between 160593 and 164183 with 100% identity.
3921_s_at 34316.8 P
Saccharomyces cerevisiae chromosome I, complete chromosome sequence. Found reverse in NC_001133 between 164540 and 165862 with 100% identity.
3922_f_at 25296.0 P
Ty1 LTR
3923_f_at 517.1 A
tRNA-Ala
3924_f_at 604.3 P
tRNA-Ser
3925_f_at 13397.0 P
Ty3 LTR Found forward in NC_001133 between 182610 and 182949 with 100% identity.
3926_f_at 17338.3 P
Ty1 LTR
3927_f_at 8904.2 P
Ty2 LTR
3928_f_at 118.5 A
Ty1 LTR
3929_s_at 85.3 A
tRNA-Thr
3930_i_at -179.8 A
Ty1 LTR
3931_f_at 995.3 A
Ty1 LTR
3884_f_at 1244.9 P
tRNA-Glu
3885_f_at 179.7 A
tRNA-Ala
3886_f_at -36.0 A
Ty3 LTR
3887_f_at 736.8 P
Ty4 LTR
3888_s_at -218.5 A
Saccharomyces cerevisiae chromosome X, complete chromosome sequence. Found forward in NC_001142 between 197614 and 198699 with 100% identity.
3889_s_at 143.5 A
Saccharomyces cerevisiae chromosome X, complete chromosome sequence. Found forward in NC_001142 between 197614 and 198699 with 100% identity.
3890_s_at -80.8 A
Saccharomyces cerevisiae chromosome X, complete chromosome sequence. Found forward in NC_001142 between 197614 and 198858 with 100% identity.
3891_s_at -314.9 A
Saccharomyces cerevisiae chromosome X, complete chromosome sequence. Found forward in NC_001142 between 198701 and 203026 with 100% identity.
3892_s_at -234.8 A
Saccharomyces cerevisiae chromosome X, complete chromosome sequence. Found forward in NC_001142 between 198701 and 203026 with 100% identity.
3893_s_at -530.1 A
Saccharomyces cerevisiae chromosome X, complete chromosome sequence. Found forward in NC_001142 between 198701 and 203026 with 100% identity.
3894_s_at -69.6 A
Saccharomyces cerevisiae chromosome X, complete chromosome sequence. Found forward in NC_001142 between 198701 and 203026 with 100% identity.
3895_s_at 28.2 A

Saccharomyces cerevisiae chromosome X, complete chromosome sequence. Found forward in NC_001142 between 198701 and 203026 with 100% identity.
3896_s_at -344.3 A
Full length Ty4
3897_s_at -18.1 A
Full length Ty4
3898_s_at -102.3 A
Full length Ty4
3899_s_at 804.7 P
Full length Ty4
3900_f_at 1000.4 P
Full length Ty4
3901_f_at 769.8 P
Ty4 LTR
3902_f_at 16842.8 P
Ty1 LTR
3903_i_at -443.0 A
Ty1 LTR
3904_f_at 5601.9 P
Ty1 LTR
3905_s_at 925.7 P
tRNA-Asp
3906_f_at 235.8 A
tRNA-Arg
3859_i_at -9.3 A
Ty1 LTR
3860_f_at 15136.7 P
Ty1 LTR
3861_f_at 41435.6 P
Ty1 LTR
3862_f_at 115.2 A
tRNA-Arg
3863_f_at -92.7 A
tRNA-Arg
3864_i_at -1693.6 A
Ty1 LTR
3865_f_at 42.2 A
Ty1 LTR
3866_at -17.9 A
Ty1 LTR
3867_s_at 984.0 P
tRNA-Val
3868_s_at 96.8 A
tRNA-Met
3869_f_at -16.2 A
tRNA-Gly
3870_s_at 403.5 A
tRNA-Lys
3871_at -376.7 A
Ty4 LTR
3872_i_at -157.0 A
Ty1 LTR
3873_f_at -255.3 A
Ty1 LTR
3874_i_at -98.9 A
Ty1 LTR

3875_f_at	-75.2	A
Ty1 LTR		
3876_at	212.8	A
Ty4 LTR		
3877_at	120.2	A
Ty1 LTR		
3878_s_at	483.2	P
tRNA-Leu		
3879_f_at	24363.8	P
Ty1 LTR		
3880_f_at	86085.3	P
Saccharomyces cerevisiae chromosome X, complete chromosome sequence. Found forward in NC_001142 between 473751 and 477716 with 100% identity.		
3881_f_at	72809.6	P
Full length Ty1		
3882_f_at	44867.2	P
Full length Ty1		
3883_f_at	27960.1	P
Ty1 LTR		
3835_s_at	124100.2	P
Saccharomyces cerevisiae chromosome X, complete chromosome sequence. Found forward in NC_001142 between 479334 and 483300 with 100% identity.		
3836_f_at	27737.8	P
Full length Ty1		
3837_f_at	24821.1	P
Ty1 LTR		
3838_s_at	-337.7	A
tRNA-Met		
3839_at	-89.4	A
Ty1 LTR		
3840_f_at	163.4	A
tRNA-Ser		
3841_at	55.6	A
Ty1 LTR		
3842_f_at	-949.7	A
tRNA-Gly		
3843_at	337.2	M
Ty1 LTR		
3844_f_at	22777.4	P
Ty1 LTR		
3845_i_at	-21.9	A
tRNA-Arg		
3846_f_at	-565.3	A
tRNA-Arg		
3847_i_at	-576.2	A
Ty1 LTR		
3848_f_at	6844.7	P
Ty1 LTR		
3849_f_at	27643.1	P
Ty1 LTR		
3850_at	343.0	P
Ty1 LTR		
3851_s_at	1786.5	P
Protein with similarity to members of the Ybr302p\/Ycr007p\/Cos8p\/Cos9p family, coded from subtelomeric region		
3852_f_at	3576.5	P

Protein with similarity to members of the Ybr302p\/Ycr007p\/Cos8p\/Cos9p family, coded from subtelomeric region
3853_f_at 186.8 A
strong similarity to subtelomeric encoded proteins
3854_f_at -309.3 A
strong similarity to Gin11p, YKL225w and other subtelomeric encoded proteins
3855_s_at -174.8 A
strong similarity to subtelomeric encoded proteins
3856_at -265.2 A
tRNA-Thr
3857_at -884.3 A
Ty1 LTR
3858_s_at -526.7 A
tRNA-Asn
3812_at -132.7 A
Ty1 LTR
3813_f_at 626.8 A
tRNA-Glu
3814_f_at 19.0 A
tRNA-Arg
3815_i_at -216.5 A
Ty1 LTR
3816_f_at -11.0 A
Ty1 LTR
3817_f_at 13875.2 P
Ty3 LTR
3818_at -168.0 A
Ty1 LTR
3819_f_at 444.2 A
tRNA-Ala
3820_f_at 1830.5 P
Ty1 LTR
3821_f_at -45.6 A
tRNA-His
3822_f_at 6694.6 P
Ty1 LTR
3823_f_at 12035.7 P
Ty1 LTR
3824_f_at 30991.7 P
Ty1 LTR
3825_at 3.4 A
Ty1 LTR
3826_at -583.0 A
Ty1 LTR
3827_f_at 200.4 A
tRNA-Arg
3828_f_at 256.5 A
Ty1 LTR
3829_f_at 31579.1 P
Ty1 LTR
3830_f_at 105.3 A
tRNA-Ala
3831_s_at -168.9 A
strong similarity to subtelomeric encoded proteins
3832_s_at -610.0 A
strong similarity to subtelomeric encoded proteins

3833_f_at -114.3 A

Ty5 LTR

3834_s_at 322.1 A

strong similarity to subtelomeric encoded proteins

3789_s_at -113.7 A

strong similarity to subtelomeric encoded proteins

3790_s_at 2583.6 P

strong similarity to subtelomeric encoded proteins

3791_s_at -181.3 A

strong similarity to subtelomeric encoded proteins

3792_s_at 7715.8 P

strong similarity to subtelomeric encoded proteins

3793_f_at 2927.7 P

Ty1 LTR

3794_f_at 92.9 A

tRNA-Ser

3795_at -122.0 A

Ty3 LTR

3796_f_at 350.1 A

tRNA-Ala

3797_f_at 22993.5 P

Ty1 LTR

3798_s_at 265813.0 P

Saccharomyces cerevisiae chromosome XII, complete chromosome sequence. Found reverse in NC_001144 between 215441 and 219403 with 100% identity.

3799_f_at 16806.2 P

Ty1 LTR

3800_at -208.8 A

Ty1 LTR

3801_f_at 108.9 A

Ty1 LTR

3802_f_at 10969.1 A

Ty3 LTR

3803_f_at -109.0 A

tRNA-Arg

3804_f_at 658.8 P

tRNA-Gln

3805_f_at 9150.9 P

Ty1 LTR

3806_s_at 41644.2 P

35S ribosomal RNA

3807_s_at 123306.2 P

35S ribosomal RNA

3808_s_at 89419.2 P

35S ribosomal RNA

3809_s_at 26054.1 P

35S ribosomal RNA

3810_s_at 21331.8 P

35S ribosomal RNA

3811_s_at 34288.9 P

35S ribosomal RNA

3764_s_at 45538.9 P

35S ribosomal RNA

3765_s_at 88415.0 P

25S ribosomal RNA

3766_s_at 112873.3 P

25S ribosomal RNA
3767_s_at 36557.5 P
18S ribosomal RNA
3768_i_at 50737.4 P
5S ribosomal RNA
3769_s_at 51931.6 P
5S ribosomal RNA
3770_i_at 35487.0 P
5S ribosomal RNA
3771_f_at 28585.4 P
Ty1 LTR
3772_f_at 109219.4 P
Full length Ty1
3773_f_at 54379.5 P
Full length Ty1
3774_f_at 148556.1 P
Saccharomyces cerevisiae chromosome XII, complete chromosome sequence. Found reverse in NC_001144 between 476334 and 480296 with 100% identity.
3775_f_at 23000.0 P
Ty1 LTR
3776_i_at 774.2 A
Ty1 LTR
3777_f_at 307.4 A
Ty1 LTR
3778_f_at 24675.5 P
Ty1 LTR
3779_f_at 82129.8 P
Saccharomyces cerevisiae chromosome XII, complete chromosome sequence. Found forward in NC_001144 between 594749 and 598706 with 100% identity.
3780_f_at 14271.8 P
Full length Ty1
3781_f_at 62232.1 P
Full length Ty1
3782_f_at 28610.5 P
Ty1 LTR
3783_at 99.5 A
Ty1 LTR
3784_at -274.1 A
Ty4 LTR
3785_f_at 29900.7 P
Ty1 LTR
3786_s_at 85431.8 P
TY1B protein Found forward in NC_001144 between 652918 and 653385 with 100% identity.
3787_f_at 78130.3 P
Saccharomyces cerevisiae chromosome XII, complete chromosome sequence. Found forward in NC_001144 between 654177 and 656387 with 100% identity.
3788_f_at 157947.4 P
Saccharomyces cerevisiae chromosome XII, complete chromosome sequence. Found forward in NC_001144 between 654177 and 656387 with 100% identity.
3740_f_at 69379.0 P
Full length Ty1
3741_f_at 73030.6 P
Full length Ty1
3742_f_at 25916.7 P
Ty1 LTR
3743_f_at 1020.6 A

tRNA-Ala
3744_i_at 2573.1 P
Ty3 LTR
3745_f_at 1471.2 P
Ty3 LTR
3746_at 234.1 A
Ty1 LTR
3747_at -56.7 A
Ty1 LTR
3748_i_at 281.2 A
Ty1 LTR
3749_r_at -118.6 A
Ty1 LTR
3750_f_at 47.2 A
Ty1 LTR
3751_f_at 23252.1 P
Ty2 LTR
3752_f_at 3419.5 P
Ty1 LTR
3753_s_at 94.4 A
tRNA-Ile
3754_s_at 47.8 A
tRNA-Ser
3755_f_at 179.6 A
Ty3 LTR
3756_i_at -47.7 A
Ty1 LTR
3757_f_at 8930.0 P
Ty1 LTR
3758_f_at 1762.9 P
tRNA-Glu
3759_f_at 7872.4 P
Ty1 LTR
3760_at 899.2 P
tRNA-Arg
3761_f_at 33654.4 P
Ty2 LTR
3762_s_at 610.0 A
Saccharomyces cerevisiae chromosome XII, complete chromosome sequence. Found forward in NC_001144 between 941478 and 942778 with 100% identity.
3763_s_at 582.7 A
Saccharomyces cerevisiae chromosome XII, complete chromosome sequence. Found forward in NC_001144 between 941478 and 942778 with 100% identity.
3717_s_at 3233.1 P
Saccharomyces cerevisiae chromosome XII, complete chromosome sequence. Found forward in NC_001144 between 942777 and 946791 with 100% identity.
3718_s_at 2485.3 P
Saccharomyces cerevisiae chromosome XII, complete chromosome sequence. Found forward in NC_001144 between 942777 and 946791 with 100% identity.
3719_s_at 5880.6 P
Saccharomyces cerevisiae chromosome XII, complete chromosome sequence. Found forward in NC_001144 between 942777 and 946791 with 100% identity.
3720_f_at 77479.6 P
Saccharomyces cerevisiae chromosome XII, complete chromosome sequence. Found forward in NC_001144 between 942777 and 946791 with 100% identity.
3721_s_at 473.8 P

Full length Ty2
3722_s_at 13350.5 P
Full length Ty2
3723_f_at 98174.0 P
Full length Ty2
3724_f_at 32420.2 P
Ty2 LTR
3725_at 552.0 A
Ty1 LTR
3726_f_at 16040.0 P
Ty2 LTR
3727_f_at 19337.2 P
Full length Ty2
3728_f_at 96891.8 P
Saccharomyces cerevisiae chromosome XII, complete chromosome sequence. Found reverse in NC_001144 between 976606 and 980109 with 100% identity.
3729_f_at 10798.9 P
Ty2 LTR
3730_at 326.4 A
Ty1 LTR
3731_s_at 117.8 A
strong similarity to subtelomeric encoded proteins
3732_s_at 272.0 A
strong similarity to subtelomeric encoded proteins
3733_s_at 250.2 A
strong similarity to subtelomeric encoded proteins
3734_s_at 654.0 M
strong similarity to subtelomeric encoded proteins
3735_f_at 16442.2 P
strong similarity to subtelomeric encoded proteins
3736_s_at 56.1 A
strong similarity to subtelomeric encoded proteins
3737_s_at 271.6 A
strong similarity to subtelomeric encoded proteins
3738_s_at 6920.6 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 4296.9 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)
3695_f_at 207.1 A
tRNA-Arg
3696_at 307.8 A
Ty1 LTR
3697_f_at 51988.5 P
Ty2 LTR
3698_f_at -1136.3 A
tRNA-Gly
3699_f_at 31353.1 P
Ty1 LTR
3700_f_at 50334.4 P
Full length Ty1
3701_f_at 28594.7 P
Ty1 LTR
3702_f_at 28491.6 P
Ty1 LTR

3703_f_at 157780.5 P
Saccharomyces cerevisiae chromosome XIII, complete chromosome sequence. Found forward in NC_001145 between 197939 and 201896 with 100% identity.
3704_f_at 97346.4 P
Full length Ty1
3705_f_at 53224.8 P
Full length Ty1
3706_f_at 19137.2 P
Ty1 LTR
3707_f_at 415.9 A
tRNA-Ser
3708_at 135.5 A
Ty4 LTR
3709_f_at 864.2 P
tRNA-Glu
3710_f_at 812.3 A
tRNA-Ala
3711_f_at 25503.7 P
Ty1 LTR
3712_s_at 613.8 A
Full length Ty1
3713_s_at 334.2 A
Full length Ty1
3714_f_at 59588.7 P
Full length Ty1
3715_f_at 27606.7 P
Ty1 LTR
3716_f_at 386.6 A
tRNA-His
3671_f_at 24010.3 P
Ty1 LTR
3672_f_at 42128.2 P
Full length Ty1
3673_f_at 25705.2 P
Ty1 LTR
3674_i_at 84.2 A
Ty1 LTR
3675_r_at -15.9 A
Ty1 LTR
3676_f_at -76.3 A
Ty1 LTR
3677_f_at 290.2 A
Ty1 LTR
3678_at -432.8 A
Ty1 LTR
3679_at -388.7 A
Ty1 LTR
3680_i_at 63.6 A
Ty1 LTR
3681_s_at 151.8 A
Ty1 LTR
3682_i_at -324.8 A
Ty1 LTR
3683_f_at 134.8 A
Ty1 LTR
3684_f_at 592.1 P

Ty4 LTR
3685_f_at 3247.6 P
Ty1 LTR
3686_f_at 85.5 A
Ty1 LTR
3687_f_at 2.6 A
tRNA-Arg
3688_f_at 254.9 P
tRNA-Ala
3689_f_at 15061.8 P
Ty2 LTR
3690_f_at -168.1 A
tRNA-Gln
3691_f_at 330.7 A
Ty4 LTR
3692_at -72.8 A
Ty1 LTR
3693_f_at 361.1 A
Ty1 LTR
3694_at 81.1 A
strong similarity to subtelomeric encoded proteins
3646_s_at -13.9 A
strong similarity to subtelomeric encoded proteins
3647_f_at 192.7 A
strong similarity to subtelomeric encoded proteins
3648_f_at 10648.6 P
Protein with similarity to subtelomerically-encoded proteins such as Cos5p, Ybr302p, Cos3p, Cos1p, Cos4p, Cos8p, Cos6p, Cos9p
3649_f_at 193.9 A
tRNA-Gly
3650_f_at -10.7 A
Ty4 LTR
3651_f_at 21889.2 P
Ty1 LTR
3652_f_at 53606.7 P
Full length Ty1
3653_f_at 23204.2 P
Ty1 LTR
3654_i_at 236.7 A
Ty3 LTR
3655_f_at -163.8 A
Ty3 LTR
3656_f_at 20779.3 P
Ty1 LTR
3657_f_at 71801.3 P
Saccharomyces cerevisiae chromosome XIV, complete chromosome sequence. Found forward in NC_001146 between 520758 and 524702 with 100% identity.
3658_f_at 86812.1 P
Full length Ty1
3659_f_at 32335.8 P
Full length Ty1
3660_f_at 22246.9 P
Ty1 LTR
3661_at 1254.2 P
Ty3 LTR
3662_f_at 12569.7 P

Ty3 LTR
3663_f_at 385.0 A
Ty4 LTR
3664_f_at 31723.2 P
Ty2 LTR
3665_f_at 89615.2 P
Full length Ty2
3666_f_at 102085.4 P
Saccharomyces cerevisiae chromosome XIV, complete chromosome sequence. Found reverse in NC_001146 between 562383 and 566402 with 100% identity.
3667_f_at 20683.6 P
Ty2 LTR
3668_f_at 550.6 P
tRNA-Pro
3669_f_at 15167.2 P
Ty1 LTR
3670_f_at 65.1 A
Ty4 LTR
3621_i_at -222.8 A
Ty3 LTR
3622_f_at 16493.1 P
Ty3 LTR
3623_f_at 14752.3 P
Ty1 LTR
3624_at 134.1 A
Ty1 LTR
3625_at 277.4 A
Protein with strong similarity to subtelomerically-encoded proteins such as Cos5p, Ybr302p, Cos3p, Cos1p, Cos4p, Cos8p, Cos6p, Cos9p
3626_i_at 36.2 A
Protein with strong similarity to subtelomerically-encoded proteins such as Cos5p, Ybr302p, Cos3p, Cos1p, Cos4p, Cos8p, Cos6p, Cos9p
3627_r_at -251.5 A
Protein with strong similarity to subtelomerically-encoded proteins such as Cos5p, Ybr302p, Cos3p, Cos1p, Cos4p, Cos8p, Cos6p, Cos9p
3628_f_at 142.7 A
Protein with strong similarity to subtelomerically-encoded proteins such as Cos5p, Ybr302p, Cos3p, Cos1p, Cos4p, Cos8p, Cos6p, Cos9p
3629_f_at 289.0 A
strong similarity to subtelomeric encoded proteins
3630_at -58.0 A
Ty1 LTR
3631_s_at 187.8 A
Ty4 LTR
3632_at -190.2 A
Ty1 LTR
3633_f_at -391.3 A
tRNA-Gly
3634_f_at 493.0 P
Ty1 LTR
3635_f_at 26541.5 P
Ty1 LTR
3636_f_at 130182.6 P
Saccharomyces cerevisiae chromosome XV, complete chromosome sequence. Found forward in NC_001147 between 119305 and 123267 with 100% identity.
3637_f_at 73719.8 P

Full length Ty1		
3638_f_at	43016.2	P
Full length Ty1		
3639_f_at	27692.7	P
Ty1 LTR		
3640_f_at	-462.4	A
tRNA-Gly		
3641_f_at	-105.9	A
Ty3 LTR		
3642_at	24.1	A
Ty1 LTR		
3643_i_at	-449.0	A
Ty1 LTR		
3644_f_at	617.6	A
Ty1 LTR		
3645_f_at	-534.1	A
tRNA-Gly		
3597_at	216.6	A
Ty1 LTR		
3598_f_at	243.1	A
tRNA-Arg		
3599_at	-270.1	A
Ty1 LTR		
3600_i_at	-965.4	A
Ty3 LTR		
3601_f_at	-113.3	A
Ty3 LTR		
3602_at	-250.2	A
Ty1 LTR		
3603_at	-164.9	A
Ty1 LTR		
3604_f_at	-294.5	A
tRNA-Gly		
3605_f_at	247.6	A
Ty1 LTR		
3606_f_at	25863.6	P
Ty1 LTR		
3607_f_at	46641.0	P
Full length Ty1		
3608_f_at	26066.3	P
Ty1 LTR		
3609_i_at	-218.6	A
Ty1 LTR		
3610_f_at	24.9	A
Ty1 LTR		
3611_f_at	-118.0	A
Ty1 LTR		
3612_f_at	22454.8	P
Ty2 LTR		
3613_i_at	101.8	A
Ty1 LTR		
3614_f_at	1735.4	A
Ty1 LTR		
3615_i_at	-48.5	A
Ty1 LTR		
3616_f_at	258.4	A

Ty1 LTR
3617_f_at 539.7 P
Ty4 LTR
3618_f_at 28713.6 P
Ty2 LTR
3619_f_at 56108.2 P
Full length Ty2
3620_f_at 59439.0 P
Saccharomyces cerevisiae chromosome XV, complete chromosome sequence. Found reverse in NC_001147 between 704417 and 708436 with 100% identity.
3572_f_at 21075.7 P
Ty2 LTR
3573_f_at 600.7 A
Ty4 LTR
3574_f_at 594.8 P
tRNA-Ala
3575_f_at 8847.7 P
Ty3 LTR
3576_f_at 334.3 A
Ty3 LTR
3577_at -237.2 A
Ty1 LTR
3578_f_at 11778.3 P
Ty2 LTR
3579_f_at 64414.6 P
Saccharomyces cerevisiae chromosome XV, complete chromosome sequence. Found forward in NC_001147 between 971863 and 975882 with 100% identity.
3580_f_at 84052.6 P
Full length Ty2
3581_f_at 10949.4 P
Ty2 LTR
3582_f_at 20755.7 P
Ty1 LTR
3583_i_at -158.5 A
Ty1 LTR
3584_f_at -17.0 A
Ty1 LTR
3585_f_at -202.8 A
Ty3 LTR
3586_f_at 24661.6 P
Ty1 LTR
3587_f_at 147127.6 P
Saccharomyces cerevisiae chromosome XVI, complete chromosome sequence. Found forward in NC_001148 between 58054 and 62016 with 100% identity.
3588_f_at 99230.3 P
Full length Ty1
3589_f_at 46969.6 P
Full length Ty1
3590_f_at 27003.1 P
Ty1 LTR
3591_f_at 11141.7 P
Ty2 LTR
3592_i_at -646.6 A
Ty1 LTR
3593_f_at 10430.7 P
Ty1 LTR

3594_f_at	1171.7	P	tRNA-Glu
3595_at	-39.4	A	Ty1 LTR
3596_f_at	19427.6	P	Ty2 LTR
3548_s_at	219.4	P	tRNA-Cys
3549_f_at	-147.4	A	Ty1 LTR
3550_i_at	237.1	A	Ty1 LTR
3551_f_at	383.0	A	Ty1 LTR
3552_f_at	93.4	A	Ty1 LTR
3553_f_at	162.2	A	Ty4 LTR
3554_f_at	740.6	P	Full length Ty4
3555_s_at	143.0	A	Saccharomyces cerevisiae chromosome XVI, complete chromosome sequence. Found reverse in NC_001148 between 437328 and 439490 with 100% identity.
3556_s_at	136.3	A	Saccharomyces cerevisiae chromosome XVI, complete chromosome sequence. Found reverse in NC_001148 between 437328 and 439490 with 100% identity.
3557_s_at	70.1	A	Saccharomyces cerevisiae chromosome XVI, complete chromosome sequence. Found reverse in NC_001148 between 439423 and 442737 with 100% identity.
3558_f_at	575.4	P	Ty4 LTR
3559_f_at	20243.4	P	Ty1 LTR
3560_at	59.2	A	Ty1 LTR
3561_f_at	-605.0	A	tRNA-Gly
3562_f_at	554.1	A	tRNA-Ser
3563_s_at	-71.8	A	tRNA-Thr
3564_f_at	17754.7	P	Ty3 LTR
3565_at	3573.6	A	Ty1 LTR
3566_i_at	-17.9	A	Ty1 LTR
3567_r_at	115.3	A	Ty1 LTR
3568_f_at	351.0	A	Ty1 LTR
3569_at	-182.2	A	Ty1 LTR
3570_f_at	2482.2	P	Ty1 LTR
3571_f_at	29033.1	P	

Ty1 LTR
3524_f_at 14461.6 P
Full length Ty1
3525_f_at 65718.3 P
Full length Ty1
3526_f_at 87288.6 P
Saccharomyces cerevisiae chromosome XVI, complete chromosome sequence. Found reverse in NC_001148 between 804996 and 808958 with 100% identity.
3527_f_at 30260.2 P
Ty1 LTR
3528_f_at 25398.5 P
Ty1 LTR
3529_f_at 69089.9 P
Full length Ty3
3530_f_at 25296.0 P
Ty1 LTR
3531_at 154.5 A
Ty1 LTR
3532_f_at 28520.7 P
Ty1 LTR
3533_f_at 21469.3 P
Full length Ty1
3534_f_at 28079.6 P
Ty1 LTR
3535_i_at 452.1 P
Ty3 LTR
3536_f_at 12365.7 P
Ty3 LTR
3537_f_at 1579.9 A
tRNA-Ala
3538_f_at -807.0 A
tRNA-Gly
3539_f_at 5767.3 P
Ty3 LTR
3540_at -149.9 A
Ty4 LTR
3541_at 90.4 A
Ty4 LTR
3542_f_at 18862.2 P
strong similarity to subtelomeric encoded proteins
3543_s_at 4427.7 P
strong similarity to subtelomeric encoded proteins
3544_at -38.2 A
strong similarity to subtelomeric encoded proteins
3545_i_at 291.6 A
Ty1 LTR
3546_f_at -135.9 A
Ty1 LTR
3547_f_at 9759.6 P
Ty2 LTR
3500_f_at -417.8 A
Ty1 LTR
3501_f_at 15407.0 P
Ty2 LTR
3502_f_at 69915.0 P
Saccharomyces cerevisiae chromosome II, complete chromosome sequence. Found forward in

NC_001134 between 31221 and 35240 with 100% identity.
3503_f_at 71845.2 P
Full length Ty2
3504_f_at 15741.1 P
Ty2 LTR
3505_s_at 137.9 A
Ty1 LTR
3506_s_at 1142.0 P
Ty4 LTR
3507_at 80.5 A
Ty1 LTR
3508_f_at -583.4 A
tRNA-Gly
3509_f_at 10357.9 P
Ty3 LTR
3510_s_at -1.6 A
Ty1 LTR
3511_f_at 21597.1 P
Ty1 LTR
3512_f_at 43039.4 P
Full length Ty1
3513_f_at 28490.5 P
Ty1 LTR
3514_f_at 48.6 A
tRNA-Ser
3515_at 239.7 A
Ty1 LTR
3516_f_at 21926.8 P
Ty1 LTR
3517_f_at 57980.8 P
Full length Ty1
3518_f_at 14723.2 P
Ty1 LTR
3519_f_at 289.3 P
Ty1 LTR
3520_s_at 113.6 A
tRNA-Val
3521_i_at 51.8 A
Ty1 LTR
3522_f_at 2537.6 P
Ty1 LTR
3523_at 157.6 A
Ty1 LTR
3477_at -155.7 A
Ty1 LTR
3478_f_at 798.3 P
tRNA-Gln
3479_f_at -53.4 A
tRNA-Arg
3480_at -81.4 A
Ty1 LTR
3481_at 144.9 A
Ty1 LTR
3482_f_at 1413.7 P
tRNA-Glu
3483_f_at 4164.1 P

Protein with similarity to members of the Cos3\/Cos5\/Cos1\/Cos4\/Cos8\/Cos6\/Cos9 family, coded from subtelomeric region		
3484_f_at	-319.4	A
Ty5 LTR		
3485_at	-250.9	A
Full length Ty5		
3486_at	-158.1	A
Full length Ty5		
3487_g_at	-182.6	A
Full length Ty5		
3488_at	58.5	A
Full length Ty5		
3489_f_at	-15.1	A
Full length Ty5		
3490_f_at	24.2	A
Ty5 LTR		
3491_f_at	1139.4	P
tRNA-Glu		
3492_f_at	5248.4	P
Ty1 LTR		
3493_f_at	42160.4	P
Ty1 LTR		
3494_f_at	18577.8	P
Ty1 LTR		
3495_f_at	757.8	P
Ty1 LTR		
3496_f_at	31296.2	P
Ty2 LTR		
3497_f_at	59315.8	P
Saccharomyces cerevisiae chromosome III, complete chromosome sequence. Found forward in NC_001135 between 86005 and 90030 with 100% identity.		
3498_f_at	71148.4	P
Full length Ty2		
3499_f_at	19804.3	P
Ty2 LTR		
3451_f_at	2059.5	P
tRNA-Pro		
3452_f_at	21958.1	P
Ty1 LTR		
3453_at	-154.4	A
strong similarity to subtelomeric encoded proteins		
3454_s_at	180.2	A
tRNA-Asn		
3455_f_at	-1093.8	A
tRNA-Gly		
3456_i_at	68.6	A
Ty1 LTR		
3457_f_at	7849.3	P
Ty1 LTR		
3458_f_at	447.2	A
Ty1 LTR		
3459_at	-251.3	A
Ty1 LTR		
3460_at	-46.5	A
Ty4 LTR		
3461_f_at	14827.9	P

Ty1 LTR
3462_f_at 662.7 P
tRNA-Gln
3463_at 286.8 A
Ty1 LTR
3464_at 147.2 A
Ty1 LTR
3465_at 56.6 A
Ty5 LTR
3466_i_at -104.6 A
Ty1 LTR
3467_f_at -823.1 A
Ty1 LTR
3468_i_at 10.0 A
Ty1 LTR
3469_f_at -172.6 A
Ty1 LTR
3470_i_at -19.1 A
Protein with strong similarity to other subtelomerically-encoded proteins such as Cos5p, Ybr302p, Cos3p, Cos1p, Cos4p, Cos8p, Cos6p, Cos9p
3471_f_at 3337.8 A
Protein with strong similarity to other subtelomerically-encoded proteins such as Cos5p, Ybr302p, Cos3p, Cos1p, Cos4p, Cos8p, Cos6p, Cos9p
3472_f_at -923.5 A
tRNA-Gly
3473_f_at 46.4 A
tRNA-Ala
3474_f_at 5408.5 P
Ty1 LTR
3475_f_at 290.6 A
Ty4 LTR
3476_f_at 377.1 A
tRNA-Ser
3427_at 361.9 A
Ty1 LTR
3428_f_at 8177.0 P
Ty1 LTR
3429_f_at 24761.5 P
Ty2 LTR
3430_f_at 118249.3 P
Full length Ty2
3431_f_at 67318.8 P
Saccharomyces cerevisiae chromosome IV, complete chromosome sequence. Found reverse in NC_001136 between 514037 and 518056 with 100% identity.
3432_f_at 19626.2 P
Ty2 LTR
3433_i_at 528.3 A
Ty1 LTR
3434_f_at 729.7 A
Ty1 LTR
3435_f_at 5540.8 P
Ty1 LTR
3436_f_at 303.8 A
tRNA-Gln
3437_f_at 177.9 A
tRNA-Arg

3438_f_at -3248.0 A
tRNA-Arg
3439_f_at 400.6 P
tRNA-Gln
3440_f_at 31044.1 P
Ty1 LTR
3441_f_at 77615.4 P
Full length Ty1
3442_f_at 73699.6 P
Full length Ty1
3443_f_at 59037.7 P
Saccharomyces cerevisiae chromosome IV, complete chromosome sequence. Found reverse in NC_001136 between 645851 and 649813 with 100% identity.
3444_f_at 35058.7 P
Ty1 LTR
3445_f_at 256.7 A
Ty3 LTR
3446_i_at -357.1 A
Ty1 LTR
3447_f_at 155.4 A
Ty1 LTR
3448_s_at 3891.8 P
Ty3 LTR
3449_i_at 59.0 A
Ty1 LTR
3450_r_at -73.0 A
Ty1 LTR
3404_f_at 500.9 P
Ty1 LTR
3405_f_at 815.3 P
tRNA-Gln
3406_f_at 26535.6 P
Ty1 LTR
3407_at -285.8 A
Saccharomyces cerevisiae chromosome IV, complete chromosome sequence. Found forward in NC_001136 between 804494 and 805681 with 100% identity.
3408_f_at 12872.9 P
Ty1 LTR
3409_f_at 81209.7 P
Saccharomyces cerevisiae chromosome IV, complete chromosome sequence. Found forward in NC_001136 between 873398 and 877417 with 100% identity.
3410_f_at 82106.2 P
Full length Ty2
3411_f_at 10788.1 P
Ty1 LTR
3412_f_at 18748.5 P
Full length Ty1
3413_f_at 70935.9 P
Full length Ty1
3414_f_at 57478.3 P
Saccharomyces cerevisiae chromosome IV, complete chromosome sequence. Found reverse in NC_001136 between 878651 and 882613 with 100% identity.
3415_i_at 120.9 A
Ty1 LTR
3416_s_at 643.2 P
Ty1 LTR

3417_f_at 15524.8 P
Ty3 LTR
3418_f_at 301.8 A
tRNA-Ser
3419_f_at 10523.0 P
Ty1 LTR
3420_f_at 76953.9 P
Saccharomyces cerevisiae chromosome IV, complete chromosome sequence. Found forward in NC_001136 between 982747 and 986766 with 100% identity.
3421_f_at 68295.3 P
Full length Ty2
3422_f_at 20780.1 P
Ty1 LTR
3423_f_at 31591.6 P
Ty1 LTR
3424_f_at 67483.1 P
Full length Ty1
3425_f_at 32752.9 P
Full length Ty1
3426_f_at 117940.0 P
Saccharomyces cerevisiae chromosome IV, complete chromosome sequence. Found reverse in NC_001136 between 987525 and 991034 with 100% identity.
3379_f_at 28452.3 P
Ty1 LTR
3380_i_at 79.2 A
Ty3 LTR
3381_f_at -213.3 A
Ty3 LTR
3382_f_at -681.4 A
tRNA-Gly
3383_f_at 838.2 P
tRNA-Glu
3384_f_at 13140.9 P
Ty3 LTR
3385_s_at 637.1 P
tRNA-Val
3386_f_at 29517.2 P
Ty1 LTR
3387_f_at 47282.6 P
Full length Ty1
3388_f_at 29552.0 P
Ty1 LTR
3389_f_at 5179.2 P
Ty1 LTR
3390_at 226.7 A
Ty3 LTR
3391_f_at 18963.0 P
Ty1 LTR
3392_f_at 41881.4 P
Ty1 LTR
3393_f_at 112758.9 P
Saccharomyces cerevisiae chromosome IV, complete chromosome sequence. Found forward in NC_001136 between 1208292 and 1212254 with 100% identity.
3394_f_at 77089.9 P
Full length Ty1
3395_f_at 64221.4 P

Full length Ty1		
3396_f_at	33074.6	P
Ty1 LTR		
3397_f_at	304.0	A
tRNA-Gly		
3398_f_at	441.9	A
tRNA-Ser		
3399_f_at	11430.0	P
Ty1 LTR		
3400_i_at	27.9	A
Ty1 LTR		
3401_f_at	-78.6	A
Ty1 LTR		
3402_at	206.9	A
Ty1 LTR		
3403_f_at	881.2	P
strong similarity to subtelomeric encoded proteins		
3356_f_at	306.0	A
strong similarity to subtelomeric encoded proteins		
3357_at	41.4	A
strong similarity to subtelomeric encoded proteins		
3358_f_at	-232.1	A
tRNA-Gly		
3359_f_at	29926.5	P
Ty1 LTR		
3360_at	-125.2	A
Ty1 LTR		
3361_f_at	-49.3	A
tRNA-Ser		
3362_at	-340.5	A
Ty1 LTR		
3363_at	-808.4	A
Ty4 LTR		
3364_f_at	200.4	A
tRNA-Gln		
3365_f_at	18314.2	P
Ty1 LTR		
3366_at	-1659.0	A
Ty1 LTR		
3367_f_at	2755.4	P
Ty1 LTR		
3368_f_at	140.6	A
tRNA-Arg		
3369_i_at	127.5	A
Ty1 LTR		
3370_f_at	338.6	A
Ty1 LTR		
3371_f_at	1579.3	P
tRNA-Glu		
3372_f_at	189.0	A
tRNA-His		
3373_at	214.2	A
Ty1 LTR		
3374_at	215.0	A
Ty1 LTR		
3375_f_at	12926.6	P

Ty3 LTR		
3376_f_at	309.0	A
tRNA-Gln		
3377_at	-34.0	A
Ty1 LTR		
3378_f_at	489.2	A
tRNA-Ser		
3332_i_at	-33.3	A
Ty1 LTR		
3333_f_at	11470.5	P
Ty1 LTR		
3334_at	110.5	A
Ty1 LTR		
3335_at	-19.3	A
Ty1 LTR		
3336_f_at	294.2	A
Ty4 LTR		
3337_i_at	174.2	A
Ty3 LTR		
3338_f_at	-124.3	A
Ty3 LTR		
3340_f_at	16827.2	P
Ty1 LTR		
3342_f_at	10254.6	P
Ty3 LTR		
3343_i_at	483.0	P
Ty1 LTR		
3344_f_at	415.2	A
Ty1 LTR		
3345_f_at	7111.0	P
Ty1 LTR		
3346_at	-425.9	A
Ty4 LTR		
3347_s_at	458.3	A
Ty1 LTR		
3348_f_at	19772.1	P
Ty1 LTR		
3350_f_at	43451.5	P
Full length Ty1		
3352_s_at	144215.1	P
Ty1 LTR		
3354_s_at	94733.4	P
Ty1 LTR		
3355_s_at	47842.8	P
Ty1 LTR		
3307_s_at	9847.4	P
Ty1 LTR		
3308_s_at	5540.8	P
Ty1 LTR		
3309_s_at	4720.7	P
Ty1 LTR		
3310_s_at	2838.2	P
Ty1 LTR		
3311_f_at	14070.0	P
Ty1 LTR		
3313_f_at	19571.5	P

Ty1 LTR
3315_f_at 52662.8 P
Ty3 LTR
3316_f_at 15669.9 P
Ty3 LTR
3317_f_at 46701.8 P
Ty1 LTR
3319_f_at 37202.6 P
Ty1 LTR
3320_i_at 2321.4 P
Ty1 LTR
3321_f_at 1391.8 A
Ty1 LTR
3322_at -317.9 A
Ty1 LTR
3323_i_at -52.6 A
Ty5 LTR
3324_at 241.2 A
Ty5 LTR
3325_f_at 595.5 A
strong similarity to subtelomeric encoded proteins
3326_at 174.2 A
strong similarity to subtelomeric encoded proteins
3327_f_at 8004.5 P
Protein with strong similarity to subtelomerically-encoded proteins such as Cos5p, Ybr302p, Cos3p, Cos1p, Cos4p, Cos8p, Cos6p, Cos9p
3328_at -101.3 A
Ty1 LTR
3329_f_at 2996.1 P
Ty1 LTR
3330_f_at 26999.9 P
Ty2 LTR
3283_f_at 77274.0 P
Saccharomyces cerevisiae chromosome VI, complete chromosome sequence. Found forward in NC_001138 between 139492 and 143511 with 100% identity.
3284_f_at 59947.2 P
Full length Ty2
3285_f_at 12077.6 P
Ty2 LTR
3286_f_at 7641.4 P
Ty1 LTR
3287_s_at 50.9 A
Ty4 LTR
3288_at 151.5 A
Ty1 LTR
3289_i_at 47.7 A
Ty1 LTR
3290_f_at 332.9 A
Ty1 LTR
3291_f_at 7347.2 P
Ty1 LTR
3294_at 86.7 A
Ty1 LTR
3296_at -225.6 A
Ty1 LTR
3297_i_at 97.6 A

Ty5 LTR		
3298_f_at	-624.9	A
Ty5 LTR		
3299_f_at	-278.6	A
strong similarity to subtelomeric encoded proteins		
3301_f_at	399.8	A
Ty4 LTR		
3302_f_at	21939.7	P
Ty1 LTR		
3303_f_at	4068.2	A
Ty1 LTR		
3304_f_at	309.9	A
Ty1 LTR		
3305_at	-217.6	A
Ty4 LTR		
3306_i_at	272.4	A
Ty1 LTR		
3258_f_at	376.2	A
Ty1 LTR		
3259_at	2290.2	P
Ty1 LTR		
3260_f_at	10761.2	P
Ty3 LTR		
3262_at	122.6	A
Ty4 LTR		
3263_i_at	148.3	A
Ty1 LTR		
3264_f_at	267.5	A
Ty1 LTR		
3267_f_at	9795.9	P
Ty3 LTR		
3268_f_at	23706.2	P
Ty1 LTR		
3269_f_at	6382.5	P
Ty1 LTR		
3270_f_at	68326.7	P
Ty1 LTR		
3271_i_at	-30.9	A
Ty3 LTR		
3272_f_at	17879.2	P
Ty3 LTR		
3274_at	319.5	A
Ty1 LTR		
3276_i_at	-629.9	A
Ty1 LTR		
3277_f_at	55.2	A
Ty1 LTR		
3279_f_at	27166.9	P
Full length Ty1		
3235_f_at	25070.7	P
Ty1 LTR		
3236_f_at	47524.0	P
Full length Ty1		
3237_f_at	67494.1	P
Full length Ty1		
3239_f_at	33127.5	P

Ty1 LTR
3240_f_at 17987.1 P
Ty2 LTR
3241_f_at 91698.0 P
Full length Ty2
3243_at -258.9 A
tRNA-Leu
3244_i_at 32.3 A
Ty1 LTR
3245_f_at 170.5 A
Ty1 LTR
3247_s_at 179.4 A
TY3B protein Found forward in NC_001139 between 707604 and 708461 with 100% identity.
3248_s_at 239.2 A
Saccharomyces cerevisiae chromosome VII, complete chromosome sequence. Found forward in NC_001139 between 708460 and 712248 with 100% identity.
3249_s_at 308.6 A
Saccharomyces cerevisiae chromosome VII, complete chromosome sequence. Found forward in NC_001139 between 708460 and 712248 with 100% identity.
3250_s_at 43.4 A
Saccharomyces cerevisiae chromosome VII, complete chromosome sequence. Found forward in NC_001139 between 708460 and 712248 with 100% identity.
3251_s_at 172.2 A
Full length Ty3
3252_s_at 404.4 A
Full length Ty3
3253_f_at 12704.9 P
Full length Ty3
3255_at 153.9 A
Ty1 LTR
3256_at -53.1 A
Ty1 LTR
3257_f_at 16833.3 P
Ty3 LTR
3212_f_at 1451.3 P
Ty1 LTR
3214_at 15.4 A
Ty1 LTR
3215_f_at 262.7 A
Ty1 LTR
3216_at -116.8 A
Ty1 LTR
3218_at -27.4 A
Ty1 LTR
3222_f_at 37715.7 P
Full length Ty2
3223_f_at 25624.3 P
Ty2 LTR
3225_f_at 47951.2 P
Full length Ty1
3226_f_at 43583.4 P
Ty1 LTR
3228_at 202.3 A
Ty3 LTR
3230_f_at 10203.3 P
Ty1 LTR

3232_f_at	225.4	A	Ty4 LTR
3233_f_at	31295.2	P	Ty1 LTR
3234_at	2593.4	P	Protein with strong similarity to other subtelomerically-encoded proteins such as Cos5p, Ybr302p, Cos3p, Cos1p, Cos4p, Cos8p, Cos6p, Cos9p
3187_s_at	905.1	P	strong similarity to subtelomeric encoded proteins
3188_at	-210.0	A	Protein with similarity to subtelomerically-encoded proteins such as Cos5p, Ybr302p, Cos3p, Cos1p, Cos4p, Cos8p, Cos6p, Cos9p
3189_i_at	-239.8	A	Protein with similarity to subtelomerically-encoded proteins such as Cos5p, Ybr302p, Cos3p, Cos1p, Cos4p, Cos8p, Cos6p, Cos9p
3190_f_at	202.0	A	Protein with similarity to subtelomerically-encoded proteins such as Cos5p, Ybr302p, Cos3p, Cos1p, Cos4p, Cos8p, Cos6p, Cos9p
3191_i_at	24.4	A	Ty5 LTR
3192_f_at	-172.6	A	Ty5 LTR
3193_at	-174.5	A	strong similarity to subtelomeric encoded proteins
3195_f_at	9223.3	P	Ty3 LTR
3196_f_at	587.7	P	Ty4 LTR
3199_f_at	35930.5	P	Ty1 LTR
3200_i_at	48.6	A	Ty1 LTR
3201_r_at	-90.3	A	Ty1 LTR
3202_f_at	-206.6	A	Ty1 LTR
3203_f_at	17687.9	P	Ty1 LTR
3204_at	37.1	A	Ty1 LTR
3206_at	-90.7	A	Ty1 LTR
3207_i_at	-45.3	A	Ty1 LTR
3208_f_at	3.6	A	Ty1 LTR
3209_f_at	15288.1	P	Ty1 LTR
3161_f_at	6407.6	P	Ty3 LTR
3162_at	304.0	A	Ty4 LTR
3163_i_at	148.1	A	Ty1 LTR
3164_f_at	-124.7	A	Ty1 LTR

3165_at	-220.9	A
Ty4 LTR		
3166_i_at	-29.1	A
Ty1 LTR		
3167_r_at	172.0	A
Ty1 LTR		
3168_f_at	-90.5	A
Ty1 LTR		
3169_f_at	53398.4	P
Ty2 LTR		
3170_i_at	119.4	A
Ty1 LTR		
3171_r_at	171.0	A
Ty1 LTR		
3172_f_at	54.1	A
Ty1 LTR		
3173_i_at	-307.8	A
Ty1 LTR		
3174_f_at	-213.3	A
Ty1 LTR		
3175_i_at	-399.3	A
Ty1 LTR		
3176_f_at	282.8	A
Ty1 LTR		
3177_f_at	-156.1	A
Ty3 LTR		
3178_f_at	-165.0	A
Ty1 LTR		
3180_f_at	60238.9	P
Full length Ty1		
3181_f_at	22190.2	P
Ty1 LTR		
3182_i_at	-579.1	A
strong similarity to subtelomeric encoded YDR544c		
3183_f_at	16755.2	P
strong similarity to subtelomeric encoded proteins		
3184_s_at	-310.5	A
strong similarity to subtelomeric encoded proteins		
3185_s_at	124.3	A
strong similarity to subtelomeric encoded proteins		
3133_f_at	9273.2	P
Ty1 LTR		
3136_s_at	1544.5	P
Saccharomyces cerevisiae chromosome IX, complete chromosome sequence. Found forward in NC_001141 between 206488 and 210129 with 100% identity.		
3137_s_at	1854.9	P
Full length Ty3		
3139_f_at	18255.8	P
Ty2 LTR		
3141_i_at	-72.4	A
Ty1 LTR		
3142_f_at	6478.0	P
Ty1 LTR		
3143_f_at	694.0	A
Ty3 LTR		
3144_f_at	556.5	P

Ty1 LTR
3145_at 314.0 A
Ty1 LTR
3147_at -276.0 A
Ty1 LTR
3148_s_at 3022.8 P
mating hormone a2
3149_at 808.2 A
Saccharomyces cerevisiae chromosome I, complete chromosome sequence. Found forward in NC_001133 between 13744 and 14743 with 100% identity.
3150_at 915.4 P
Saccharomyces cerevisiae chromosome I, complete chromosome sequence. Found forward in NC_001133 between 14744 and 15743 with 100% identity.
3151_g_at 1011.5 P
Saccharomyces cerevisiae chromosome I, complete chromosome sequence. Found forward in NC_001133 between 14744 and 15743 with 100% identity.
3152_at 1766.0 P
Saccharomyces cerevisiae chromosome I, complete chromosome sequence. Found forward in NC_001133 between 15744 and 16743 with 100% identity.
3153_at 933.8 P
Saccharomyces cerevisiae chromosome I, complete chromosome sequence. Found forward in NC_001133 between 16744 and 17743 with 100% identity.
3154_at 642.1 P
Saccharomyces cerevisiae chromosome I, complete chromosome sequence. Found forward in NC_001133 between 17744 and 18743 with 100% identity.
3155_at 930.6 P
Saccharomyces cerevisiae chromosome I, complete chromosome sequence. Found forward in NC_001133 between 18744 and 19729 with 100% identity.
3156_at 592.0 A
Saccharomyces cerevisiae chromosome I, complete chromosome sequence. Found forward in NC_001133 between 88357 and 89356 with 100% identity.
3157_at -430.5 A
Saccharomyces cerevisiae chromosome I, complete chromosome sequence. Found forward in NC_001133 between 89357 and 90356 with 100% identity.
3158_at 399.0 P
Saccharomyces cerevisiae chromosome I, complete chromosome sequence. Found forward in NC_001133 between 90357 and 91356 with 100% identity.
3159_at 554.8 P
Saccharomyces cerevisiae chromosome I, complete chromosome sequence. Found forward in NC_001133 between 91357 and 92356 with 100% identity.
3088_at 313.8 A
Saccharomyces cerevisiae chromosome I, complete chromosome sequence. Found forward in NC_001133 between 92357 and 93356 with 100% identity.
3089_g_at 728.6 P
Saccharomyces cerevisiae chromosome I, complete chromosome sequence. Found forward in NC_001133 between 92357 and 93356 with 100% identity.
3090_s_at 1059.9 P
Saccharomyces cerevisiae chromosome I, complete chromosome sequence. Found forward in NC_001133 between 93357 and 93988 with 100% identity.
3091_at 416.5 P
Saccharomyces cerevisiae chromosome I, complete chromosome sequence. Found forward in NC_001133 between 159789 and 160788 with 100% identity.
3092_f_at 2584.6 P
Saccharomyces cerevisiae chromosome I, complete chromosome sequence. Found forward in NC_001133 between 160789 and 161788 with 100% identity.
3093_f_at 5336.3 P

Saccharomyces cerevisiae chromosome I, complete chromosome sequence. Found forward in NC_001133 between 161789 and 162788 with 100% identity.
3096_f_at 2212.2 P
Saccharomyces cerevisiae chromosome I, complete chromosome sequence. Found forward in NC_001133 between 164789 and 165788 with 100% identity.
3097_at 658.7 P
Saccharomyces cerevisiae chromosome I, complete chromosome sequence. Found forward in NC_001133 between 165789 and 166468 with 100% identity.
3098_at 963.4 P
Saccharomyces cerevisiae chromosome I, complete chromosome sequence. Found forward in NC_001133 between 208649 and 209648 with 100% identity.
3099_at 666.6 P
Saccharomyces cerevisiae chromosome I, complete chromosome sequence. Found forward in NC_001133 between 209649 and 210648 with 100% identity.
3100_s_at 1134.6 P
Saccharomyces cerevisiae chromosome I, complete chromosome sequence. Found forward in NC_001133 between 210649 and 211648 with 100% identity.
3101_at 756.9 P
Saccharomyces cerevisiae chromosome I, complete chromosome sequence. Found forward in NC_001133 between 211649 and 212648 with 100% identity.
3102_s_at 930.5 P
Saccharomyces cerevisiae chromosome I, complete chromosome sequence. Found forward in NC_001133 between 212649 and 213648 with 100% identity.
3103_at 675.0 P
Saccharomyces cerevisiae chromosome I, complete chromosome sequence. Found forward in NC_001133 between 213649 and 214648 with 100% identity.
3104_at 505.4 P
Saccharomyces cerevisiae chromosome I, complete chromosome sequence. Found forward in NC_001133 between 214649 and 215648 with 100% identity.
3105_g_at 907.5 P
Saccharomyces cerevisiae chromosome I, complete chromosome sequence. Found forward in NC_001133 between 214649 and 215648 with 100% identity.
3106_s_at 1004.1 P
Saccharomyces cerevisiae chromosome I, complete chromosome sequence. Found forward in NC_001133 between 215649 and 216648 with 100% identity.
3107_s_at 4346.9 P
Saccharomyces cerevisiae chromosome I, complete chromosome sequence. Found forward in NC_001133 between 216649 and 217143 with 100% identity.
3108_at 612.6 P
Saccharomyces cerevisiae chromosome X, complete chromosome sequence. Found forward in NC_001142 between 9138 and 10137 with 100% identity.
3109_at 144.8 A
Saccharomyces cerevisiae chromosome X, complete chromosome sequence. Found forward in NC_001142 between 10138 and 11137 with 100% identity.
3110_s_at 566.0 P
Saccharomyces cerevisiae chromosome X, complete chromosome sequence. Found forward in NC_001142 between 11138 and 12137 with 100% identity.
3111_s_at -540.0 P
Saccharomyces cerevisiae chromosome X, complete chromosome sequence. Found forward in NC_001142 between 12138 and 13137 with 100% identity.
3112_s_at 357.0 A
Saccharomyces cerevisiae chromosome X, complete chromosome sequence. Found forward in NC_001142 between 13138 and 14137 with 100% identity.
3113_s_at 977.5 P
Saccharomyces cerevisiae chromosome X, complete chromosome sequence. Found forward in NC_001142 between 14138 and 15137 with 100% identity.

3114_s_at 1291.3 P
Saccharomyces cerevisiae chromosome X, complete chromosome sequence. Found forward in NC_001142 between 15138 and 15624 with 100% identity.
3115_at 597.8 P
Saccharomyces cerevisiae chromosome X, complete chromosome sequence. Found forward in NC_001142 between 41889 and 42888 with 100% identity.
3116_at 1652.3 P
Saccharomyces cerevisiae chromosome X, complete chromosome sequence. Found forward in NC_001142 between 42889 and 43888 with 100% identity.
3117_at 808.6 P
Saccharomyces cerevisiae chromosome X, complete chromosome sequence. Found forward in NC_001142 between 43889 and 44888 with 100% identity.
3118_at -167.6 P
Saccharomyces cerevisiae chromosome X, complete chromosome sequence. Found forward in NC_001142 between 44889 and 45888 with 100% identity.
3119_at 726.3 P
Saccharomyces cerevisiae chromosome X, complete chromosome sequence. Found forward in NC_001142 between 45889 and 46888 with 100% identity.
3120_at 917.1 P
Saccharomyces cerevisiae chromosome X, complete chromosome sequence. Found forward in NC_001142 between 46889 and 47659 with 100% identity.
3121_at 1886.0 P
Saccharomyces cerevisiae chromosome X, complete chromosome sequence. Found forward in NC_001142 between 165921 and 166920 with 100% identity.
3122_at 1125.7 P
Saccharomyces cerevisiae chromosome X, complete chromosome sequence. Found forward in NC_001142 between 166921 and 167920 with 100% identity.
3123_at 3463.4 P
Saccharomyces cerevisiae chromosome X, complete chromosome sequence. Found forward in NC_001142 between 167921 and 168920 with 100% identity.
3124_at 1582.6 P
Saccharomyces cerevisiae chromosome X, complete chromosome sequence. Found forward in NC_001142 between 168921 and 169920 with 100% identity.
3125_at 2137.8 P
Saccharomyces cerevisiae chromosome X, complete chromosome sequence. Found forward in NC_001142 between 169921 and 170920 with 100% identity.
3126_at 1205.8 P
Saccharomyces cerevisiae chromosome X, complete chromosome sequence. Found forward in NC_001142 between 170921 and 171920 with 100% identity.
3127_at 1746.4 P
Saccharomyces cerevisiae chromosome X, complete chromosome sequence. Found forward in NC_001142 between 171921 and 172694 with 100% identity.
3128_at 602.6 A
Saccharomyces cerevisiae chromosome X, complete chromosome sequence. Found forward in NC_001142 between 196825 and 197824 with 100% identity.
3129_at -109.5 A
Saccharomyces cerevisiae chromosome X, complete chromosome sequence. Found forward in NC_001142 between 203825 and 204824 with 100% identity.
3130_at -31.4 A
Saccharomyces cerevisiae chromosome X, complete chromosome sequence. Found forward in NC_001142 between 204825 and 205824 with 100% identity.
3131_g_at 3.3 A
Saccharomyces cerevisiae chromosome X, complete chromosome sequence. Found forward in NC_001142 between 204825 and 205824 with 100% identity.
3045_s_at 331.2 A
Saccharomyces cerevisiae chromosome X, complete chromosome sequence. Found forward in

NC_001142 between 205825 and 206646 with 100% identity.
3046_at 82.0 A
Saccharomyces cerevisiae chromosome X, complete chromosome sequence. Found forward in NC_001142 between 212197 and 213196 with 100% identity.
3047_at 7358.6 A
Saccharomyces cerevisiae chromosome X, complete chromosome sequence. Found forward in NC_001142 between 213197 and 214196 with 100% identity.
3048_at -254.2 A
Saccharomyces cerevisiae chromosome X, complete chromosome sequence. Found forward in NC_001142 between 214197 and 215196 with 100% identity.
3049_at 247.1 A
Saccharomyces cerevisiae chromosome X, complete chromosome sequence. Found forward in NC_001142 between 215197 and 216196 with 100% identity.
3050_at -85.2 A
Saccharomyces cerevisiae chromosome X, complete chromosome sequence. Found forward in NC_001142 between 216197 and 217196 with 100% identity.
3051_at 83.8 A
Saccharomyces cerevisiae chromosome X, complete chromosome sequence. Found forward in NC_001142 between 217197 and 217402 with 100% identity.
3052_at 229.3 A
Saccharomyces cerevisiae chromosome X, complete chromosome sequence. Found forward in NC_001142 between 254933 and 255932 with 100% identity.
3053_at 147.4 A
Saccharomyces cerevisiae chromosome X, complete chromosome sequence. Found forward in NC_001142 between 255933 and 256932 with 100% identity.
3054_at -197.3 A
Saccharomyces cerevisiae chromosome X, complete chromosome sequence. Found forward in NC_001142 between 256933 and 257932 with 100% identity.
3055_g_at 80.8 A
Saccharomyces cerevisiae chromosome X, complete chromosome sequence. Found forward in NC_001142 between 256933 and 257932 with 100% identity.
3056_s_at 285.6 A
Saccharomyces cerevisiae chromosome X, complete chromosome sequence. Found forward in NC_001142 between 257933 and 258932 with 100% identity.
3057_s_at 928.8 A
Saccharomyces cerevisiae chromosome X, complete chromosome sequence. Found forward in NC_001142 between 258933 and 259932 with 100% identity.
3058_s_at 77.5 A
Saccharomyces cerevisiae chromosome X, complete chromosome sequence. Found forward in NC_001142 between 259933 and 260143 with 100% identity.
3059_at 107.1 A
Saccharomyces cerevisiae chromosome X, complete chromosome sequence. Found forward in NC_001142 between 368944 and 369943 with 100% identity.
3060_at 66.4 A
Saccharomyces cerevisiae chromosome X, complete chromosome sequence. Found forward in NC_001142 between 369944 and 370943 with 100% identity.
3061_at -12.1 A
Saccharomyces cerevisiae chromosome X, complete chromosome sequence. Found forward in NC_001142 between 370944 and 371943 with 100% identity.
3062_at 204.8 A
Saccharomyces cerevisiae chromosome X, complete chromosome sequence. Found forward in NC_001142 between 371944 and 372943 with 100% identity.
3063_at 462.8 A
Saccharomyces cerevisiae chromosome X, complete chromosome sequence. Found forward in NC_001142 between 372944 and 373943 with 100% identity.
3064_at 669.0 A

Saccharomyces cerevisiae chromosome X, complete chromosome sequence. Found forward in NC_001142 between 373944 and 374811 with 100% identity.
3065_g_at	-75.8	A
Saccharomyces cerevisiae chromosome X, complete chromosome sequence. Found forward in NC_001142 between 373944 and 374811 with 100% identity.
3066_at	33.0	A
Saccharomyces cerevisiae chromosome X, complete chromosome sequence. Found forward in NC_001142 between 424301 and 425300 with 100% identity.
3067_g_at	121.2	A
Saccharomyces cerevisiae chromosome X, complete chromosome sequence. Found forward in NC_001142 between 424301 and 425300 with 100% identity.
3068_s_at	-67.9	A
Saccharomyces cerevisiae chromosome X, complete chromosome sequence. Found forward in NC_001142 between 425301 and 426300 with 100% identity.
3069_s_at	-258.3	A
Saccharomyces cerevisiae chromosome X, complete chromosome sequence. Found forward in NC_001142 between 426301 and 427300 with 100% identity.
3070_s_at	-1164.9	A
Saccharomyces cerevisiae chromosome X, complete chromosome sequence. Found forward in NC_001142 between 427301 and 428300 with 100% identity.
3071_s_at	285.7	A
Saccharomyces cerevisiae chromosome X, complete chromosome sequence. Found forward in NC_001142 between 428301 and 429300 with 100% identity.
3072_s_at	819.5	A
Saccharomyces cerevisiae chromosome X, complete chromosome sequence. Found forward in NC_001142 between 429301 and 430300 with 100% identity.
3073_s_at	-24.3	A
Saccharomyces cerevisiae chromosome X, complete chromosome sequence. Found forward in NC_001142 between 430301 and 430425 with 100% identity.
3074_at	-266.2	A
Saccharomyces cerevisiae chromosome X, complete chromosome sequence. Found forward in NC_001142 between 510427 and 511426 with 100% identity.
3075_at	-1000.8	A
Saccharomyces cerevisiae chromosome X, complete chromosome sequence. Found forward in NC_001142 between 511427 and 512426 with 100% identity.
3076_at	186.2	A
Saccharomyces cerevisiae chromosome X, complete chromosome sequence. Found forward in NC_001142 between 512427 and 513426 with 100% identity.
3077_at	169.5	A
Saccharomyces cerevisiae chromosome X, complete chromosome sequence. Found forward in NC_001142 between 513427 and 514426 with 100% identity.
3078_g_at	257.2	A
Saccharomyces cerevisiae chromosome X, complete chromosome sequence. Found forward in NC_001142 between 513427 and 514426 with 100% identity.
3079_s_at	253.7	A
Saccharomyces cerevisiae chromosome X, complete chromosome sequence. Found forward in NC_001142 between 514427 and 515426 with 100% identity.
3080_f_at	581.1	P
Saccharomyces cerevisiae chromosome X, complete chromosome sequence. Found forward in NC_001142 between 515427 and 515477 with 100% identity.
3081_at	878.8	A
Saccharomyces cerevisiae chromosome X, complete chromosome sequence. Found forward in NC_001142 between 557997 and 558996 with 100% identity.
3082_at	-1467.9	A
Saccharomyces cerevisiae chromosome X, complete chromosome sequence. Found forward in NC_001142 between 558997 and 559996 with 100% identity.

3083_g_at -11978.4 A
Saccharomyces cerevisiae chromosome X, complete chromosome sequence. Found forward in NC_001142 between 558997 and 559996 with 100% identity.
3084_s_at -52.1 A
Saccharomyces cerevisiae chromosome X, complete chromosome sequence. Found forward in NC_001142 between 559997 and 560996 with 100% identity.
3085_s_at -244.6 A
Saccharomyces cerevisiae chromosome X, complete chromosome sequence. Found forward in NC_001142 between 560997 and 561996 with 100% identity.
3086_s_at -34.2 A
Saccharomyces cerevisiae chromosome X, complete chromosome sequence. Found forward in NC_001142 between 561997 and 562996 with 100% identity.
3087_s_at -206.9 A
Saccharomyces cerevisiae chromosome X, complete chromosome sequence. Found forward in NC_001142 between 562997 and 563996 with 100% identity.
3003_s_at 1080.5 A
Saccharomyces cerevisiae chromosome X, complete chromosome sequence. Found forward in NC_001142 between 563997 and 564996 with 100% identity.
3004_s_at 495.4 A
Saccharomyces cerevisiae chromosome X, complete chromosome sequence. Found forward in NC_001142 between 564997 and 565996 with 100% identity.
3005_at -24.0 A
Saccharomyces cerevisiae chromosome X, complete chromosome sequence. Found forward in NC_001142 between 595249 and 596248 with 100% identity.
3006_at -245.1 A
Saccharomyces cerevisiae chromosome X, complete chromosome sequence. Found forward in NC_001142 between 596249 and 597248 with 100% identity.
3007_at 518.8 A
Saccharomyces cerevisiae chromosome X, complete chromosome sequence. Found forward in NC_001142 between 597249 and 598248 with 100% identity.
3008_at -7.6 A
Saccharomyces cerevisiae chromosome X, complete chromosome sequence. Found forward in NC_001142 between 598249 and 599248 with 100% identity.
3009_g_at 528.8 A
Saccharomyces cerevisiae chromosome X, complete chromosome sequence. Found forward in NC_001142 between 598249 and 599248 with 100% identity.
3010_s_at 131.2 A
Saccharomyces cerevisiae chromosome X, complete chromosome sequence. Found forward in NC_001142 between 599249 and 600248 with 100% identity.
3011_s_at -61.6 A
Saccharomyces cerevisiae chromosome X, complete chromosome sequence. Found forward in NC_001142 between 600249 and 601248 with 100% identity.
3012_s_at 5255.0 A
Saccharomyces cerevisiae chromosome X, complete chromosome sequence. Found forward in NC_001142 between 601249 and 602248 with 100% identity.
3013_at 557.2 A
Saccharomyces cerevisiae chromosome X, complete chromosome sequence. Found forward in NC_001142 between 629774 and 630773 with 100% identity.
3014_at 128.4 A
Saccharomyces cerevisiae chromosome X, complete chromosome sequence. Found forward in NC_001142 between 630774 and 631773 with 100% identity.
3015_at -340.5 A
Saccharomyces cerevisiae chromosome X, complete chromosome sequence. Found forward in NC_001142 between 631774 and 632773 with 100% identity.
3016_at 133.7 A
Saccharomyces cerevisiae chromosome X, complete chromosome sequence. Found forward in

NC_001142 between 632774 and 633773 with 100% identity.
3017_g_at -179.2 A
Saccharomyces cerevisiae chromosome X, complete chromosome sequence. Found forward in NC_001142 between 632774 and 633773 with 100% identity.
3018_s_at 49.4 A
Saccharomyces cerevisiae chromosome X, complete chromosome sequence. Found forward in NC_001142 between 633774 and 634773 with 100% identity.
3019_at -36.1 A
Saccharomyces cerevisiae chromosome X, complete chromosome sequence. Found forward in NC_001142 between 690939 and 691938 with 100% identity.
3020_at -82.3 A
Saccharomyces cerevisiae chromosome X, complete chromosome sequence. Found forward in NC_001142 between 691939 and 692938 with 100% identity.
3021_at 76.6 A
Saccharomyces cerevisiae chromosome X, complete chromosome sequence. Found forward in NC_001142 between 692939 and 693938 with 100% identity.
3022_at -273.3 A
Saccharomyces cerevisiae chromosome X, complete chromosome sequence. Found forward in NC_001142 between 693939 and 694938 with 100% identity.
3023_at 150.1 A
Saccharomyces cerevisiae chromosome X, complete chromosome sequence. Found forward in NC_001142 between 694939 and 695938 with 100% identity.
3024_g_at 752.2 A
Saccharomyces cerevisiae chromosome X, complete chromosome sequence. Found forward in NC_001142 between 694939 and 695938 with 100% identity.
3025_s_at 249.5 A
Saccharomyces cerevisiae chromosome X, complete chromosome sequence. Found forward in NC_001142 between 695939 and 696138 with 100% identity.
3026_at 1237.5 A
Saccharomyces cerevisiae chromosome X, complete chromosome sequence. Found forward in NC_001142 between 712444 and 713443 with 100% identity.
3027_at 281.0 A
Saccharomyces cerevisiae chromosome X, complete chromosome sequence. Found forward in NC_001142 between 713444 and 714443 with 100% identity.
3028_at -107.6 A
Saccharomyces cerevisiae chromosome X, complete chromosome sequence. Found forward in NC_001142 between 714444 and 715443 with 100% identity.
3029_at -7.1 A
Saccharomyces cerevisiae chromosome X, complete chromosome sequence. Found forward in NC_001142 between 715444 and 716443 with 100% identity.
3030_at 453.4 A
Saccharomyces cerevisiae chromosome X, complete chromosome sequence. Found forward in NC_001142 between 716444 and 717443 with 100% identity.
3031_at -177.8 A
Saccharomyces cerevisiae chromosome X, complete chromosome sequence. Found forward in NC_001142 between 717444 and 718443 with 100% identity.
3032_at 85.8 A
Saccharomyces cerevisiae chromosome X, complete chromosome sequence. Found forward in NC_001142 between 718444 and 719443 with 100% identity.
3033_s_at 68.6 A
Saccharomyces cerevisiae chromosome X, complete chromosome sequence. Found forward in NC_001142 between 719444 and 720443 with 100% identity.
3034_at 750.3 A
Saccharomyces cerevisiae chromosome XI, complete chromosome sequence. Found forward in NC_001143 between 9592 and 10591 with 100% identity.
3035_at 340.5 A

Saccharomyces cerevisiae chromosome XI, complete chromosome sequence. Found forward in NC_001143 between 10592 and 11591 with 100% identity.
3036_at 681.1 A
Saccharomyces cerevisiae chromosome XI, complete chromosome sequence. Found forward in NC_001143 between 11592 and 12591 with 100% identity.
3037_at -156.5 A
Saccharomyces cerevisiae chromosome XI, complete chromosome sequence. Found forward in NC_001143 between 12592 and 13591 with 100% identity.
3038_at 194.3 A
Saccharomyces cerevisiae chromosome XI, complete chromosome sequence. Found forward in NC_001143 between 13592 and 14591 with 100% identity.
3039_s_at 634.0 P
Saccharomyces cerevisiae chromosome XI, complete chromosome sequence. Found forward in NC_001143 between 14592 and 15208 with 100% identity.
3040_at 611.0 P
Saccharomyces cerevisiae chromosome XI, complete chromosome sequence. Found forward in NC_001143 between 56435 and 57434 with 100% identity.
3041_at -1468.0 A
Saccharomyces cerevisiae chromosome XI, complete chromosome sequence. Found forward in NC_001143 between 57435 and 58434 with 100% identity.
3042_at 253.7 A
Saccharomyces cerevisiae chromosome XI, complete chromosome sequence. Found forward in NC_001143 between 58435 and 59434 with 100% identity.
3043_at -14.2 A
Saccharomyces cerevisiae chromosome XI, complete chromosome sequence. Found forward in NC_001143 between 59435 and 60434 with 100% identity.
3044_at -84.8 A
Saccharomyces cerevisiae chromosome XI, complete chromosome sequence. Found forward in NC_001143 between 60435 and 61434 with 100% identity.
2960_at -150.7 A
Saccharomyces cerevisiae chromosome XI, complete chromosome sequence. Found forward in NC_001143 between 61435 and 62434 with 100% identity.
2961_at 414.4 P
Saccharomyces cerevisiae chromosome XI, complete chromosome sequence. Found forward in NC_001143 between 62435 and 63434 with 100% identity.
2962_at 212.2 A
Saccharomyces cerevisiae chromosome XI, complete chromosome sequence. Found forward in NC_001143 between 63435 and 63899 with 100% identity.
2963_at -261.4 A
Saccharomyces cerevisiae chromosome XI, complete chromosome sequence. Found forward in NC_001143 between 99643 and 100642 with 100% identity.
2964_at 180.8 A
Saccharomyces cerevisiae chromosome XI, complete chromosome sequence. Found forward in NC_001143 between 100643 and 101642 with 100% identity.
2965_g_at -92.1 A
Saccharomyces cerevisiae chromosome XI, complete chromosome sequence. Found forward in NC_001143 between 100643 and 101642 with 100% identity.
2966_s_at -343.9 A
Saccharomyces cerevisiae chromosome XI, complete chromosome sequence. Found forward in NC_001143 between 101643 and 102642 with 100% identity.
2967_s_at 4012.9 P
Saccharomyces cerevisiae chromosome XI, complete chromosome sequence. Found forward in NC_001143 between 102643 and 103642 with 100% identity.
2968_s_at 1517.1 P
Saccharomyces cerevisiae chromosome XI, complete chromosome sequence. Found forward in NC_001143 between 103643 and 104642 with 100% identity.

2969_s_at	3451.2	P	Saccharomyces cerevisiae chromosome XI, complete chromosome sequence. Found forward in NC_001143 between 104643 and 105642 with 100% identity.
2970_s_at	17429.4	P	Saccharomyces cerevisiae chromosome XI, complete chromosome sequence. Found forward in NC_001143 between 105643 and 106328 with 100% identity.
2971_at	-823.7	A	Saccharomyces cerevisiae chromosome XI, complete chromosome sequence. Found forward in NC_001143 between 411757 and 412756 with 100% identity.
2972_at	-501.8	A	Saccharomyces cerevisiae chromosome XI, complete chromosome sequence. Found forward in NC_001143 between 412757 and 413756 with 100% identity.
2973_at	-361.5	A	Saccharomyces cerevisiae chromosome XI, complete chromosome sequence. Found forward in NC_001143 between 413757 and 414756 with 100% identity.
2974_at	-827.6	A	Saccharomyces cerevisiae chromosome XI, complete chromosome sequence. Found forward in NC_001143 between 414757 and 415756 with 100% identity.
2975_at	-541.2	A	Saccharomyces cerevisiae chromosome XI, complete chromosome sequence. Found forward in NC_001143 between 415757 and 416756 with 100% identity.
2976_at	-213.6	A	Saccharomyces cerevisiae chromosome XI, complete chromosome sequence. Found forward in NC_001143 between 416757 and 417146 with 100% identity.
2977_at	4153.7	A	Saccharomyces cerevisiae chromosome XI, complete chromosome sequence. Found forward in NC_001143 between 535784 and 536783 with 100% identity.
2978_at	-239.4	A	Saccharomyces cerevisiae chromosome XI, complete chromosome sequence. Found forward in NC_001143 between 536784 and 537783 with 100% identity.
2979_at	2883.9	P	Saccharomyces cerevisiae chromosome XI, complete chromosome sequence. Found forward in NC_001143 between 537784 and 538783 with 100% identity.
2980_at	400.7	A	Saccharomyces cerevisiae chromosome XI, complete chromosome sequence. Found forward in NC_001143 between 538784 and 539783 with 100% identity.
2981_at	56.0	A	Saccharomyces cerevisiae chromosome XI, complete chromosome sequence. Found forward in NC_001143 between 539784 and 540783 with 100% identity.
2982_at	407.9	A	Saccharomyces cerevisiae chromosome XI, complete chromosome sequence. Found forward in NC_001143 between 540784 and 541783 with 100% identity.
2983_at	-197.7	A	Saccharomyces cerevisiae chromosome XI, complete chromosome sequence. Found forward in NC_001143 between 541784 and 542783 with 100% identity.
2984_at	44.4	A	Saccharomyces cerevisiae chromosome XI, complete chromosome sequence. Found forward in NC_001143 between 542784 and 543783 with 100% identity.
2985_at	-40.3	A	Saccharomyces cerevisiae chromosome XI, complete chromosome sequence. Found forward in NC_001143 between 543784 and 544783 with 100% identity.
2986_at	296.8	A	Saccharomyces cerevisiae chromosome XI, complete chromosome sequence. Found forward in NC_001143 between 544784 and 545783 with 100% identity.
2987_at	-38.4	A	Saccharomyces cerevisiae chromosome XI, complete chromosome sequence. Found forward in

NC_001143 between 545784 and 546783 with 100% identity.

2988_at -577.2 A

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

2989_at -199.5 A

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

2990_g_at 476.4 P

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

2991_at 52.7 A

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

2992_g_at 45.2 A

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

2993_s_at 89.1 A

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

2994_s_at -73.8 A

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

2995_s_at 680.6 A

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

2996_s_at 233.3 A

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

2997_s_at 744.2 P

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

2998_at 404.2 A

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

2999_at -191.1 A

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

3000_at -67.4 A

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

3001_at 23.6 A

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

3002_g_at -28.8 A

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

2917_s_at 77.0 A

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

2918_s_at -123.2 A

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

2919_s_at 1753.5 A

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

2920_at 109.2 A

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

2921_at 99.7 A

Saccharomyces cerevisiae chromosome XI, complete chromosome sequence. Found forward in NC_001143 between 650494 and 651493 with 100% identity.

2922_at 336.8 A

Saccharomyces cerevisiae chromosome XI, complete chromosome sequence. Found forward in NC_001143 between 651494 and 652493 with 100% identity.

2923_at -298.9 A

Saccharomyces cerevisiae chromosome XI, complete chromosome sequence. Found forward in NC_001143 between 652494 and 653493 with 100% identity.

2924_g_at -89.9 A

Saccharomyces cerevisiae chromosome XI, complete chromosome sequence. Found forward in NC_001143 between 652494 and 653493 with 100% identity.

2925_s_at 552.8 P

Saccharomyces cerevisiae chromosome XI, complete chromosome sequence. Found forward in NC_001143 between 653494 and 654493 with 100% identity.

2926_s_at -4.2 A

Saccharomyces cerevisiae chromosome XI, complete chromosome sequence. Found forward in NC_001143 between 654494 and 655493 with 100% identity.

2927_s_at 443.0 P

Saccharomyces cerevisiae chromosome XI, complete chromosome sequence. Found forward in NC_001143 between 655494 and 655865 with 100% identity.

2928_at 269.2 A

Saccharomyces cerevisiae chromosome XI, complete chromosome sequence. Found forward in NC_001143 between 662918 and 663917 with 100% identity.

2929_at 14639.8 A

Saccharomyces cerevisiae chromosome XI, complete chromosome sequence. Found forward in NC_001143 between 663918 and 664917 with 100% identity.

2930_at 286.5 A

Saccharomyces cerevisiae chromosome XI, complete chromosome sequence. Found forward in NC_001143 between 664918 and 665917 with 100% identity.

2931_at -82.5 A

Saccharomyces cerevisiae chromosome XI, complete chromosome sequence. Found forward in NC_001143 between 665918 and 666445 with 100% identity.

2932_at -162.3 A

Saccharomyces cerevisiae chromosome XII, complete chromosome sequence. Found forward in NC_001144 between 54710 and 55709 with 100% identity.

2933_at 223.6 M

Saccharomyces cerevisiae chromosome XII, complete chromosome sequence. Found forward in NC_001144 between 55710 and 56709 with 100% identity.

2934_at -121.8 A

Saccharomyces cerevisiae chromosome XII, complete chromosome sequence. Found forward in NC_001144 between 56710 and 57709 with 100% identity.

2935_at 3900.5 P

Saccharomyces cerevisiae chromosome XII, complete chromosome sequence. Found forward in NC_001144 between 57710 and 58709 with 100% identity.

2936_at 15.5 A

Saccharomyces cerevisiae chromosome XII, complete chromosome sequence. Found forward in NC_001144 between 58710 and 59709 with 100% identity.

2937_at -1367.6 A

Saccharomyces cerevisiae chromosome XII, complete chromosome sequence. Found forward in NC_001144 between 59710 and 60709 with 100% identity.

2938_at -866.2 A

Saccharomyces cerevisiae chromosome XII, complete chromosome sequence. Found forward in NC_001144 between 60710 and 61709 with 100% identity.

2939_at -1227.1 A
Saccharomyces cerevisiae chromosome XII, complete chromosome sequence. Found forward in NC_001144 between 61710 and 62709 with 100% identity.
2940_at -1521.4 A
Saccharomyces cerevisiae chromosome XII, complete chromosome sequence. Found forward in NC_001144 between 62710 and 63709 with 100% identity.
2941_at -2683.0 A
Saccharomyces cerevisiae chromosome XII, complete chromosome sequence. Found forward in NC_001144 between 63710 and 64061 with 100% identity.
2942_at -949.7 A
Saccharomyces cerevisiae chromosome XII, complete chromosome sequence. Found forward in NC_001144 between 99543 and 100542 with 100% identity.
2943_at -1559.2 A
Saccharomyces cerevisiae chromosome XII, complete chromosome sequence. Found forward in NC_001144 between 100543 and 101542 with 100% identity.
2944_g_at -1449.6 A
Saccharomyces cerevisiae chromosome XII, complete chromosome sequence. Found forward in NC_001144 between 100543 and 101542 with 100% identity.
2945_s_at -1743.2 A
Saccharomyces cerevisiae chromosome XII, complete chromosome sequence. Found forward in NC_001144 between 101543 and 102542 with 100% identity.
2946_s_at -1689.5 A
Saccharomyces cerevisiae chromosome XII, complete chromosome sequence. Found forward in NC_001144 between 102543 and 103542 with 100% identity.
2947_s_at -1241.2 A
Saccharomyces cerevisiae chromosome XII, complete chromosome sequence. Found forward in NC_001144 between 103543 and 104542 with 100% identity.
2948_s_at -2279.3 A
Saccharomyces cerevisiae chromosome XII, complete chromosome sequence. Found forward in NC_001144 between 104543 and 104846 with 100% identity.
2949_at -755.7 A
Saccharomyces cerevisiae chromosome XII, complete chromosome sequence. Found forward in NC_001144 between 188164 and 189163 with 100% identity.
2950_at -1156.1 A
Saccharomyces cerevisiae chromosome XII, complete chromosome sequence. Found forward in NC_001144 between 189164 and 190163 with 100% identity.
2951_at -1929.2 A
Saccharomyces cerevisiae chromosome XII, complete chromosome sequence. Found forward in NC_001144 between 190164 and 191163 with 100% identity.
2952_at -3207.6 A
Saccharomyces cerevisiae chromosome XII, complete chromosome sequence. Found forward in NC_001144 between 191164 and 192163 with 100% identity.
2953_at -5594.1 A
Saccharomyces cerevisiae chromosome XII, complete chromosome sequence. Found forward in NC_001144 between 192164 and 193163 with 100% identity.
2954_at -2500.4 A
Saccharomyces cerevisiae chromosome XII, complete chromosome sequence. Found forward in NC_001144 between 193164 and 194163 with 100% identity.
2955_at -1804.2 A
Saccharomyces cerevisiae chromosome XII, complete chromosome sequence. Found forward in NC_001144 between 194164 and 194675 with 100% identity.
2956_g_at -366.9 A
Saccharomyces cerevisiae chromosome XII, complete chromosome sequence. Found forward in NC_001144 between 194164 and 194675 with 100% identity.
2957_at -2050.3 A
Saccharomyces cerevisiae chromosome XII, complete chromosome sequence. Found forward in

NC_001144 between 307356 and 308355 with 100% identity.
2958_at -2763.0 A
Saccharomyces cerevisiae chromosome XII, complete chromosome sequence. Found forward in NC_001144 between 308356 and 309355 with 100% identity.
2959_at -609.3 A
Saccharomyces cerevisiae chromosome XII, complete chromosome sequence. Found forward in NC_001144 between 309356 and 310355 with 100% identity.
2875_at -482.7 A
Saccharomyces cerevisiae chromosome XII, complete chromosome sequence. Found forward in NC_001144 between 310356 and 311355 with 100% identity.
2876_at -1757.8 A
Saccharomyces cerevisiae chromosome XII, complete chromosome sequence. Found forward in NC_001144 between 311356 and 312355 with 100% identity.
2877_at -259.4 A
Saccharomyces cerevisiae chromosome XII, complete chromosome sequence. Found forward in NC_001144 between 312356 and 313355 with 100% identity.
2878_at -209.3 A
Saccharomyces cerevisiae chromosome XII, complete chromosome sequence. Found forward in NC_001144 between 313356 and 314355 with 100% identity.
2879_at -241.5 A
Saccharomyces cerevisiae chromosome XII, complete chromosome sequence. Found forward in NC_001144 between 314356 and 315355 with 100% identity.
2880_at 67.2 A
Saccharomyces cerevisiae chromosome XII, complete chromosome sequence. Found forward in NC_001144 between 315356 and 315877 with 100% identity.
2881_at 199.4 A
Saccharomyces cerevisiae chromosome XII, complete chromosome sequence. Found forward in NC_001144 between 330178 and 331177 with 100% identity.
2882_at 618.6 A
Saccharomyces cerevisiae chromosome XII, complete chromosome sequence. Found forward in NC_001144 between 331178 and 332177 with 100% identity.
2883_at -135.2 A
Saccharomyces cerevisiae chromosome XII, complete chromosome sequence. Found forward in NC_001144 between 332178 and 333177 with 100% identity.
2884_g_at 2268.4 A
Saccharomyces cerevisiae chromosome XII, complete chromosome sequence. Found forward in NC_001144 between 332178 and 333177 with 100% identity.
2885_s_at -140.7 A
Saccharomyces cerevisiae chromosome XII, complete chromosome sequence. Found forward in NC_001144 between 333178 and 334177 with 100% identity.
2886_s_at 623.9 P
Saccharomyces cerevisiae chromosome XII, complete chromosome sequence. Found forward in NC_001144 between 334178 and 335177 with 100% identity.
2887_s_at 530.5 A
Saccharomyces cerevisiae chromosome XII, complete chromosome sequence. Found forward in NC_001144 between 335178 and 335534 with 100% identity.
2888_at 362.1 A
Saccharomyces cerevisiae chromosome XII, complete chromosome sequence. Found forward in NC_001144 between 349507 and 350506 with 100% identity.
2889_at 25.7 A
Saccharomyces cerevisiae chromosome XII, complete chromosome sequence. Found forward in NC_001144 between 350507 and 351506 with 100% identity.
2890_at -308.0 A
Saccharomyces cerevisiae chromosome XII, complete chromosome sequence. Found forward in NC_001144 between 351507 and 352506 with 100% identity.
2891_at -1407.3 A

Saccharomyces cerevisiae chromosome XII, complete chromosome sequence. Found forward in NC_001144 between 352507 and 353506 with 100% identity.

2892_at -216.0 A

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

2893_at 113.2 A

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

2894_at -782.2 A

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

2895_at 1099.3 A

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

2896_at 159.8 A

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

2897_at 369.7 A

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

2898_at -566.3 A

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

2899_at -436.6 A

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

2900_at -3071.3 A

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

2901_at 16.0 A

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

2902_at -107.3 A

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

2903_g_at -155.8 A

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

2904_s_at -640.0 A

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

2905_at 48.8 A

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

2906_at -65.0 A

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

2907_at -905.5 A

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

2908_at -376.7 A

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

2909_at 112.6 A

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

2910_at -128.6 A
Saccharomyces cerevisiae chromosome XII, complete chromosome sequence. Found forward in NC_001144 between 634184 and 635183 with 100% identity.
2911_s_at 2357.2 P
Saccharomyces cerevisiae chromosome XII, complete chromosome sequence. Found forward in NC_001144 between 635184 and 635584 with 100% identity.
2912_at 225.7 A
Saccharomyces cerevisiae chromosome XII, complete chromosome sequence. Found forward in NC_001144 between 769817 and 770816 with 100% identity.
2913_at 1159.3 A
Saccharomyces cerevisiae chromosome XII, complete chromosome sequence. Found forward in NC_001144 between 770817 and 771816 with 100% identity.
2914_at 192.5 A
Saccharomyces cerevisiae chromosome XII, complete chromosome sequence. Found forward in NC_001144 between 771817 and 772816 with 100% identity.
2915_g_at 141.7 A
Saccharomyces cerevisiae chromosome XII, complete chromosome sequence. Found forward in NC_001144 between 771817 and 772816 with 100% identity.
2916_s_at 146.0 A
Saccharomyces cerevisiae chromosome XII, complete chromosome sequence. Found forward in NC_001144 between 772817 and 773816 with 100% identity.
2832_s_at 17.5 A
Saccharomyces cerevisiae chromosome XII, complete chromosome sequence. Found forward in NC_001144 between 773817 and 774816 with 100% identity.
2833_s_at -97.3 A
Saccharomyces cerevisiae chromosome XII, complete chromosome sequence. Found forward in NC_001144 between 774817 and 775803 with 100% identity.
2834_at 174.0 A
Saccharomyces cerevisiae chromosome XII, complete chromosome sequence. Found forward in NC_001144 between 808817 and 809816 with 100% identity.
2835_at 1034.6 P
Saccharomyces cerevisiae chromosome XII, complete chromosome sequence. Found forward in NC_001144 between 809817 and 810816 with 100% identity.
2836_g_at -574.4 P
Saccharomyces cerevisiae chromosome XII, complete chromosome sequence. Found forward in NC_001144 between 809817 and 810816 with 100% identity.
2837_s_at 235.7 P
Saccharomyces cerevisiae chromosome XII, complete chromosome sequence. Found forward in NC_001144 between 810817 and 811816 with 100% identity.
2838_s_at 354.3 A
Saccharomyces cerevisiae chromosome XII, complete chromosome sequence. Found forward in NC_001144 between 811817 and 812816 with 100% identity.
2839_s_at 572.0 P
Saccharomyces cerevisiae chromosome XII, complete chromosome sequence. Found forward in NC_001144 between 812817 and 813816 with 100% identity.
2840_s_at 5219.5 P
Saccharomyces cerevisiae chromosome XII, complete chromosome sequence. Found forward in NC_001144 between 813817 and 814816 with 100% identity.
2841_s_at 13079.8 P
Saccharomyces cerevisiae chromosome XII, complete chromosome sequence. Found forward in NC_001144 between 814817 and 815126 with 100% identity.
2842_at 387.7 A
Saccharomyces cerevisiae chromosome XII, complete chromosome sequence. Found forward in NC_001144 between 934909 and 935908 with 100% identity.
2843_at 784.8 P
Saccharomyces cerevisiae chromosome XII, complete chromosome sequence. Found forward in

NC_001144 between 935909 and 936908 with 100% identity.
2844_at 143.4 A
Saccharomyces cerevisiae chromosome XII, complete chromosome sequence. Found forward in NC_001144 between 936909 and 937908 with 100% identity.
2845_g_at -81.5 A
Saccharomyces cerevisiae chromosome XII, complete chromosome sequence. Found forward in NC_001144 between 936909 and 937908 with 100% identity.
2846_s_at 400.4 A
Saccharomyces cerevisiae chromosome XII, complete chromosome sequence. Found forward in NC_001144 between 937909 and 938908 with 100% identity.
2847_s_at 779.2 P
Saccharomyces cerevisiae chromosome XII, complete chromosome sequence. Found forward in NC_001144 between 938909 and 939908 with 100% identity.
2848_s_at 1160.6 P
Saccharomyces cerevisiae chromosome XII, complete chromosome sequence. Found forward in NC_001144 between 939909 and 940476 with 100% identity.
2849_at 527.4 A
Saccharomyces cerevisiae chromosome XII, complete chromosome sequence. Found forward in NC_001144 between 965554 and 966553 with 100% identity.
2850_g_at 13008.3 A
Saccharomyces cerevisiae chromosome XII, complete chromosome sequence. Found forward in NC_001144 between 965554 and 966553 with 100% identity.
2851_s_at 139.1 A
Saccharomyces cerevisiae chromosome XII, complete chromosome sequence. Found forward in NC_001144 between 966554 and 967553 with 100% identity.
2852_s_at 4.2 A
Saccharomyces cerevisiae chromosome XII, complete chromosome sequence. Found forward in NC_001144 between 967554 and 968553 with 100% identity.
2853_s_at 85.6 A
Saccharomyces cerevisiae chromosome XII, complete chromosome sequence. Found forward in NC_001144 between 968554 and 969553 with 100% identity.
2854_s_at 176.1 P
Saccharomyces cerevisiae chromosome XII, complete chromosome sequence. Found forward in NC_001144 between 969554 and 970553 with 100% identity.
2855_s_at 587.7 P
Saccharomyces cerevisiae chromosome XII, complete chromosome sequence. Found forward in NC_001144 between 970554 and 971189 with 100% identity.
2856_at 246.6 M
Saccharomyces cerevisiae chromosome XII, complete chromosome sequence. Found forward in NC_001144 between 979430 and 980429 with 100% identity.
2857_at 991.7 P
Saccharomyces cerevisiae chromosome XII, complete chromosome sequence. Found forward in NC_001144 between 980430 and 981429 with 100% identity.
2858_at 500.0 A
Saccharomyces cerevisiae chromosome XII, complete chromosome sequence. Found forward in NC_001144 between 981430 and 982429 with 100% identity.
2859_at 890.9 A
Saccharomyces cerevisiae chromosome XII, complete chromosome sequence. Found forward in NC_001144 between 982430 and 983429 with 100% identity.
2860_g_at -6777.0 A
Saccharomyces cerevisiae chromosome XII, complete chromosome sequence. Found forward in NC_001144 between 982430 and 983429 with 100% identity.
2861_s_at 166.5 A
Saccharomyces cerevisiae chromosome XII, complete chromosome sequence. Found forward in NC_001144 between 983430 and 984429 with 100% identity.
2862_s_at 777.1 P

Saccharomyces cerevisiae chromosome XII, complete chromosome sequence. Found forward in NC_001144 between 984430 and 985429 with 100% identity.
2863_s_at 734.9 P
Saccharomyces cerevisiae chromosome XII, complete chromosome sequence. Found forward in NC_001144 between 985430 and 986311 with 100% identity.
2864_at 767.3 P
Saccharomyces cerevisiae chromosome XII, complete chromosome sequence. Found forward in NC_001144 between 992726 and 993725 with 100% identity.
2865_g_at 917.0 P
Saccharomyces cerevisiae chromosome XII, complete chromosome sequence. Found forward in NC_001144 between 992726 and 993725 with 100% identity.
2866_s_at 787.7 P
Saccharomyces cerevisiae chromosome XII, complete chromosome sequence. Found forward in NC_001144 between 993726 and 994725 with 100% identity.
2867_s_at 2881.1 P
Saccharomyces cerevisiae chromosome XII, complete chromosome sequence. Found forward in NC_001144 between 994726 and 995725 with 100% identity.
2868_s_at -1112.3 P
Saccharomyces cerevisiae chromosome XII, complete chromosome sequence. Found forward in NC_001144 between 995726 and 996725 with 100% identity.
2869_s_at 385.2 A
Saccharomyces cerevisiae chromosome XII, complete chromosome sequence. Found forward in NC_001144 between 996726 and 997725 with 100% identity.
2870_s_at 939.8 P
Saccharomyces cerevisiae chromosome XII, complete chromosome sequence. Found forward in NC_001144 between 997726 and 998725 with 100% identity.
2871_s_at 2458.7 P
Saccharomyces cerevisiae chromosome XII, complete chromosome sequence. Found forward in NC_001144 between 998726 and 999623 with 100% identity.
2872_at 673.8 P
Saccharomyces cerevisiae chromosome XII, complete chromosome sequence. Found forward in NC_001144 between 1042294 and 1043293 with 100% identity.
2873_at 591.9 P
Saccharomyces cerevisiae chromosome XII, complete chromosome sequence. Found forward in NC_001144 between 1043294 and 1044293 with 100% identity.
2874_g_at 178.0 A
Saccharomyces cerevisiae chromosome XII, complete chromosome sequence. Found forward in NC_001144 between 1043294 and 1044293 with 100% identity.
2789_s_at 845.6 P
Saccharomyces cerevisiae chromosome XII, complete chromosome sequence. Found forward in NC_001144 between 1044294 and 1045293 with 100% identity.
2790_s_at 806.2 P
Saccharomyces cerevisiae chromosome XII, complete chromosome sequence. Found forward in NC_001144 between 1045294 and 1046293 with 100% identity.
2791_s_at 95.4 A
Saccharomyces cerevisiae chromosome XII, complete chromosome sequence. Found forward in NC_001144 between 1046294 and 1047293 with 100% identity.
2792_s_at 54.2 A
Saccharomyces cerevisiae chromosome XII, complete chromosome sequence. Found forward in NC_001144 between 1047294 and 1048293 with 100% identity.
2793_s_at 29.7 A
Saccharomyces cerevisiae chromosome XII, complete chromosome sequence. Found forward in NC_001144 between 1048294 and 1049293 with 100% identity.
2794_s_at 443.1 A
Saccharomyces cerevisiae chromosome XII, complete chromosome sequence. Found forward in NC_001144 between 1049294 and 1050293 with 100% identity.

2795_s_at 376.4 P
Saccharomyces cerevisiae chromosome XII, complete chromosome sequence. Found forward in NC_001144 between 1050294 and 1051293 with 100% identity.
2796_f_at 647.9 P
Saccharomyces cerevisiae chromosome XII, complete chromosome sequence. Found forward in NC_001144 between 1051294 and 1051379 with 100% identity.
2797_at 393.7 P
Saccharomyces cerevisiae chromosome XII, complete chromosome sequence. Found forward in NC_001144 between 1071425 and 1072424 with 100% identity.
2798_g_at -74.7 A
Saccharomyces cerevisiae chromosome XII, complete chromosome sequence. Found forward in NC_001144 between 1071425 and 1072424 with 100% identity.
2799_at -180.2 A
Saccharomyces cerevisiae chromosome XIII, complete chromosome sequence. Found forward in NC_001145 between 63082 and 64081 with 100% identity.
2800_at 437.0 P
Saccharomyces cerevisiae chromosome XIII, complete chromosome sequence. Found forward in NC_001145 between 64082 and 65081 with 100% identity.
2801_at 176.4 A
Saccharomyces cerevisiae chromosome XIII, complete chromosome sequence. Found forward in NC_001145 between 65082 and 66081 with 100% identity.
2802_at 342.1 A
Saccharomyces cerevisiae chromosome XIII, complete chromosome sequence. Found forward in NC_001145 between 66082 and 67081 with 100% identity.
2803_at -2671.6 A
Saccharomyces cerevisiae chromosome XIII, complete chromosome sequence. Found forward in NC_001145 between 67082 and 68081 with 100% identity.
2804_at -54.6 A
Saccharomyces cerevisiae chromosome XIII, complete chromosome sequence. Found forward in NC_001145 between 68082 and 69081 with 100% identity.
2805_g_at 409.6 P
Saccharomyces cerevisiae chromosome XIII, complete chromosome sequence. Found forward in NC_001145 between 68082 and 69081 with 100% identity.
2806_s_at 1268.3 P
Saccharomyces cerevisiae chromosome XIII, complete chromosome sequence. Found forward in NC_001145 between 69082 and 69200 with 100% identity.
2807_at 280.1 A
Saccharomyces cerevisiae chromosome XIII, complete chromosome sequence. Found forward in NC_001145 between 153719 and 154718 with 100% identity.
2808_at -326.0 A
Saccharomyces cerevisiae chromosome XIII, complete chromosome sequence. Found forward in NC_001145 between 154719 and 155718 with 100% identity.
2809_at -11.9 A
Saccharomyces cerevisiae chromosome XIII, complete chromosome sequence. Found forward in NC_001145 between 155719 and 156718 with 100% identity.
2810_at 22.0 A
Saccharomyces cerevisiae chromosome XIII, complete chromosome sequence. Found forward in NC_001145 between 156719 and 157718 with 100% identity.
2811_at -39.4 A
Saccharomyces cerevisiae chromosome XIII, complete chromosome sequence. Found forward in NC_001145 between 157719 and 158718 with 100% identity.
2812_at -1699.0 A
Saccharomyces cerevisiae chromosome XIII, complete chromosome sequence. Found forward in NC_001145 between 183363 and 184362 with 100% identity.
2813_at 95.8 A
Saccharomyces cerevisiae chromosome XIII, complete chromosome sequence. Found forward in

NC_001145 between 189363 and 190244 with 100% identity.
2814_at 81.7 A
Saccharomyces cerevisiae chromosome XIII, complete chromosome sequence. Found forward in NC_001145 between 195413 and 196412 with 100% identity.
2815_at 592.7 P
Saccharomyces cerevisiae chromosome XIII, complete chromosome sequence. Found forward in NC_001145 between 201413 and 202412 with 100% identity.
2816_at 3322.4 P
Saccharomyces cerevisiae chromosome XIII, complete chromosome sequence. Found forward in NC_001145 between 202413 and 202775 with 100% identity.
2817_at 1485.6 P
Saccharomyces cerevisiae chromosome XIII, complete chromosome sequence. Found forward in NC_001145 between 356810 and 357809 with 100% identity.
2818_at 9092.5 P
Saccharomyces cerevisiae chromosome XIII, complete chromosome sequence. Found forward in NC_001145 between 357810 and 358809 with 100% identity.
2819_s_at 1372.5 P
Saccharomyces cerevisiae chromosome XIII, complete chromosome sequence. Found forward in NC_001145 between 358810 and 359809 with 100% identity.
2821_at -130.4 A
Saccharomyces cerevisiae chromosome XIII, complete chromosome sequence. Found forward in NC_001145 between 360810 and 361809 with 100% identity.
2822_at 631.0 A
Saccharomyces cerevisiae chromosome XIII, complete chromosome sequence. Found forward in NC_001145 between 361810 and 362701 with 100% identity.
2823_at 337.3 P
Saccharomyces cerevisiae chromosome XIII, complete chromosome sequence. Found forward in NC_001145 between 368593 and 369592 with 100% identity.
2824_at 898.1 A
Saccharomyces cerevisiae chromosome XIII, complete chromosome sequence. Found forward in NC_001145 between 369593 and 370592 with 100% identity.
2825_at 396.9 A
Saccharomyces cerevisiae chromosome XIII, complete chromosome sequence. Found forward in NC_001145 between 370593 and 371592 with 100% identity.
2826_at -150.2 A
Saccharomyces cerevisiae chromosome XIII, complete chromosome sequence. Found forward in NC_001145 between 371593 and 372592 with 100% identity.
2827_g_at 17.3 A
Saccharomyces cerevisiae chromosome XIII, complete chromosome sequence. Found forward in NC_001145 between 371593 and 372592 with 100% identity.
2828_at 141.9 A
Saccharomyces cerevisiae chromosome XIII, complete chromosome sequence. Found forward in NC_001145 between 372593 and 373592 with 100% identity.
2829_f_at 31768.3 P
Saccharomyces cerevisiae chromosome XIII, complete chromosome sequence. Found forward in NC_001145 between 373593 and 374592 with 100% identity.
2748_at 119.6 A
Saccharomyces cerevisiae chromosome XIII, complete chromosome sequence. Found forward in NC_001145 between 378593 and 379592 with 100% identity.
2749_s_at 469.2 P
Saccharomyces cerevisiae chromosome XIII, complete chromosome sequence. Found forward in NC_001145 between 379593 and 379699 with 100% identity.
2750_at -89.0 A
Saccharomyces cerevisiae chromosome XIII, complete chromosome sequence. Found forward in NC_001145 between 677692 and 678691 with 100% identity.
2751_at -14.5 A

Saccharomyces cerevisiae chromosome XIII, complete chromosome sequence. Found forward in NC_001145 between 678692 and 679691 with 100% identity.
2752_at 433.4 A
Saccharomyces cerevisiae chromosome XIII, complete chromosome sequence. Found forward in NC_001145 between 679692 and 680691 with 100% identity.
2753_at 92.7 A
Saccharomyces cerevisiae chromosome XIII, complete chromosome sequence. Found forward in NC_001145 between 680692 and 681691 with 100% identity.
2754_at -181.3 A
Saccharomyces cerevisiae chromosome XIII, complete chromosome sequence. Found forward in NC_001145 between 681692 and 682691 with 100% identity.
2755_at 97.8 A
Saccharomyces cerevisiae chromosome XIII, complete chromosome sequence. Found forward in NC_001145 between 682692 and 683691 with 100% identity.
2756_at -1189.5 P
Saccharomyces cerevisiae chromosome XIII, complete chromosome sequence. Found forward in NC_001145 between 683692 and 684691 with 100% identity.
2757_g_at 2524.4 P
Saccharomyces cerevisiae chromosome XIII, complete chromosome sequence. Found forward in NC_001145 between 683692 and 684691 with 100% identity.
2758_s_at 2198.8 P
Saccharomyces cerevisiae chromosome XIII, complete chromosome sequence. Found forward in NC_001145 between 684692 and 685297 with 100% identity.
2759_at -290.6 A
Saccharomyces cerevisiae chromosome XIII, complete chromosome sequence. Found forward in NC_001145 between 704078 and 705077 with 100% identity.
2760_at 448.3 P
Saccharomyces cerevisiae chromosome XIII, complete chromosome sequence. Found forward in NC_001145 between 705078 and 706077 with 100% identity.
2761_at 375.6 A
Saccharomyces cerevisiae chromosome XIII, complete chromosome sequence. Found forward in NC_001145 between 706078 and 707077 with 100% identity.
2762_at 290.7 A
Saccharomyces cerevisiae chromosome XIII, complete chromosome sequence. Found forward in NC_001145 between 707078 and 708077 with 100% identity.
2763_s_at -112.3 A
Saccharomyces cerevisiae chromosome XIII, complete chromosome sequence. Found forward in NC_001145 between 708078 and 709077 with 100% identity.
2764_s_at 227.4 A
Saccharomyces cerevisiae chromosome XIII, complete chromosome sequence. Found forward in NC_001145 between 709078 and 710077 with 100% identity.
2765_s_at -212.5 A
Saccharomyces cerevisiae chromosome XIII, complete chromosome sequence. Found forward in NC_001145 between 710078 and 711077 with 100% identity.
2766_s_at 864.8 P
Saccharomyces cerevisiae chromosome XIII, complete chromosome sequence. Found forward in NC_001145 between 711078 and 711608 with 100% identity.
2767_at 630.6 A
Saccharomyces cerevisiae chromosome XIII, complete chromosome sequence. Found forward in NC_001145 between 726433 and 727432 with 100% identity.
2768_at 182.0 P
Saccharomyces cerevisiae chromosome XIII, complete chromosome sequence. Found forward in NC_001145 between 727433 and 728432 with 100% identity.
2769_at 87.9 P
Saccharomyces cerevisiae chromosome XIII, complete chromosome sequence. Found forward in NC_001145 between 728433 and 729432 with 100% identity.

2770_at 289.8 A
Saccharomyces cerevisiae chromosome XIII, complete chromosome sequence. Found forward in NC_001145 between 729433 and 730432 with 100% identity.
2771_at 670.8 P
Saccharomyces cerevisiae chromosome XIII, complete chromosome sequence. Found forward in NC_001145 between 730433 and 731432 with 100% identity.
2772_at 329.3 A
Saccharomyces cerevisiae chromosome XIII, complete chromosome sequence. Found forward in NC_001145 between 731433 and 731964 with 100% identity.
2773_at 75.2 A
Saccharomyces cerevisiae chromosome XIII, complete chromosome sequence. Found forward in NC_001145 between 827528 and 828527 with 100% identity.
2774_at -88.6 A
Saccharomyces cerevisiae chromosome XIII, complete chromosome sequence. Found forward in NC_001145 between 828528 and 829527 with 100% identity.
2775_at -4034.8 A
Saccharomyces cerevisiae chromosome XIII, complete chromosome sequence. Found forward in NC_001145 between 829528 and 830527 with 100% identity.
2776_at -403.7 A
Saccharomyces cerevisiae chromosome XIII, complete chromosome sequence. Found forward in NC_001145 between 830528 and 831527 with 100% identity.
2777_at -89.0 A
Saccharomyces cerevisiae chromosome XIII, complete chromosome sequence. Found forward in NC_001145 between 831528 and 832527 with 100% identity.
2778_g_at 583.4 P
Saccharomyces cerevisiae chromosome XIII, complete chromosome sequence. Found forward in NC_001145 between 831528 and 832527 with 100% identity.
2779_s_at 67.1 A
Saccharomyces cerevisiae chromosome XIII, complete chromosome sequence. Found forward in NC_001145 between 832528 and 832753 with 100% identity.
2780_at 244.1 A
Saccharomyces cerevisiae chromosome XIII, complete chromosome sequence. Found forward in NC_001145 between 842936 and 843935 with 100% identity.
2781_at 85.6 A
Saccharomyces cerevisiae chromosome XIII, complete chromosome sequence. Found forward in NC_001145 between 843936 and 844935 with 100% identity.
2782_at 384.4 A
Saccharomyces cerevisiae chromosome XIII, complete chromosome sequence. Found forward in NC_001145 between 844936 and 845935 with 100% identity.
2783_g_at 171.4 A
Saccharomyces cerevisiae chromosome XIII, complete chromosome sequence. Found forward in NC_001145 between 844936 and 845935 with 100% identity.
2784_s_at 638.5 A
Saccharomyces cerevisiae chromosome XIII, complete chromosome sequence. Found forward in NC_001145 between 845936 and 846935 with 100% identity.
2785_s_at 517.1 A
Saccharomyces cerevisiae chromosome XIII, complete chromosome sequence. Found forward in NC_001145 between 846936 and 847935 with 100% identity.
2786_s_at 849.1 P
Saccharomyces cerevisiae chromosome XIII, complete chromosome sequence. Found forward in NC_001145 between 847936 and 847986 with 100% identity.
2787_at 318.6 A
Saccharomyces cerevisiae chromosome XIII, complete chromosome sequence. Found forward in NC_001145 between 879563 and 880562 with 100% identity.
2788_at 158.5 A
Saccharomyces cerevisiae chromosome XIII, complete chromosome sequence. Found forward in

NC_001145 between 880563 and 881562 with 100% identity.

2703_g_at -230.0 A

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

2704_s_at 581.5 A

Saccharomyces cerevisiae chromosome XIII, complete chromosome sequence. Found forward in NC_001145 between 881563 and 882562 with 100% identity.

2705_s_at -3.4 A

Saccharomyces cerevisiae chromosome XIII, complete chromosome sequence. Found forward in NC_001145 between 882563 and 883562 with 100% identity.

2706_s_at 14305.2 A

Saccharomyces cerevisiae chromosome XIII, complete chromosome sequence. Found forward in NC_001145 between 883563 and 884562 with 100% identity.

2707_s_at -947.8 A

Saccharomyces cerevisiae chromosome XIII, complete chromosome sequence. Found forward in NC_001145 between 884563 and 885562 with 100% identity.

2708_s_at 196.8 A

Saccharomyces cerevisiae chromosome XIII, complete chromosome sequence. Found forward in NC_001145 between 885563 and 886016 with 100% identity.

2709_s_at 288.0 P

Saccharomyces cerevisiae chromosome XIV, complete chromosome sequence. Found forward in NC_001146 between 871 and 1870 with 100% identity.

2710_s_at 520.4 P

Saccharomyces cerevisiae chromosome XIV, complete chromosome sequence. Found forward in NC_001146 between 1871 and 2870 with 100% identity.

2711_s_at 487.4 P

Saccharomyces cerevisiae chromosome XIV, complete chromosome sequence. Found forward in NC_001146 between 2871 and 3870 with 100% identity.

2712_s_at -590.1 A

Saccharomyces cerevisiae chromosome XIV, complete chromosome sequence. Found forward in NC_001146 between 3871 and 4870 with 100% identity.

2713_s_at 230.5 A

Saccharomyces cerevisiae chromosome XIV, complete chromosome sequence. Found forward in NC_001146 between 4871 and 5870 with 100% identity.

2714_s_at 1660.2 P

Saccharomyces cerevisiae chromosome XIV, complete chromosome sequence. Found forward in NC_001146 between 5871 and 6080 with 100% identity.

2715_at 132.5 A

Saccharomyces cerevisiae chromosome XIV, complete chromosome sequence. Found forward in NC_001146 between 130021 and 131020 with 100% identity.

2716_at 1482.3 M

Saccharomyces cerevisiae chromosome XIV, complete chromosome sequence. Found forward in NC_001146 between 131021 and 132020 with 100% identity.

2717_at -96.0 A

Saccharomyces cerevisiae chromosome XIV, complete chromosome sequence. Found forward in NC_001146 between 132021 and 133020 with 100% identity.

2718_at 607.4 A

Saccharomyces cerevisiae chromosome XIV, complete chromosome sequence. Found forward in NC_001146 between 133021 and 134020 with 100% identity.

2719_at -2123.8 A

Saccharomyces cerevisiae chromosome XIV, complete chromosome sequence. Found forward in NC_001146 between 134021 and 135020 with 100% identity.

2720_at -164.3 A

Saccharomyces cerevisiae chromosome XIV, complete chromosome sequence. Found forward in NC_001146 between 135021 and 135939 with 100% identity.

2721_at -97.0 A

Saccharomyces cerevisiae chromosome XIV, complete chromosome sequence. Found forward in NC_001146 between 147395 and 148394 with 100% identity.

2722_g_at 281.8 A

Saccharomyces cerevisiae chromosome XIV, complete chromosome sequence. Found forward in NC_001146 between 147395 and 148394 with 100% identity.

2723_s_at -410.4 A

Saccharomyces cerevisiae chromosome XIV, complete chromosome sequence. Found forward in NC_001146 between 148395 and 149394 with 100% identity.

2724_s_at -103.1 A

Saccharomyces cerevisiae chromosome XIV, complete chromosome sequence. Found forward in NC_001146 between 149395 and 150394 with 100% identity.

2725_s_at 2.2 A

Saccharomyces cerevisiae chromosome XIV, complete chromosome sequence. Found forward in NC_001146 between 150395 and 151394 with 100% identity.

2726_s_at -89.8 A

Saccharomyces cerevisiae chromosome XIV, complete chromosome sequence. Found forward in NC_001146 between 151395 and 152394 with 100% identity.

2727_s_at -23.4 A

Saccharomyces cerevisiae chromosome XIV, complete chromosome sequence. Found forward in NC_001146 between 152395 and 153394 with 100% identity.

2728_s_at 615.2 P

Saccharomyces cerevisiae chromosome XIV, complete chromosome sequence. Found forward in NC_001146 between 153395 and 154379 with 100% identity.

2729_at 187.8 A

Saccharomyces cerevisiae chromosome XIV, complete chromosome sequence. Found forward in NC_001146 between 161130 and 162129 with 100% identity.

2730_at -67.6 A

Saccharomyces cerevisiae chromosome XIV, complete chromosome sequence. Found forward in NC_001146 between 162130 and 163129 with 100% identity.

2731_at 595.2 A

Saccharomyces cerevisiae chromosome XIV, complete chromosome sequence. Found forward in NC_001146 between 163130 and 164129 with 100% identity.

2732_at -62.1 A

Saccharomyces cerevisiae chromosome XIV, complete chromosome sequence. Found forward in NC_001146 between 164130 and 165129 with 100% identity.

2733_g_at 140.1 M

Saccharomyces cerevisiae chromosome XIV, complete chromosome sequence. Found forward in NC_001146 between 164130 and 165129 with 100% identity.

2734_s_at -192.0 A

Saccharomyces cerevisiae chromosome XIV, complete chromosome sequence. Found forward in NC_001146 between 165130 and 166129 with 100% identity.

2735_s_at 461.6 A

Saccharomyces cerevisiae chromosome XIV, complete chromosome sequence. Found forward in NC_001146 between 166130 and 166596 with 100% identity.

2736_at 230.1 A

Saccharomyces cerevisiae chromosome XIV, complete chromosome sequence. Found forward in NC_001146 between 173087 and 174086 with 100% identity.

2737_at 280.1 A

Saccharomyces cerevisiae chromosome XIV, complete chromosome sequence. Found forward in NC_001146 between 174087 and 175086 with 100% identity.

2738_at -16.8 A

Saccharomyces cerevisiae chromosome XIV, complete chromosome sequence. Found forward in NC_001146 between 175087 and 176086 with 100% identity.

2739_g_at -14.2 A

Saccharomyces cerevisiae chromosome XIV, complete chromosome sequence. Found forward in NC_001146 between 175087 and 176086 with 100% identity.

2740_s_at 205.2 A
Saccharomyces cerevisiae chromosome XIV, complete chromosome sequence. Found forward in NC_001146 between 176087 and 177086 with 100% identity.
2741_s_at 84.4 A
Saccharomyces cerevisiae chromosome XIV, complete chromosome sequence. Found forward in NC_001146 between 177087 and 178086 with 100% identity.
2742_s_at 739.1 A
Saccharomyces cerevisiae chromosome XIV, complete chromosome sequence. Found forward in NC_001146 between 178087 and 178847 with 100% identity.
2743_at 145.9 A
Saccharomyces cerevisiae chromosome XIV, complete chromosome sequence. Found forward in NC_001146 between 309454 and 310453 with 100% identity.
2744_at 79.9 A
Saccharomyces cerevisiae chromosome XIV, complete chromosome sequence. Found forward in NC_001146 between 310454 and 311453 with 100% identity.
2745_g_at 546.1 P
Saccharomyces cerevisiae chromosome XIV, complete chromosome sequence. Found forward in NC_001146 between 310454 and 311453 with 100% identity.
2660_s_at -266.6 A
Saccharomyces cerevisiae chromosome XIV, complete chromosome sequence. Found forward in NC_001146 between 311454 and 312453 with 100% identity.
2661_s_at 117.0 A
Saccharomyces cerevisiae chromosome XIV, complete chromosome sequence. Found forward in NC_001146 between 312454 and 313453 with 100% identity.
2662_s_at 75.6 A
Saccharomyces cerevisiae chromosome XIV, complete chromosome sequence. Found forward in NC_001146 between 313454 and 314453 with 100% identity.
2663_s_at 123.4 A
Saccharomyces cerevisiae chromosome XIV, complete chromosome sequence. Found forward in NC_001146 between 314454 and 315379 with 100% identity.
2664_at 522.1 A
Saccharomyces cerevisiae chromosome XIV, complete chromosome sequence. Found forward in NC_001146 between 524084 and 525083 with 100% identity.
2665_at 382.6 P
Saccharomyces cerevisiae chromosome XIV, complete chromosome sequence. Found forward in NC_001146 between 525084 and 526083 with 100% identity.
2666_s_at -12191.5 A
Saccharomyces cerevisiae chromosome XIV, complete chromosome sequence. Found forward in NC_001146 between 526084 and 527083 with 100% identity.
2667_s_at 286.4 A
Saccharomyces cerevisiae chromosome XIV, complete chromosome sequence. Found forward in NC_001146 between 527084 and 528083 with 100% identity.
2668_s_at 488.4 P
Saccharomyces cerevisiae chromosome XIV, complete chromosome sequence. Found forward in NC_001146 between 528084 and 529079 with 100% identity.
2669_at 3411.4 P
Saccharomyces cerevisiae chromosome XIV, complete chromosome sequence. Found forward in NC_001146 between 655170 and 656169 with 100% identity.
2670_at 539.2 P
Saccharomyces cerevisiae chromosome XIV, complete chromosome sequence. Found forward in NC_001146 between 656170 and 657169 with 100% identity.
2671_at -55.0 A
Saccharomyces cerevisiae chromosome XIV, complete chromosome sequence. Found forward in NC_001146 between 657170 and 658169 with 100% identity.
2672_at 148.5 A
Saccharomyces cerevisiae chromosome XIV, complete chromosome sequence. Found forward in

NC_001146 between 658170 and 659169 with 100% identity.
2673_at -435.8 A
Saccharomyces cerevisiae chromosome XIV, complete chromosome sequence. Found forward in NC_001146 between 659170 and 660169 with 100% identity.
2674_at -1405.1 A
Saccharomyces cerevisiae chromosome XIV, complete chromosome sequence. Found forward in NC_001146 between 660170 and 661169 with 100% identity.
2675_at 200.1 A
Saccharomyces cerevisiae chromosome XIV, complete chromosome sequence. Found forward in NC_001146 between 661170 and 661997 with 100% identity.
2676_at 433.4 A
Saccharomyces cerevisiae chromosome XIV, complete chromosome sequence. Found forward in NC_001146 between 681191 and 682190 with 100% identity.
2677_at 52.1 A
Saccharomyces cerevisiae chromosome XIV, complete chromosome sequence. Found forward in NC_001146 between 682191 and 683190 with 100% identity.
2678_at -493.0 A
Saccharomyces cerevisiae chromosome XIV, complete chromosome sequence. Found forward in NC_001146 between 683191 and 684190 with 100% identity.
2679_at 351.6 A
Saccharomyces cerevisiae chromosome XIV, complete chromosome sequence. Found forward in NC_001146 between 684191 and 685190 with 100% identity.
2680_at -102.5 A
Saccharomyces cerevisiae chromosome XIV, complete chromosome sequence. Found forward in NC_001146 between 685191 and 686190 with 100% identity.
2681_g_at 238.4 A
Saccharomyces cerevisiae chromosome XIV, complete chromosome sequence. Found forward in NC_001146 between 685191 and 686190 with 100% identity.
2682_s_at 12.3 A
Saccharomyces cerevisiae chromosome XIV, complete chromosome sequence. Found forward in NC_001146 between 686191 and 686613 with 100% identity.
2683_at -154.2 A
Saccharomyces cerevisiae chromosome XIV, complete chromosome sequence. Found forward in NC_001146 between 761618 and 762617 with 100% identity.
2684_at -238.1 A
Saccharomyces cerevisiae chromosome XIV, complete chromosome sequence. Found forward in NC_001146 between 762618 and 763617 with 100% identity.
2685_at 1434.8 P
Saccharomyces cerevisiae chromosome XIV, complete chromosome sequence. Found forward in NC_001146 between 763618 and 764617 with 100% identity.
2686_at 382.2 A
Saccharomyces cerevisiae chromosome XIV, complete chromosome sequence. Found forward in NC_001146 between 764618 and 765617 with 100% identity.
2687_g_at -495.7 A
Saccharomyces cerevisiae chromosome XIV, complete chromosome sequence. Found forward in NC_001146 between 764618 and 765617 with 100% identity.
2688_s_at 235.3 A
Saccharomyces cerevisiae chromosome XIV, complete chromosome sequence. Found forward in NC_001146 between 765618 and 766617 with 100% identity.
2689_s_at -248.1 A
Saccharomyces cerevisiae chromosome XIV, complete chromosome sequence. Found forward in NC_001146 between 766618 and 767617 with 100% identity.
2690_s_at 40.1 A
Saccharomyces cerevisiae chromosome XIV, complete chromosome sequence. Found forward in NC_001146 between 767618 and 768617 with 100% identity.
2691_s_at -368.4 A

Saccharomyces cerevisiae chromosome XIV, complete chromosome sequence. Found forward in NC_001146 between 768618 and 768871 with 100% identity.
2692_at -19.4 A
Saccharomyces cerevisiae chromosome XV, complete chromosome sequence. Found forward in NC_001147 between 2078 and 3077 with 100% identity.
2693_at -163.2 A
Saccharomyces cerevisiae chromosome XV, complete chromosome sequence. Found forward in NC_001147 between 3078 and 4077 with 100% identity.
2694_at -5879.5 A
Saccharomyces cerevisiae chromosome XV, complete chromosome sequence. Found forward in NC_001147 between 4078 and 5077 with 100% identity.
2695_at -254.4 A
Saccharomyces cerevisiae chromosome XV, complete chromosome sequence. Found forward in NC_001147 between 5078 and 6077 with 100% identity.
2696_at 309.7 A
Saccharomyces cerevisiae chromosome XV, complete chromosome sequence. Found forward in NC_001147 between 6078 and 7077 with 100% identity.
2697_g_at 158.4 A
Saccharomyces cerevisiae chromosome XV, complete chromosome sequence. Found forward in NC_001147 between 6078 and 7077 with 100% identity.
2698_s_at -86.2 A
Saccharomyces cerevisiae chromosome XV, complete chromosome sequence. Found forward in NC_001147 between 7078 and 7615 with 100% identity.
2699_at 316.2 A
Saccharomyces cerevisiae chromosome XV, complete chromosome sequence. Found forward in NC_001147 between 169973 and 170972 with 100% identity.
2700_at 2.3 A
Saccharomyces cerevisiae chromosome XV, complete chromosome sequence. Found forward in NC_001147 between 170973 and 171972 with 100% identity.
2701_g_at 192.3 A
Saccharomyces cerevisiae chromosome XV, complete chromosome sequence. Found forward in NC_001147 between 170973 and 171972 with 100% identity.
2702_s_at -1804.6 A
Saccharomyces cerevisiae chromosome XV, complete chromosome sequence. Found forward in NC_001147 between 171973 and 172972 with 100% identity.
2618_s_at 15.6 A
Saccharomyces cerevisiae chromosome XV, complete chromosome sequence. Found forward in NC_001147 between 172973 and 173972 with 100% identity.
2619_s_at -496.9 A
Saccharomyces cerevisiae chromosome XV, complete chromosome sequence. Found forward in NC_001147 between 173973 and 174972 with 100% identity.
2620_s_at -102.7 A
Saccharomyces cerevisiae chromosome XV, complete chromosome sequence. Found forward in NC_001147 between 174973 and 175972 with 100% identity.
2621_s_at -126.7 A
Saccharomyces cerevisiae chromosome XV, complete chromosome sequence. Found forward in NC_001147 between 175973 and 176972 with 100% identity.
2622_s_at 554.3 A
Saccharomyces cerevisiae chromosome XV, complete chromosome sequence. Found forward in NC_001147 between 176973 and 177972 with 100% identity.
2623_s_at -420.6 A
Saccharomyces cerevisiae chromosome XV, complete chromosome sequence. Found forward in NC_001147 between 177973 and 178972 with 100% identity.
2624_s_at 240.8 A
Saccharomyces cerevisiae chromosome XV, complete chromosome sequence. Found forward in NC_001147 between 178973 and 179808 with 100% identity.

2625_at 128.8 A
Saccharomyces cerevisiae chromosome XV, complete chromosome sequence. Found forward in NC_001147 between 346694 and 347693 with 100% identity.
2626_at 1618.7 A
Saccharomyces cerevisiae chromosome XV, complete chromosome sequence. Found forward in NC_001147 between 347694 and 348693 with 100% identity.
2627_at 228.0 A
Saccharomyces cerevisiae chromosome XV, complete chromosome sequence. Found forward in NC_001147 between 348694 and 349693 with 100% identity.
2628_s_at 143.8 A
Saccharomyces cerevisiae chromosome XV, complete chromosome sequence. Found forward in NC_001147 between 349694 and 350693 with 100% identity.
2629_s_at 2748.6 P
Saccharomyces cerevisiae chromosome XV, complete chromosome sequence. Found forward in NC_001147 between 350694 and 351693 with 100% identity.
2630_s_at 436.1 P
Saccharomyces cerevisiae chromosome XV, complete chromosome sequence. Found forward in NC_001147 between 351694 and 352693 with 100% identity.
2631_s_at 624.6 P
Saccharomyces cerevisiae chromosome XV, complete chromosome sequence. Found forward in NC_001147 between 352694 and 353362 with 100% identity.
2632_at 332.0 A
Saccharomyces cerevisiae chromosome XV, complete chromosome sequence. Found forward in NC_001147 between 540261 and 541260 with 100% identity.
2633_at 100.8 A
Saccharomyces cerevisiae chromosome XV, complete chromosome sequence. Found forward in NC_001147 between 541261 and 542260 with 100% identity.
2634_at 5711.8 P
Saccharomyces cerevisiae chromosome XV, complete chromosome sequence. Found forward in NC_001147 between 542261 and 543260 with 100% identity.
2635_at 502.1 A
Saccharomyces cerevisiae chromosome XV, complete chromosome sequence. Found forward in NC_001147 between 543261 and 544260 with 100% identity.
2636_at -72.9 A
Saccharomyces cerevisiae chromosome XV, complete chromosome sequence. Found forward in NC_001147 between 544261 and 545260 with 100% identity.
2637_g_at 971.1 P
Saccharomyces cerevisiae chromosome XV, complete chromosome sequence. Found forward in NC_001147 between 544261 and 545260 with 100% identity.
2638_s_at 1933.2 P
Saccharomyces cerevisiae chromosome XV, complete chromosome sequence. Found forward in NC_001147 between 545261 and 545831 with 100% identity.
2639_at 308.2 A
Saccharomyces cerevisiae chromosome XV, complete chromosome sequence. Found forward in NC_001147 between 618016 and 619015 with 100% identity.
2640_at 221.7 A
Saccharomyces cerevisiae chromosome XV, complete chromosome sequence. Found forward in NC_001147 between 619016 and 620015 with 100% identity.
2641_g_at 1352.1 M
Saccharomyces cerevisiae chromosome XV, complete chromosome sequence. Found forward in NC_001147 between 619016 and 620015 with 100% identity.
2642_s_at 1423.8 P
Saccharomyces cerevisiae chromosome XV, complete chromosome sequence. Found forward in NC_001147 between 620016 and 621015 with 100% identity.
2643_s_at 4508.9 P
Saccharomyces cerevisiae chromosome XV, complete chromosome sequence. Found forward in

NC_001147 between 621016 and 622015 with 100% identity.
2644_s_at 6419.0 P
Saccharomyces cerevisiae chromosome XV, complete chromosome sequence. Found forward in NC_001147 between 622016 and 623015 with 100% identity.
2645_s_at 50753.5 P
Saccharomyces cerevisiae chromosome XV, complete chromosome sequence. Found forward in NC_001147 between 623016 and 623873 with 100% identity.
2646_at 2479.7 A
Saccharomyces cerevisiae chromosome XV, complete chromosome sequence. Found forward in NC_001147 between 730506 and 731505 with 100% identity.
2647_at 30.1 A
Saccharomyces cerevisiae chromosome XV, complete chromosome sequence. Found forward in NC_001147 between 731506 and 732505 with 100% identity.
2648_at 1099.1 A
Saccharomyces cerevisiae chromosome XV, complete chromosome sequence. Found forward in NC_001147 between 732506 and 733505 with 100% identity.
2649_at -1868.6 A
Saccharomyces cerevisiae chromosome XV, complete chromosome sequence. Found forward in NC_001147 between 733506 and 734505 with 100% identity.
2650_g_at 130.5 A
Saccharomyces cerevisiae chromosome XV, complete chromosome sequence. Found forward in NC_001147 between 733506 and 734505 with 100% identity.
2651_s_at 375.0 P
Saccharomyces cerevisiae chromosome XV, complete chromosome sequence. Found forward in NC_001147 between 734506 and 735505 with 100% identity.
2652_s_at 698.1 P
Saccharomyces cerevisiae chromosome XV, complete chromosome sequence. Found forward in NC_001147 between 735506 and 735675 with 100% identity.
2653_at 652.6 A
Saccharomyces cerevisiae chromosome XV, complete chromosome sequence. Found forward in NC_001147 between 855642 and 856641 with 100% identity.
2654_at 118.5 A
Saccharomyces cerevisiae chromosome XV, complete chromosome sequence. Found forward in NC_001147 between 856642 and 857641 with 100% identity.
2655_at 7879.6 P
Saccharomyces cerevisiae chromosome XV, complete chromosome sequence. Found forward in NC_001147 between 857642 and 858641 with 100% identity.
2656_at -390.5 A
Saccharomyces cerevisiae chromosome XV, complete chromosome sequence. Found forward in NC_001147 between 858642 and 859641 with 100% identity.
2657_at -76.1 A
Saccharomyces cerevisiae chromosome XV, complete chromosome sequence. Found forward in NC_001147 between 859642 and 860641 with 100% identity.
2658_at -29.2 A
Saccharomyces cerevisiae chromosome XV, complete chromosome sequence. Found forward in NC_001147 between 860642 and 861641 with 100% identity.
2659_g_at 9.7 A
Saccharomyces cerevisiae chromosome XV, complete chromosome sequence. Found forward in NC_001147 between 860642 and 861641 with 100% identity.
2575_s_at 357.5 A
Saccharomyces cerevisiae chromosome XV, complete chromosome sequence. Found forward in NC_001147 between 861642 and 862641 with 100% identity.
2576_s_at 235.8 A
Saccharomyces cerevisiae chromosome XV, complete chromosome sequence. Found forward in NC_001147 between 862642 and 863641 with 100% identity.
2577_s_at -15.6 A

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

2578_s_at 336.3 A

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

2579_at 921.3 P

Saccharomyces cerevisiae chromosome XV, complete chromosome sequence. Found forward in NC_001147 between 946724 and 947723 with 100% identity.

2580_at 9050.3 P

Saccharomyces cerevisiae chromosome XV, complete chromosome sequence. Found forward in NC_001147 between 947724 and 948723 with 100% identity.

2581_at 303.3 A

Saccharomyces cerevisiae chromosome XV, complete chromosome sequence. Found forward in NC_001147 between 948724 and 949723 with 100% identity.

2582_at -454.4 A

Saccharomyces cerevisiae chromosome XV, complete chromosome sequence. Found forward in NC_001147 between 949724 and 950723 with 100% identity.

2583_g_at -154.8 A

Saccharomyces cerevisiae chromosome XV, complete chromosome sequence. Found forward in NC_001147 between 949724 and 950723 with 100% identity.

2584_s_at 134.5 A

Saccharomyces cerevisiae chromosome XV, complete chromosome sequence. Found forward in NC_001147 between 950724 and 951723 with 100% identity.

2585_s_at 529.8 P

Saccharomyces cerevisiae chromosome XV, complete chromosome sequence. Found forward in NC_001147 between 951724 and 952723 with 100% identity.

2586_s_at 344.2 A

Saccharomyces cerevisiae chromosome XV, complete chromosome sequence. Found forward in NC_001147 between 952724 and 953361 with 100% identity.

2587_at 333.7 A

Saccharomyces cerevisiae chromosome XV, complete chromosome sequence. Found forward in NC_001147 between 959693 and 960692 with 100% identity.

2588_at 98.7 A

Saccharomyces cerevisiae chromosome XV, complete chromosome sequence. Found forward in NC_001147 between 960693 and 961692 with 100% identity.

2589_g_at 195.8 A

Saccharomyces cerevisiae chromosome XV, complete chromosome sequence. Found forward in NC_001147 between 960693 and 961692 with 100% identity.

2590_s_at 957.3 P

Saccharomyces cerevisiae chromosome XV, complete chromosome sequence. Found forward in NC_001147 between 961693 and 962692 with 100% identity.

2591_s_at 662.8 A

Saccharomyces cerevisiae chromosome XV, complete chromosome sequence. Found forward in NC_001147 between 962693 and 963692 with 100% identity.

2592_s_at 256.5 P

Saccharomyces cerevisiae chromosome XV, complete chromosome sequence. Found forward in NC_001147 between 963693 and 964692 with 100% identity.

2593_s_at 3557.0 P

Saccharomyces cerevisiae chromosome XV, complete chromosome sequence. Found forward in NC_001147 between 964693 and 965472 with 100% identity.

2594_at 145.7 A

Saccharomyces cerevisiae chromosome XVI, complete chromosome sequence. Found forward in NC_001148 between 19079 and 20078 with 100% identity.

2595_at -30.1 A

Saccharomyces cerevisiae chromosome XVI, complete chromosome sequence. Found forward in NC_001148 between 20079 and 21078 with 100% identity.

2596_at -1217.7 A
Saccharomyces cerevisiae chromosome XVI, complete chromosome sequence. Found forward in NC_001148 between 21079 and 22078 with 100% identity.
2597_at -377.3 A
Saccharomyces cerevisiae chromosome XVI, complete chromosome sequence. Found forward in NC_001148 between 22079 and 23078 with 100% identity.
2598_g_at -3.8 A
Saccharomyces cerevisiae chromosome XVI, complete chromosome sequence. Found forward in NC_001148 between 22079 and 23078 with 100% identity.
2599_s_at 491.8 P
Saccharomyces cerevisiae chromosome XVI, complete chromosome sequence. Found forward in NC_001148 between 23079 and 24078 with 100% identity.
2600_s_at -15.7 A
Saccharomyces cerevisiae chromosome XVI, complete chromosome sequence. Found forward in NC_001148 between 24079 and 24201 with 100% identity.
2601_at -429.9 A
Saccharomyces cerevisiae chromosome XVI, complete chromosome sequence. Found forward in NC_001148 between 108147 and 109146 with 100% identity.
2602_g_at -1676.9 A
Saccharomyces cerevisiae chromosome XVI, complete chromosome sequence. Found forward in NC_001148 between 108147 and 109146 with 100% identity.
2603_s_at 195.9 A
Saccharomyces cerevisiae chromosome XVI, complete chromosome sequence. Found forward in NC_001148 between 109147 and 110146 with 100% identity.
2604_s_at 1373.1 P
Saccharomyces cerevisiae chromosome XVI, complete chromosome sequence. Found forward in NC_001148 between 110147 and 111146 with 100% identity.
2605_s_at 1296.6 P
Saccharomyces cerevisiae chromosome XVI, complete chromosome sequence. Found forward in NC_001148 between 111147 and 112146 with 100% identity.
2606_s_at 5009.0 P
Saccharomyces cerevisiae chromosome XVI, complete chromosome sequence. Found forward in NC_001148 between 112147 and 113146 with 100% identity.
2607_s_at 22618.5 P
Saccharomyces cerevisiae chromosome XVI, complete chromosome sequence. Found forward in NC_001148 between 113147 and 113815 with 100% identity.
2608_at 609.2 A
Saccharomyces cerevisiae chromosome XVI, complete chromosome sequence. Found forward in NC_001148 between 140119 and 141118 with 100% identity.
2609_at 1712.8 A
Saccharomyces cerevisiae chromosome XVI, complete chromosome sequence. Found forward in NC_001148 between 141119 and 142118 with 100% identity.
2610_at 512.2 A
Saccharomyces cerevisiae chromosome XVI, complete chromosome sequence. Found forward in NC_001148 between 142119 and 143118 with 100% identity.
2611_at -2165.7 A
Saccharomyces cerevisiae chromosome XVI, complete chromosome sequence. Found forward in NC_001148 between 143119 and 144118 with 100% identity.
2612_g_at 250.3 A
Saccharomyces cerevisiae chromosome XVI, complete chromosome sequence. Found forward in NC_001148 between 143119 and 144118 with 100% identity.
2613_s_at 143.4 A
Saccharomyces cerevisiae chromosome XVI, complete chromosome sequence. Found forward in NC_001148 between 144119 and 145118 with 100% identity.
2614_s_at 187.3 A
Saccharomyces cerevisiae chromosome XVI, complete chromosome sequence. Found forward in

NC_001148 between 145119 and 146118 with 100% identity.
2615_s_at 372.9 A
Saccharomyces cerevisiae chromosome XVI, complete chromosome sequence. Found forward in NC_001148 between 146119 and 146628 with 100% identity.
2616_at -73.7 A
Saccharomyces cerevisiae chromosome XVI, complete chromosome sequence. Found forward in NC_001148 between 385268 and 386267 with 100% identity.
2617_at -446.9 A
Saccharomyces cerevisiae chromosome XVI, complete chromosome sequence. Found forward in NC_001148 between 386268 and 387267 with 100% identity.
2532_g_at -141.7 A
Saccharomyces cerevisiae chromosome XVI, complete chromosome sequence. Found forward in NC_001148 between 386268 and 387267 with 100% identity.
2533_s_at 7.9 A
Saccharomyces cerevisiae chromosome XVI, complete chromosome sequence. Found forward in NC_001148 between 387268 and 388267 with 100% identity.
2534_s_at -74.4 A
Saccharomyces cerevisiae chromosome XVI, complete chromosome sequence. Found forward in NC_001148 between 388268 and 389267 with 100% identity.
2535_s_at 106.0 A
Saccharomyces cerevisiae chromosome XVI, complete chromosome sequence. Found forward in NC_001148 between 389268 and 390267 with 100% identity.
2536_s_at 234.0 A
Saccharomyces cerevisiae chromosome XVI, complete chromosome sequence. Found forward in NC_001148 between 390268 and 391267 with 100% identity.
2537_s_at 80.4 A
Saccharomyces cerevisiae chromosome XVI, complete chromosome sequence. Found forward in NC_001148 between 391268 and 392267 with 100% identity.
2538_s_at 695.4 P
Saccharomyces cerevisiae chromosome XVI, complete chromosome sequence. Found forward in NC_001148 between 392268 and 393149 with 100% identity.
2539_at 296.3 A
Saccharomyces cerevisiae chromosome XVI, complete chromosome sequence. Found forward in NC_001148 between 398975 and 399974 with 100% identity.
2540_at 505.7 P
Saccharomyces cerevisiae chromosome XVI, complete chromosome sequence. Found forward in NC_001148 between 399975 and 400974 with 100% identity.
2541_at -533.5 A
Saccharomyces cerevisiae chromosome XVI, complete chromosome sequence. Found forward in NC_001148 between 400975 and 401974 with 100% identity.
2542_at 37.7 A
Saccharomyces cerevisiae chromosome XVI, complete chromosome sequence. Found forward in NC_001148 between 401975 and 402974 with 100% identity.
2543_at -1095.6 A
Saccharomyces cerevisiae chromosome XVI, complete chromosome sequence. Found forward in NC_001148 between 402975 and 403974 with 100% identity.
2544_at -119.0 A
Saccharomyces cerevisiae chromosome XVI, complete chromosome sequence. Found forward in NC_001148 between 403975 and 404451 with 100% identity.
2545_at -32.5 A
Saccharomyces cerevisiae chromosome XVI, complete chromosome sequence. Found forward in NC_001148 between 435759 and 436758 with 100% identity.
2546_at 190.1 A
Saccharomyces cerevisiae chromosome XVI, complete chromosome sequence. Found forward in NC_001148 between 436759 and 437758 with 100% identity.
2547_at -39.0 A

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

2548_at -40.3 A

Saccharomyces cerevisiae chromosome XVI, complete chromosome sequence. Found forward in NC_001148 between 438759 and 439758 with 100% identity.

2549_at -142.0 A

Saccharomyces cerevisiae chromosome XVI, complete chromosome sequence. Found forward in NC_001148 between 439759 and 440758 with 100% identity.

2550_at -251.2 A

Saccharomyces cerevisiae chromosome XVI, complete chromosome sequence. Found forward in NC_001148 between 440759 and 441758 with 100% identity.

2551_at 1009.6 P

Saccharomyces cerevisiae chromosome XVI, complete chromosome sequence. Found forward in NC_001148 between 441759 and 442758 with 100% identity.

2552_at -234.8 A

Saccharomyces cerevisiae chromosome XVI, complete chromosome sequence. Found forward in NC_001148 between 442759 and 443758 with 100% identity.

2553_at -82.5 A

Saccharomyces cerevisiae chromosome XVI, complete chromosome sequence. Found forward in NC_001148 between 443759 and 444574 with 100% identity.

2554_at 478.8 A

Saccharomyces cerevisiae chromosome XVI, complete chromosome sequence. Found forward in NC_001148 between 446337 and 447336 with 100% identity.

2555_at 2168.3 A

Saccharomyces cerevisiae chromosome XVI, complete chromosome sequence. Found forward in NC_001148 between 447337 and 448336 with 100% identity.

2556_at -107.4 A

Saccharomyces cerevisiae chromosome XVI, complete chromosome sequence. Found forward in NC_001148 between 448337 and 449336 with 100% identity.

2557_at 113.2 A

Saccharomyces cerevisiae chromosome XVI, complete chromosome sequence. Found forward in NC_001148 between 449337 and 450336 with 100% identity.

2558_at 200.6 A

Saccharomyces cerevisiae chromosome XVI, complete chromosome sequence. Found forward in NC_001148 between 450337 and 451336 with 100% identity.

2559_at 285.9 A

Saccharomyces cerevisiae chromosome XVI, complete chromosome sequence. Found forward in NC_001148 between 451337 and 451904 with 100% identity.

2560_at -1623.4 A

Saccharomyces cerevisiae chromosome XVI, complete chromosome sequence. Found forward in NC_001148 between 519230 and 520229 with 100% identity.

2561_at 237.1 A

Saccharomyces cerevisiae chromosome XVI, complete chromosome sequence. Found forward in NC_001148 between 520230 and 521229 with 100% identity.

2562_g_at -306.7 A

Saccharomyces cerevisiae chromosome XVI, complete chromosome sequence. Found forward in NC_001148 between 520230 and 521229 with 100% identity.

2563_s_at 1166.6 A

Saccharomyces cerevisiae chromosome XVI, complete chromosome sequence. Found forward in NC_001148 between 521230 and 522229 with 100% identity.

2564_s_at 3436.1 A

Saccharomyces cerevisiae chromosome XVI, complete chromosome sequence. Found forward in NC_001148 between 522230 and 523229 with 100% identity.

2565_s_at 946.4 A

Saccharomyces cerevisiae chromosome XVI, complete chromosome sequence. Found forward in NC_001148 between 523230 and 524229 with 100% identity.

2566_s_at -264.8 A
Saccharomyces cerevisiae chromosome XVI, complete chromosome sequence. Found forward in NC_001148 between 524230 and 524453 with 100% identity.
2567_at 438.8 A
Saccharomyces cerevisiae chromosome XVI, complete chromosome sequence. Found forward in NC_001148 between 536315 and 537314 with 100% identity.
2568_at 218.4 A
Saccharomyces cerevisiae chromosome XVI, complete chromosome sequence. Found forward in NC_001148 between 537315 and 538314 with 100% identity.
2569_at -82.7 A
Saccharomyces cerevisiae chromosome XVI, complete chromosome sequence. Found forward in NC_001148 between 538315 and 539314 with 100% identity.
2570_at 62.4 A
Saccharomyces cerevisiae chromosome XVI, complete chromosome sequence. Found forward in NC_001148 between 539315 and 540314 with 100% identity.
2571_s_at -82.2 A
Saccharomyces cerevisiae chromosome XVI, complete chromosome sequence. Found forward in NC_001148 between 540315 and 541314 with 100% identity.
2572_s_at 272.9 A
Saccharomyces cerevisiae chromosome XVI, complete chromosome sequence. Found forward in NC_001148 between 541315 and 541465 with 100% identity.
2573_at 239.6 A
Saccharomyces cerevisiae chromosome XVI, complete chromosome sequence. Found forward in NC_001148 between 542577 and 543576 with 100% identity.
2574_at 241.3 A
Saccharomyces cerevisiae chromosome XVI, complete chromosome sequence. Found forward in NC_001148 between 543577 and 544576 with 100% identity.
2489_at -126.2 A
Saccharomyces cerevisiae chromosome XVI, complete chromosome sequence. Found forward in NC_001148 between 544577 and 545576 with 100% identity.
2490_s_at -401.8 A
Saccharomyces cerevisiae chromosome XVI, complete chromosome sequence. Found forward in NC_001148 between 545577 and 546576 with 100% identity.
2491_s_at 531.6 A
Saccharomyces cerevisiae chromosome XVI, complete chromosome sequence. Found forward in NC_001148 between 546577 and 547576 with 100% identity.
2492_f_at 418.8 P
Saccharomyces cerevisiae chromosome XVI, complete chromosome sequence. Found forward in NC_001148 between 547577 and 547638 with 100% identity.
2493_at -638.8 A
Saccharomyces cerevisiae chromosome XVI, complete chromosome sequence. Found forward in NC_001148 between 624964 and 625963 with 100% identity.
2494_at 367.5 A
Saccharomyces cerevisiae chromosome XVI, complete chromosome sequence. Found forward in NC_001148 between 625964 and 626963 with 100% identity.
2495_at -187.6 A
Saccharomyces cerevisiae chromosome XVI, complete chromosome sequence. Found forward in NC_001148 between 626964 and 627963 with 100% identity.
2496_g_at -539.0 A
Saccharomyces cerevisiae chromosome XVI, complete chromosome sequence. Found forward in NC_001148 between 626964 and 627963 with 100% identity.
2497_s_at 440.4 A
Saccharomyces cerevisiae chromosome XVI, complete chromosome sequence. Found forward in NC_001148 between 627964 and 628963 with 100% identity.
2498_s_at 315.5 A
Saccharomyces cerevisiae chromosome XVI, complete chromosome sequence. Found forward in

NC_001148 between 628964 and 629963 with 100% identity.
2499_s_at -73.9 A
Saccharomyces cerevisiae chromosome XVI, complete chromosome sequence. Found forward in NC_001148 between 629964 and 630740 with 100% identity.
2500_at 649.6 P
Saccharomyces cerevisiae chromosome XVI, complete chromosome sequence. Found forward in NC_001148 between 759478 and 760477 with 100% identity.
2501_g_at 393.4 A
Saccharomyces cerevisiae chromosome XVI, complete chromosome sequence. Found forward in NC_001148 between 759478 and 760477 with 100% identity.
2502_s_at -69.0 A
Saccharomyces cerevisiae chromosome XVI, complete chromosome sequence. Found forward in NC_001148 between 760478 and 761477 with 100% identity.
2503_s_at -23.1 A
Saccharomyces cerevisiae chromosome XVI, complete chromosome sequence. Found forward in NC_001148 between 761478 and 762477 with 100% identity.
2504_s_at -243.8 A
Saccharomyces cerevisiae chromosome XVI, complete chromosome sequence. Found forward in NC_001148 between 762478 and 763477 with 100% identity.
2505_s_at 107.2 A
Saccharomyces cerevisiae chromosome XVI, complete chromosome sequence. Found forward in NC_001148 between 763478 and 764477 with 100% identity.
2506_s_at 691.9 P
Saccharomyces cerevisiae chromosome XVI, complete chromosome sequence. Found forward in NC_001148 between 764478 and 765477 with 100% identity.
2507_s_at -229.7 A
Saccharomyces cerevisiae chromosome XVI, complete chromosome sequence. Found forward in NC_001148 between 765478 and 766477 with 100% identity.
2508_s_at 779.0 P
Saccharomyces cerevisiae chromosome XVI, complete chromosome sequence. Found forward in NC_001148 between 766478 and 766991 with 100% identity.
2509_at 1908.2 P
Saccharomyces cerevisiae chromosome XVI, complete chromosome sequence. Found forward in NC_001148 between 869140 and 870139 with 100% identity.
2510_at -14.4 A
Saccharomyces cerevisiae chromosome XVI, complete chromosome sequence. Found forward in NC_001148 between 870140 and 871139 with 100% identity.
2511_g_at 185.0 A
Saccharomyces cerevisiae chromosome XVI, complete chromosome sequence. Found forward in NC_001148 between 870140 and 871139 with 100% identity.
2512_s_at 44.8 A
Saccharomyces cerevisiae chromosome XVI, complete chromosome sequence. Found forward in NC_001148 between 871140 and 872139 with 100% identity.
2513_s_at 21.8 A
Saccharomyces cerevisiae chromosome XVI, complete chromosome sequence. Found forward in NC_001148 between 872140 and 873139 with 100% identity.
2514_s_at -40.4 A
Saccharomyces cerevisiae chromosome XVI, complete chromosome sequence. Found forward in NC_001148 between 873140 and 874139 with 100% identity.
2515_s_at 5903.5 A
Saccharomyces cerevisiae chromosome XVI, complete chromosome sequence. Found forward in NC_001148 between 874140 and 874421 with 100% identity.
2516_at -58.0 A
Saccharomyces cerevisiae chromosome II, complete chromosome sequence. Found forward in NC_001134 between 25441 and 26440 with 100% identity.
2517_at 306.1 A

Saccharomyces cerevisiae chromosome II, complete chromosome sequence. Found forward in NC_001134 between 26441 and 27440 with 100% identity.

2518_at 364.3 A

Saccharomyces cerevisiae chromosome II, complete chromosome sequence. Found forward in NC_001134 between 27441 and 28440 with 100% identity.

2519_at -423.4 A

Saccharomyces cerevisiae chromosome II, complete chromosome sequence. Found forward in NC_001134 between 28441 and 29440 with 100% identity.

2520_at -221.6 A

Saccharomyces cerevisiae chromosome II, complete chromosome sequence. Found forward in NC_001134 between 29441 and 30440 with 100% identity.

2521_f_at -683.7 A

Saccharomyces cerevisiae chromosome II, complete chromosome sequence. Found forward in NC_001134 between 35441 and 35606 with 100% identity.

2522_at -62.9 A

Saccharomyces cerevisiae chromosome II, complete chromosome sequence. Found forward in NC_001134 between 51513 and 52512 with 100% identity.

2523_at -24.8 A

Saccharomyces cerevisiae chromosome II, complete chromosome sequence. Found forward in NC_001134 between 52513 and 53512 with 100% identity.

2524_at 174.0 A

Saccharomyces cerevisiae chromosome II, complete chromosome sequence. Found forward in NC_001134 between 53513 and 54512 with 100% identity.

2525_at 994.1 A

Saccharomyces cerevisiae chromosome II, complete chromosome sequence. Found forward in NC_001134 between 54513 and 55512 with 100% identity.

2526_at 54.4 A

Saccharomyces cerevisiae chromosome II, complete chromosome sequence. Found forward in NC_001134 between 55513 and 56512 with 100% identity.

2527_at -266.8 A

Saccharomyces cerevisiae chromosome II, complete chromosome sequence. Found forward in NC_001134 between 56513 and 57512 with 100% identity.

2528_at -447.7 A

Saccharomyces cerevisiae chromosome II, complete chromosome sequence. Found forward in NC_001134 between 57513 and 58512 with 100% identity.

2529_at -740.1 A

Saccharomyces cerevisiae chromosome II, complete chromosome sequence. Found forward in NC_001134 between 58513 and 59512 with 100% identity.

2530_at -1254.8 A

Saccharomyces cerevisiae chromosome II, complete chromosome sequence. Found forward in NC_001134 between 59513 and 59815 with 100% identity.

2531_at -11.3 A

Saccharomyces cerevisiae chromosome II, complete chromosome sequence. Found forward in NC_001134 between 73564 and 74563 with 100% identity.

2446_at 728.7 A

Saccharomyces cerevisiae chromosome II, complete chromosome sequence. Found forward in NC_001134 between 74564 and 75563 with 100% identity.

2447_g_at -661.0 A

Saccharomyces cerevisiae chromosome II, complete chromosome sequence. Found forward in NC_001134 between 74564 and 75563 with 100% identity.

2448_s_at 177.8 A

Saccharomyces cerevisiae chromosome II, complete chromosome sequence. Found forward in NC_001134 between 75564 and 76563 with 100% identity.

2449_s_at 358.0 A

Saccharomyces cerevisiae chromosome II, complete chromosome sequence. Found forward in NC_001134 between 76564 and 77563 with 100% identity.

2450_s_at 31.2 A
Saccharomyces cerevisiae chromosome II, complete chromosome sequence. Found forward in NC_001134 between 77564 and 78563 with 100% identity.
2451_s_at 879.0 P
Saccharomyces cerevisiae chromosome II, complete chromosome sequence. Found forward in NC_001134 between 78564 and 79261 with 100% identity.
2452_at -240.7 A
Saccharomyces cerevisiae chromosome II, complete chromosome sequence. Found forward in NC_001134 between 187307 and 188306 with 100% identity.
2453_at -143.8 A
Saccharomyces cerevisiae chromosome II, complete chromosome sequence. Found forward in NC_001134 between 188307 and 189306 with 100% identity.
2454_at 46.5 A
Saccharomyces cerevisiae chromosome II, complete chromosome sequence. Found forward in NC_001134 between 189307 and 190306 with 100% identity.
2455_at 120.0 A
Saccharomyces cerevisiae chromosome II, complete chromosome sequence. Found forward in NC_001134 between 190307 and 191306 with 100% identity.
2456_at 232.4 A
Saccharomyces cerevisiae chromosome II, complete chromosome sequence. Found forward in NC_001134 between 191307 and 192306 with 100% identity.
2457_at 5.3 A
Saccharomyces cerevisiae chromosome II, complete chromosome sequence. Found forward in NC_001134 between 192307 and 192975 with 100% identity.
2458_g_at 1572.9 P
Saccharomyces cerevisiae chromosome II, complete chromosome sequence. Found forward in NC_001134 between 192307 and 192975 with 100% identity.
2459_at 789.9 P
Saccharomyces cerevisiae chromosome II, complete chromosome sequence. Found forward in NC_001134 between 220363 and 221362 with 100% identity.
2460_at -182.0 A
Saccharomyces cerevisiae chromosome II, complete chromosome sequence. Found forward in NC_001134 between 226363 and 227362 with 100% identity.
2461_at 169.5 A
Saccharomyces cerevisiae chromosome II, complete chromosome sequence. Found forward in NC_001134 between 227363 and 228362 with 100% identity.
2462_g_at 56.3 A
Saccharomyces cerevisiae chromosome II, complete chromosome sequence. Found forward in NC_001134 between 227363 and 228362 with 100% identity.
2463_s_at 190.6 A
Saccharomyces cerevisiae chromosome II, complete chromosome sequence. Found forward in NC_001134 between 228363 and 229362 with 100% identity.
2464_s_at 528.8 A
Saccharomyces cerevisiae chromosome II, complete chromosome sequence. Found forward in NC_001134 between 229363 and 230362 with 100% identity.
2465_s_at 144.8 A
Saccharomyces cerevisiae chromosome II, complete chromosome sequence. Found forward in NC_001134 between 230363 and 231362 with 100% identity.
2466_s_at 45.5 A
Saccharomyces cerevisiae chromosome II, complete chromosome sequence. Found forward in NC_001134 between 231363 and 232362 with 100% identity.
2467_s_at -150.6 A
Saccharomyces cerevisiae chromosome II, complete chromosome sequence. Found forward in NC_001134 between 232363 and 233362 with 100% identity.
2468_s_at 177.7 A
Saccharomyces cerevisiae chromosome II, complete chromosome sequence. Found forward in

NC_001134 between 233363 and 234362 with 100% identity.

2469_s_at 902.2 P

Saccharomyces cerevisiae chromosome II, complete chromosome sequence. Found forward in NC_001134 between 234363 and 234580 with 100% identity.

2470_at 360.7 A

Saccharomyces cerevisiae chromosome II, complete chromosome sequence. Found forward in NC_001134 between 505265 and 506264 with 100% identity.

2471_g_at -320.7 A

Saccharomyces cerevisiae chromosome II, complete chromosome sequence. Found forward in NC_001134 between 505265 and 506264 with 100% identity.

2472_s_at -2.0 A

Saccharomyces cerevisiae chromosome II, complete chromosome sequence. Found forward in NC_001134 between 506265 and 507264 with 100% identity.

2473_s_at -128.1 A

Saccharomyces cerevisiae chromosome II, complete chromosome sequence. Found forward in NC_001134 between 507265 and 508264 with 100% identity.

2474_s_at 9.9 A

Saccharomyces cerevisiae chromosome II, complete chromosome sequence. Found forward in NC_001134 between 508265 and 509264 with 100% identity.

2475_s_at 74.8 A

Saccharomyces cerevisiae chromosome II, complete chromosome sequence. Found forward in NC_001134 between 509265 and 510264 with 100% identity.

2476_s_at 46.9 A

Saccharomyces cerevisiae chromosome II, complete chromosome sequence. Found forward in NC_001134 between 510265 and 511264 with 100% identity.

2477_s_at -4308.8 A

Saccharomyces cerevisiae chromosome II, complete chromosome sequence. Found forward in NC_001134 between 511265 and 512233 with 100% identity.

2478_at 221.1 A

Saccharomyces cerevisiae chromosome II, complete chromosome sequence. Found forward in NC_001134 between 517809 and 518808 with 100% identity.

2479_at 261.5 A

Saccharomyces cerevisiae chromosome II, complete chromosome sequence. Found forward in NC_001134 between 518809 and 519808 with 100% identity.

2480_at 170.9 A

Saccharomyces cerevisiae chromosome II, complete chromosome sequence. Found forward in NC_001134 between 519809 and 520808 with 100% identity.

2481_at 172.7 A

Saccharomyces cerevisiae chromosome II, complete chromosome sequence. Found forward in NC_001134 between 520809 and 521808 with 100% identity.

2482_at -265.8 A

Saccharomyces cerevisiae chromosome II, complete chromosome sequence. Found forward in NC_001134 between 521809 and 522808 with 100% identity.

2483_at 1627.2 A

Saccharomyces cerevisiae chromosome II, complete chromosome sequence. Found forward in NC_001134 between 522809 and 523808 with 100% identity.

2484_at -360.8 A

Saccharomyces cerevisiae chromosome II, complete chromosome sequence. Found forward in NC_001134 between 523809 and 524808 with 100% identity.

2485_at -515.5 A

Saccharomyces cerevisiae chromosome II, complete chromosome sequence. Found forward in NC_001134 between 524809 and 525808 with 100% identity.

2486_at 114.4 A

Saccharomyces cerevisiae chromosome II, complete chromosome sequence. Found forward in NC_001134 between 525809 and 526808 with 100% identity.

2487_at 279.4 A

Saccharomyces cerevisiae chromosome II, complete chromosome sequence. Found forward in NC_001134 between 526809 and 526984 with 100% identity.
2488_at 304.9 A
Saccharomyces cerevisiae chromosome II, complete chromosome sequence. Found forward in NC_001134 between 637162 and 638161 with 100% identity.
2421_at 230.1 A
Saccharomyces cerevisiae chromosome II, complete chromosome sequence. Found forward in NC_001134 between 638162 and 639161 with 100% identity.
2422_at 133.0 A
Saccharomyces cerevisiae chromosome II, complete chromosome sequence. Found forward in NC_001134 between 639162 and 640161 with 100% identity.
2423_at -24.8 A
Saccharomyces cerevisiae chromosome II, complete chromosome sequence. Found forward in NC_001134 between 640162 and 641161 with 100% identity.
2424_at 149.9 A
Saccharomyces cerevisiae chromosome II, complete chromosome sequence. Found forward in NC_001134 between 641162 and 642161 with 100% identity.
2425_at -38.2 A
Saccharomyces cerevisiae chromosome II, complete chromosome sequence. Found forward in NC_001134 between 642162 and 642542 with 100% identity.
2426_at 138.4 A
Saccharomyces cerevisiae chromosome II, complete chromosome sequence. Found forward in NC_001134 between 751813 and 752812 with 100% identity.
2427_at -2242.6 A
Saccharomyces cerevisiae chromosome II, complete chromosome sequence. Found forward in NC_001134 between 752813 and 753812 with 100% identity.
2428_at -192.0 A
Saccharomyces cerevisiae chromosome II, complete chromosome sequence. Found forward in NC_001134 between 753813 and 754812 with 100% identity.
2429_at -202.0 A
Saccharomyces cerevisiae chromosome II, complete chromosome sequence. Found forward in NC_001134 between 754813 and 755812 with 100% identity.
2430_at 13.6 A
Saccharomyces cerevisiae chromosome II, complete chromosome sequence. Found forward in NC_001134 between 755813 and 756812 with 100% identity.
2431_at -278.4 A
Saccharomyces cerevisiae chromosome II, complete chromosome sequence. Found forward in NC_001134 between 756813 and 757578 with 100% identity.
2432_at 791.9 P
Saccharomyces cerevisiae chromosome III, complete chromosome sequence. Found forward in NC_001135 between 82220 and 83219 with 100% identity.
2433_at 1187.8 P
Saccharomyces cerevisiae chromosome III, complete chromosome sequence. Found forward in NC_001135 between 83220 and 84219 with 100% identity.
2434_at 1240.1 A
Saccharomyces cerevisiae chromosome III, complete chromosome sequence. Found forward in NC_001135 between 84220 and 85219 with 100% identity.
2435_at -245.0 A
Saccharomyces cerevisiae chromosome III, complete chromosome sequence. Found forward in NC_001135 between 90220 and 91219 with 100% identity.
2436_g_at 205.0 A
Saccharomyces cerevisiae chromosome III, complete chromosome sequence. Found forward in NC_001135 between 90220 and 91219 with 100% identity.
2437_s_at 744.7 P
Saccharomyces cerevisiae chromosome III, complete chromosome sequence. Found forward in NC_001135 between 91220 and 91533 with 100% identity.

2438_at 201.4 A
Saccharomyces cerevisiae chromosome III, complete chromosome sequence. Found forward in NC_001135 between 177526 and 178525 with 100% identity.
2439_g_at -113.2 A
Saccharomyces cerevisiae chromosome III, complete chromosome sequence. Found forward in NC_001135 between 177526 and 178525 with 100% identity.
2440_s_at 57.7 A
Saccharomyces cerevisiae chromosome III, complete chromosome sequence. Found forward in NC_001135 between 178526 and 179525 with 100% identity.
2441_s_at 174.4 A
Saccharomyces cerevisiae chromosome III, complete chromosome sequence. Found forward in NC_001135 between 179526 and 180525 with 100% identity.
2442_s_at 529.4 P
Saccharomyces cerevisiae chromosome III, complete chromosome sequence. Found forward in NC_001135 between 180526 and 181525 with 100% identity.
2443_s_at 126.4 A
Saccharomyces cerevisiae chromosome III, complete chromosome sequence. Found forward in NC_001135 between 181526 and 182525 with 100% identity.
2444_s_at -74.7 A
Saccharomyces cerevisiae chromosome III, complete chromosome sequence. Found forward in NC_001135 between 182526 and 183525 with 100% identity.
2445_s_at 254.7 A
Saccharomyces cerevisiae chromosome III, complete chromosome sequence. Found forward in NC_001135 between 183526 and 184252 with 100% identity.
2395_at -193.2 A
Saccharomyces cerevisiae chromosome III, complete chromosome sequence. Found forward in NC_001135 between 275986 and 276985 with 100% identity.
2396_at 151.1 A
Saccharomyces cerevisiae chromosome III, complete chromosome sequence. Found forward in NC_001135 between 276986 and 277985 with 100% identity.
2397_at -347.1 A
Saccharomyces cerevisiae chromosome III, complete chromosome sequence. Found forward in NC_001135 between 277986 and 278985 with 100% identity.
2398_g_at 700.9 P
Saccharomyces cerevisiae chromosome III, complete chromosome sequence. Found forward in NC_001135 between 277986 and 278985 with 100% identity.
2399_s_at 172.2 A
Saccharomyces cerevisiae chromosome III, complete chromosome sequence. Found forward in NC_001135 between 278986 and 279985 with 100% identity.
2400_s_at -186.4 A
Saccharomyces cerevisiae chromosome III, complete chromosome sequence. Found forward in NC_001135 between 279986 and 280985 with 100% identity.
2401_s_at -66.9 A
Saccharomyces cerevisiae chromosome III, complete chromosome sequence. Found forward in NC_001135 between 280986 and 281985 with 100% identity.
2402_s_at -167.4 A
Saccharomyces cerevisiae chromosome III, complete chromosome sequence. Found forward in NC_001135 between 281986 and 282985 with 100% identity.
2403_s_at 654.1 P
Saccharomyces cerevisiae chromosome III, complete chromosome sequence. Found forward in NC_001135 between 282986 and 283985 with 100% identity.
2404_s_at 307.7 A
Saccharomyces cerevisiae chromosome III, complete chromosome sequence. Found forward in NC_001135 between 283986 and 284665 with 100% identity.
2405_at 236.3 A
Saccharomyces cerevisiae chromosome IV, complete chromosome sequence. Found forward in

NC_001136 between 79795 and 80794 with 100% identity.
2406_at -230.5 A
Saccharomyces cerevisiae chromosome IV, complete chromosome sequence. Found forward in NC_001136 between 80795 and 81794 with 100% identity.
2407_at 217.0 A
Saccharomyces cerevisiae chromosome IV, complete chromosome sequence. Found forward in NC_001136 between 81795 and 82794 with 100% identity.
2408_at 29.0 A
Saccharomyces cerevisiae chromosome IV, complete chromosome sequence. Found forward in NC_001136 between 82795 and 83794 with 100% identity.
2409_at 680.9 A
Saccharomyces cerevisiae chromosome IV, complete chromosome sequence. Found forward in NC_001136 between 83795 and 84794 with 100% identity.
2410_g_at 85.1 A
Saccharomyces cerevisiae chromosome IV, complete chromosome sequence. Found forward in NC_001136 between 83795 and 84794 with 100% identity.
2411_s_at 416.3 A
Saccharomyces cerevisiae chromosome IV, complete chromosome sequence. Found forward in NC_001136 between 84795 and 85486 with 100% identity.
2412_at -1664.9 A
Saccharomyces cerevisiae chromosome IV, complete chromosome sequence. Found forward in NC_001136 between 149704 and 150703 with 100% identity.
2413_at -85.3 A
Saccharomyces cerevisiae chromosome IV, complete chromosome sequence. Found forward in NC_001136 between 150704 and 151703 with 100% identity.
2414_at 659.6 A
Saccharomyces cerevisiae chromosome IV, complete chromosome sequence. Found forward in NC_001136 between 151704 and 152703 with 100% identity.
2415_at -24.8 A
Saccharomyces cerevisiae chromosome IV, complete chromosome sequence. Found forward in NC_001136 between 152704 and 153703 with 100% identity.
2416_at -356.5 A
Saccharomyces cerevisiae chromosome IV, complete chromosome sequence. Found forward in NC_001136 between 153704 and 154703 with 100% identity.
2417_at 650.5 A
Saccharomyces cerevisiae chromosome IV, complete chromosome sequence. Found forward in NC_001136 between 154704 and 155703 with 100% identity.
2418_at -52.6 A
Saccharomyces cerevisiae chromosome IV, complete chromosome sequence. Found forward in NC_001136 between 155704 and 156703 with 100% identity.
2419_g_at 331.6 A
Saccharomyces cerevisiae chromosome IV, complete chromosome sequence. Found forward in NC_001136 between 155704 and 156703 with 100% identity.
2420_s_at 77.3 A
Saccharomyces cerevisiae chromosome IV, complete chromosome sequence. Found forward in NC_001136 between 156704 and 157405 with 100% identity.
2352_at -1270.9 A
Saccharomyces cerevisiae chromosome IV, complete chromosome sequence. Found forward in NC_001136 between 205861 and 206860 with 100% identity.
2353_at 691.0 P
Saccharomyces cerevisiae chromosome IV, complete chromosome sequence. Found forward in NC_001136 between 206861 and 207860 with 100% identity.
2354_at 320.1 A
Saccharomyces cerevisiae chromosome IV, complete chromosome sequence. Found forward in NC_001136 between 207861 and 208860 with 100% identity.
2355_at -442.7 A

Saccharomyces cerevisiae chromosome IV, complete chromosome sequence. Found forward in NC_001136 between 208861 and 209860 with 100% identity.
2356_at -278.9 A
Saccharomyces cerevisiae chromosome IV, complete chromosome sequence. Found forward in NC_001136 between 209861 and 210860 with 100% identity.
2357_at 428.7 A
Saccharomyces cerevisiae chromosome IV, complete chromosome sequence. Found forward in NC_001136 between 210861 and 211376 with 100% identity.
2358_at 12.1 A
Saccharomyces cerevisiae chromosome IV, complete chromosome sequence. Found forward in NC_001136 between 257132 and 258131 with 100% identity.
2359_at 208.5 P
Saccharomyces cerevisiae chromosome IV, complete chromosome sequence. Found forward in NC_001136 between 258132 and 259131 with 100% identity.
2360_g_at 153.0 A
Saccharomyces cerevisiae chromosome IV, complete chromosome sequence. Found forward in NC_001136 between 258132 and 259131 with 100% identity.
2361_s_at 735.9 A
Saccharomyces cerevisiae chromosome IV, complete chromosome sequence. Found forward in NC_001136 between 259132 and 260131 with 100% identity.
2362_s_at 374.0 A
Saccharomyces cerevisiae chromosome IV, complete chromosome sequence. Found forward in NC_001136 between 260132 and 261131 with 100% identity.
2363_s_at 79.0 A
Saccharomyces cerevisiae chromosome IV, complete chromosome sequence. Found forward in NC_001136 between 261132 and 262131 with 100% identity.
2364_s_at 16.4 A
Saccharomyces cerevisiae chromosome IV, complete chromosome sequence. Found forward in NC_001136 between 262132 and 262724 with 100% identity.
2365_at -200.6 A
Saccharomyces cerevisiae chromosome IV, complete chromosome sequence. Found forward in NC_001136 between 344736 and 345735 with 100% identity.
2366_s_at -245.1 A
Saccharomyces cerevisiae chromosome IV, complete chromosome sequence. Found forward in NC_001136 between 345736 and 346735 with 100% identity.
2367_s_at 837.0 P
Saccharomyces cerevisiae chromosome IV, complete chromosome sequence. Found forward in NC_001136 between 346736 and 347735 with 100% identity.
2368_s_at -253.1 A
Saccharomyces cerevisiae chromosome IV, complete chromosome sequence. Found forward in NC_001136 between 347736 and 348735 with 100% identity.
2369_s_at 98.8 A
Saccharomyces cerevisiae chromosome IV, complete chromosome sequence. Found forward in NC_001136 between 348736 and 349735 with 100% identity.

2370_s_at 1168.7 A
Saccharomyces cerevisiae chromosome IV, complete chromosome sequence. Found forward in NC_001136 between 349736 and 350536 with 100% identity.
2371_at -1865.8 A
Saccharomyces cerevisiae chromosome IV, complete chromosome sequence. Found forward in NC_001136 between 618990 and 619989 with 100% identity.
2372_at 159.1 A
Saccharomyces cerevisiae chromosome IV, complete chromosome sequence. Found forward in NC_001136 between 619990 and 620989 with 100% identity.
2373_at -177.2 A
Saccharomyces cerevisiae chromosome IV, complete chromosome sequence. Found forward in

NC_001136 between 620990 and 621989 with 100% identity.
2374_at 292.8 A
Saccharomyces cerevisiae chromosome IV, complete chromosome sequence. Found forward in NC_001136 between 621990 and 622989 with 100% identity.
2375_s_at 1057.9 A
Saccharomyces cerevisiae chromosome IV, complete chromosome sequence. Found forward in NC_001136 between 622990 and 623989 with 100% identity.
2376_s_at 500.2 P
Saccharomyces cerevisiae chromosome IV, complete chromosome sequence. Found forward in NC_001136 between 623990 and 624214 with 100% identity.
2377_at 2389.1 A
Saccharomyces cerevisiae chromosome IV, complete chromosome sequence. Found forward in NC_001136 between 630598 and 631597 with 100% identity.
2378_g_at 691.6 P
Saccharomyces cerevisiae chromosome IV, complete chromosome sequence. Found forward in NC_001136 between 630598 and 631597 with 100% identity.
2379_s_at 1623.5 P
Saccharomyces cerevisiae chromosome IV, complete chromosome sequence. Found forward in NC_001136 between 631598 and 632597 with 100% identity.
2380_s_at 436.5 P
Saccharomyces cerevisiae chromosome IV, complete chromosome sequence. Found forward in NC_001136 between 632598 and 633597 with 100% identity.
2381_s_at 377.6 A
Saccharomyces cerevisiae chromosome IV, complete chromosome sequence. Found forward in NC_001136 between 633598 and 634597 with 100% identity.
2382_s_at 412.2 P
Saccharomyces cerevisiae chromosome IV, complete chromosome sequence. Found forward in NC_001136 between 634598 and 635597 with 100% identity.
2383_at -8.9 A
Saccharomyces cerevisiae chromosome IV, complete chromosome sequence. Found forward in NC_001136 between 735394 and 736393 with 100% identity.
2384_at 340.6 A
Saccharomyces cerevisiae chromosome IV, complete chromosome sequence. Found forward in NC_001136 between 736394 and 737393 with 100% identity.
2385_at -220.3 A
Saccharomyces cerevisiae chromosome IV, complete chromosome sequence. Found forward in NC_001136 between 737394 and 738393 with 100% identity.
2386_at 161.5 A
Saccharomyces cerevisiae chromosome IV, complete chromosome sequence. Found forward in NC_001136 between 738394 and 739393 with 100% identity.
2387_at -78.6 A
Saccharomyces cerevisiae chromosome IV, complete chromosome sequence. Found forward in NC_001136 between 739394 and 740393 with 100% identity.
2388_s_at 292.0 A
Saccharomyces cerevisiae chromosome IV, complete chromosome sequence. Found forward in NC_001136 between 756048 and 757047 with 100% identity.
2389_s_at 148.8 A
Saccharomyces cerevisiae chromosome IV, complete chromosome sequence. Found forward in NC_001136 between 757048 and 758047 with 100% identity.
2390_s_at 12.2 A
Saccharomyces cerevisiae chromosome IV, complete chromosome sequence. Found forward in NC_001136 between 759048 and 760047 with 100% identity.
2391_s_at -16.6 A
Saccharomyces cerevisiae chromosome IV, complete chromosome sequence. Found forward in NC_001136 between 760048 and 761047 with 100% identity.
2392_s_at -82.5 A

			Saccharomyces cerevisiae chromosome IV, complete chromosome sequence. Found forward in NC_001136 between 761048 and 762047 with 100% identity.
2393_s_at	189.7	A	Saccharomyces cerevisiae chromosome IV, complete chromosome sequence. Found forward in NC_001136 between 762048 and 763047 with 100% identity.
2394_s_at	982.8	P	Saccharomyces cerevisiae chromosome IV, complete chromosome sequence. Found forward in NC_001136 between 763048 and 763367 with 100% identity.
2309_at	308.6	A	Saccharomyces cerevisiae chromosome IV, complete chromosome sequence. Found forward in NC_001136 between 796686 and 797685 with 100% identity.
2310_at	-39.2	A	Saccharomyces cerevisiae chromosome IV, complete chromosome sequence. Found forward in NC_001136 between 797686 and 798685 with 100% identity.
2311_at	153.0	A	Saccharomyces cerevisiae chromosome IV, complete chromosome sequence. Found forward in NC_001136 between 798686 and 799685 with 100% identity.
2312_at	1691.4	A	Saccharomyces cerevisiae chromosome IV, complete chromosome sequence. Found forward in NC_001136 between 799686 and 800685 with 100% identity.
2313_at	4530.9	P	Saccharomyces cerevisiae chromosome IV, complete chromosome sequence. Found forward in NC_001136 between 800686 and 801685 with 100% identity.
2314_at	550.1	A	Saccharomyces cerevisiae chromosome IV, complete chromosome sequence. Found forward in NC_001136 between 801686 and 802685 with 100% identity.
2315_at	8.3	A	Saccharomyces cerevisiae chromosome IV, complete chromosome sequence. Found forward in NC_001136 between 802686 and 803685 with 100% identity.
2316_at	-9.9	A	Saccharomyces cerevisiae chromosome IV, complete chromosome sequence. Found forward in NC_001136 between 877250 and 878249 with 100% identity.
2317_at	3385.3	P	Saccharomyces cerevisiae chromosome IV, complete chromosome sequence. Found forward in NC_001136 between 878250 and 879249 with 100% identity.
2319_f_at	6640.5	P	Saccharomyces cerevisiae chromosome IV, complete chromosome sequence. Found forward in NC_001136 between 647450 and 647656 with 100% identity.
2320_at	-96.8	A	Saccharomyces cerevisiae chromosome IV, complete chromosome sequence. Found forward in NC_001136 between 1133751 and 1134750 with 100% identity.
2321_at	-134.7	A	Saccharomyces cerevisiae chromosome IV, complete chromosome sequence. Found forward in NC_001136 between 1134751 and 1135750 with 100% identity.
2322_at	17.4	A	Saccharomyces cerevisiae chromosome IV, complete chromosome sequence. Found forward in NC_001136 between 1135751 and 1136750 with 100% identity.
2323_g_at	-16.8	A	Saccharomyces cerevisiae chromosome IV, complete chromosome sequence. Found forward in NC_001136 between 1135751 and 1136750 with 100% identity.
2324_s_at	-125.5	A	Saccharomyces cerevisiae chromosome IV, complete chromosome sequence. Found forward in NC_001136 between 1136751 and 1137750 with 100% identity.
2325_s_at	208.1	A	Saccharomyces cerevisiae chromosome IV, complete chromosome sequence. Found forward in NC_001136 between 1137751 and 1138750 with 100% identity.

2326_s_at 156.3 A
Saccharomyces cerevisiae chromosome IV, complete chromosome sequence. Found forward in NC_001136 between 1138751 and 1139750 with 100% identity.
2327_s_at 37.7 A
Saccharomyces cerevisiae chromosome IV, complete chromosome sequence. Found forward in NC_001136 between 1139751 and 1139967 with 100% identity.
2328_at 108.5 A
Saccharomyces cerevisiae chromosome IV, complete chromosome sequence. Found forward in NC_001136 between 1305061 and 1306060 with 100% identity.
2329_at 167.4 A
Saccharomyces cerevisiae chromosome IV, complete chromosome sequence. Found forward in NC_001136 between 1306061 and 1307060 with 100% identity.
2330_g_at 593.6 P
Saccharomyces cerevisiae chromosome IV, complete chromosome sequence. Found forward in NC_001136 between 1306061 and 1307060 with 100% identity.
2331_s_at 64.5 A
Saccharomyces cerevisiae chromosome IV, complete chromosome sequence. Found forward in NC_001136 between 1307061 and 1308060 with 100% identity.
2332_s_at 337.2 A
Saccharomyces cerevisiae chromosome IV, complete chromosome sequence. Found forward in NC_001136 between 1308061 and 1309060 with 100% identity.
2333_s_at 310.0 A
Saccharomyces cerevisiae chromosome IV, complete chromosome sequence. Found forward in NC_001136 between 1309061 and 1310060 with 100% identity.
2334_s_at 187.6 A
Saccharomyces cerevisiae chromosome IV, complete chromosome sequence. Found forward in NC_001136 between 1310061 and 1311060 with 100% identity.
2335_s_at 925.4 P
Saccharomyces cerevisiae chromosome IV, complete chromosome sequence. Found forward in NC_001136 between 1311061 and 1311164 with 100% identity.
2336_at 1170.1 A
Saccharomyces cerevisiae chromosome IV, complete chromosome sequence. Found forward in NC_001136 between 1346165 and 1347164 with 100% identity.
2337_at 305.4 A
Saccharomyces cerevisiae chromosome IV, complete chromosome sequence. Found forward in NC_001136 between 1347165 and 1348164 with 100% identity.
2338_at 305.4 A
Saccharomyces cerevisiae chromosome IV, complete chromosome sequence. Found forward in NC_001136 between 1348165 and 1349164 with 100% identity.
2339_at 520.5 P
Saccharomyces cerevisiae chromosome IV, complete chromosome sequence. Found forward in NC_001136 between 1349165 and 1350164 with 100% identity.
2340_at -775.7 A
Saccharomyces cerevisiae chromosome IV, complete chromosome sequence. Found forward in NC_001136 between 1350165 and 1351164 with 100% identity.
2341_g_at -58.2 A
Saccharomyces cerevisiae chromosome IV, complete chromosome sequence. Found forward in NC_001136 between 1350165 and 1351164 with 100% identity.
2342_s_at -139.6 A
Saccharomyces cerevisiae chromosome IV, complete chromosome sequence. Found forward in NC_001136 between 1351165 and 1351842 with 100% identity.
2343_at 1126.9 A
Saccharomyces cerevisiae chromosome IV, complete chromosome sequence. Found forward in NC_001136 between 1369375 and 1370374 with 100% identity.
2344_g_at 2366.0 A
Saccharomyces cerevisiae chromosome IV, complete chromosome sequence. Found forward in

NC_001136 between 1369375 and 1370374 with 100% identity.
2345_s_at	-60.1	A
Saccharomyces cerevisiae chromosome IV, complete chromosome sequence. Found forward in NC_001136 between 1370375 and 1371374 with 100% identity.
2346_s_at	-111.1	A
Saccharomyces cerevisiae chromosome IV, complete chromosome sequence. Found forward in NC_001136 between 1371375 and 1372374 with 100% identity.
2347_s_at	-227.3	A
Saccharomyces cerevisiae chromosome IV, complete chromosome sequence. Found forward in NC_001136 between 1372375 and 1373374 with 100% identity.
2348_s_at	86.0	A
Saccharomyces cerevisiae chromosome IV, complete chromosome sequence. Found forward in NC_001136 between 1373375 and 1374374 with 100% identity.
2349_s_at	-65.0	A
Saccharomyces cerevisiae chromosome IV, complete chromosome sequence. Found forward in NC_001136 between 1374375 and 1375374 with 100% identity.
2350_s_at	1118.0	P
Saccharomyces cerevisiae chromosome IV, complete chromosome sequence. Found forward in NC_001136 between 1375375 and 1376374 with 100% identity.
2351_s_at	361.0	A
Saccharomyces cerevisiae chromosome IV, complete chromosome sequence. Found forward in NC_001136 between 1376375 and 1377374 with 100% identity.
2266_s_at	325.6	A
Saccharomyces cerevisiae chromosome IV, complete chromosome sequence. Found forward in NC_001136 between 1377375 and 1378374 with 100% identity.
2267_s_at	185.7	A
Saccharomyces cerevisiae chromosome IV, complete chromosome sequence. Found forward in NC_001136 between 1378375 and 1379085 with 100% identity.
2268_at	-48.3	A
Saccharomyces cerevisiae chromosome V, complete chromosome sequence. Found forward in NC_001137 between 7553 and 8552 with 100% identity.
2269_at	159.9	A
Saccharomyces cerevisiae chromosome V, complete chromosome sequence. Found forward in NC_001137 between 8553 and 9552 with 100% identity.
2270_at	102.2	A
Saccharomyces cerevisiae chromosome V, complete chromosome sequence. Found forward in NC_001137 between 9553 and 10552 with 100% identity.
2271_at	-143.2	A
Saccharomyces cerevisiae chromosome V, complete chromosome sequence. Found forward in NC_001137 between 10553 and 11552 with 100% identity.
2272_at	413.5	P
Saccharomyces cerevisiae chromosome V, complete chromosome sequence. Found forward in NC_001137 between 11553 and 12552 with 100% identity.
2273_at	-9050.2	A
Saccharomyces cerevisiae chromosome V, complete chromosome sequence. Found forward in NC_001137 between 12553 and 13552 with 100% identity.
2274_at	-7.6	A
Saccharomyces cerevisiae chromosome V, complete chromosome sequence. Found forward in NC_001137 between 13553 and 13915 with 100% identity.
2275_g_at	-1724.6	A
Saccharomyces cerevisiae chromosome V, complete chromosome sequence. Found forward in NC_001137 between 13553 and 13915 with 100% identity.
2276_at	-507.3	A
Saccharomyces cerevisiae chromosome V, complete chromosome sequence. Found forward in NC_001137 between 109004 and 110003 with 100% identity.
2277_at	52.2	A

Saccharomyces cerevisiae chromosome V, complete chromosome sequence. Found forward in NC_001137 between 110004 and 111003 with 100% identity.
2278_at	-11.3	A
Saccharomyces cerevisiae chromosome V, complete chromosome sequence. Found forward in NC_001137 between 111004 and 112003 with 100% identity.
2279_g_at	405.7	A
Saccharomyces cerevisiae chromosome V, complete chromosome sequence. Found forward in NC_001137 between 111004 and 112003 with 100% identity.
2280_s_at	-252.0	A
Saccharomyces cerevisiae chromosome V, complete chromosome sequence. Found forward in NC_001137 between 112004 and 113003 with 100% identity.
2281_s_at	-95.4	A
Saccharomyces cerevisiae chromosome V, complete chromosome sequence. Found forward in NC_001137 between 113004 and 114003 with 100% identity.
2282_s_at	205.9	A
Saccharomyces cerevisiae chromosome V, complete chromosome sequence. Found forward in NC_001137 between 114004 and 115003 with 100% identity.
2283_s_at	1210.2	P
Saccharomyces cerevisiae chromosome V, complete chromosome sequence. Found forward in NC_001137 between 115004 and 115300 with 100% identity.
2284_at	-40.0	A
Saccharomyces cerevisiae chromosome V, complete chromosome sequence. Found forward in NC_001137 between 425685 and 426684 with 100% identity.
2285_at	107.1	A
Saccharomyces cerevisiae chromosome V, complete chromosome sequence. Found forward in NC_001137 between 426685 and 427684 with 100% identity.
2286_at	720.8	A
Saccharomyces cerevisiae chromosome V, complete chromosome sequence. Found forward in NC_001137 between 427685 and 428684 with 100% identity.
2287_at	47.5	A
Saccharomyces cerevisiae chromosome V, complete chromosome sequence. Found forward in NC_001137 between 428685 and 429684 with 100% identity.
2288_at	931.6	A
Saccharomyces cerevisiae chromosome V, complete chromosome sequence. Found forward in NC_001137 between 429685 and 430684 with 100% identity.
2289_at	-494.5	A
Saccharomyces cerevisiae chromosome V, complete chromosome sequence. Found forward in NC_001137 between 430685 and 431126 with 100% identity.
2290_at	-803.0	A
Saccharomyces cerevisiae chromosome V, complete chromosome sequence. Found forward in NC_001137 between 442412 and 443411 with 100% identity.
2291_g_at	3259.5	A
Saccharomyces cerevisiae chromosome V, complete chromosome sequence. Found forward in NC_001137 between 442412 and 443411 with 100% identity.
2294_f_at	18970.9	P
Saccharomyces cerevisiae chromosome V, complete chromosome sequence. Found forward in NC_001137 between 446412 and 447411 with 100% identity.
2295_at	212.6	A
Saccharomyces cerevisiae chromosome V, complete chromosome sequence. Found forward in NC_001137 between 476841 and 477840 with 100% identity.
2296_at	317.6	A
Saccharomyces cerevisiae chromosome V, complete chromosome sequence. Found forward in NC_001137 between 477841 and 478840 with 100% identity.
2297_at	67.3	A
Saccharomyces cerevisiae chromosome V, complete chromosome sequence. Found forward in NC_001137 between 478841 and 479840 with 100% identity.

2298_at -426.2 A

Saccharomyces cerevisiae chromosome V, complete chromosome sequence. Found forward in NC_001137 between 479841 and 480840 with 100% identity.

2299_at 175.8 A

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

2300_at 670.0 A

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

2301_at 52.3 A

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

2302_at 306.9 P

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

2303_f_at 18010.4 P

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

2306_at 295.4 A

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

2307_at 280.7 M

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

2308_at -1613.4 A

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

2223_at 133.5 A

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

2224_at 9.0 A

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

2225_at 773.6 A

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

2226_at 407.9 M

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

2227_at -301.5 A

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

2228_at 71.5 A

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

2229_at 281.3 A

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

2230_at 551.3 A

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

2231_at -417.0 A

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

2232_at 18.8 A

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

NC_001138 between 72614 and 73613 with 100% identity.
2233_at -3587.8 A
Saccharomyces cerevisiae chromosome VI, complete chromosome sequence. Found forward in NC_001138 between 73614 and 74613 with 100% identity.
2234_at -3.2 A
Saccharomyces cerevisiae chromosome VI, complete chromosome sequence. Found forward in NC_001138 between 74614 and 74871 with 100% identity.
2235_at 413.2 A
Saccharomyces cerevisiae chromosome VI, complete chromosome sequence. Found forward in NC_001138 between 136029 and 137028 with 100% identity.
2236_at -185.4 A
Saccharomyces cerevisiae chromosome VI, complete chromosome sequence. Found forward in NC_001138 between 137029 and 138028 with 100% identity.
2237_at -125.1 A
Saccharomyces cerevisiae chromosome VI, complete chromosome sequence. Found forward in NC_001138 between 143029 and 144028 with 100% identity.
2238_at -1302.6 A
Saccharomyces cerevisiae chromosome VI, complete chromosome sequence. Found forward in NC_001138 between 144029 and 145028 with 100% identity.
2239_at 942.2 A
Saccharomyces cerevisiae chromosome VI, complete chromosome sequence. Found forward in NC_001138 between 145029 and 145108 with 100% identity.
2240_at -288.9 A
Saccharomyces cerevisiae chromosome VI, complete chromosome sequence. Found forward in NC_001138 between 184470 and 185469 with 100% identity.
2241_s_at 38.5 A
Saccharomyces cerevisiae chromosome VI, complete chromosome sequence. Found forward in NC_001138 between 185470 and 186469 with 100% identity.
2242_s_at 158.4 A
Saccharomyces cerevisiae chromosome VI, complete chromosome sequence. Found forward in NC_001138 between 186470 and 187469 with 100% identity.
2243_s_at -31.7 A
Saccharomyces cerevisiae chromosome VI, complete chromosome sequence. Found forward in NC_001138 between 187470 and 188469 with 100% identity.
2244_s_at 506.1 P
Saccharomyces cerevisiae chromosome VI, complete chromosome sequence. Found forward in NC_001138 between 188470 and 189469 with 100% identity.
2245_s_at 922.4 A
Saccharomyces cerevisiae chromosome VI, complete chromosome sequence. Found forward in NC_001138 between 189470 and 190469 with 100% identity.
2246_s_at 567.3 A
Saccharomyces cerevisiae chromosome VI, complete chromosome sequence. Found forward in NC_001138 between 190470 and 190825 with 100% identity.
2247_at 338.4 P
Saccharomyces cerevisiae chromosome VII, complete chromosome sequence. Found forward in NC_001139 between 16307 and 17306 with 100% identity.
2248_at 157.7 A
Saccharomyces cerevisiae chromosome VII, complete chromosome sequence. Found forward in NC_001139 between 17307 and 18306 with 100% identity.
2249_at -180.8 A
Saccharomyces cerevisiae chromosome VII, complete chromosome sequence. Found forward in NC_001139 between 18307 and 19306 with 100% identity.
2250_at 2950.4 P
Saccharomyces cerevisiae chromosome VII, complete chromosome sequence. Found forward in NC_001139 between 19307 and 20306 with 100% identity.
2251_at 34.5 A

Saccharomyces cerevisiae chromosome VII, complete chromosome sequence. Found forward in NC_001139 between 20307 and 21306 with 100% identity.
2252_g_at 148.6 A
Saccharomyces cerevisiae chromosome VII, complete chromosome sequence. Found forward in NC_001139 between 20307 and 21306 with 100% identity.
2253_s_at -641.7 A
Saccharomyces cerevisiae chromosome VII, complete chromosome sequence. Found forward in NC_001139 between 21307 and 21608 with 100% identity.
2254_at 204.7 A
Saccharomyces cerevisiae chromosome VII, complete chromosome sequence. Found forward in NC_001139 between 103045 and 104044 with 100% identity.
2255_at 16.0 A
Saccharomyces cerevisiae chromosome VII, complete chromosome sequence. Found forward in NC_001139 between 104045 and 105044 with 100% identity.
2256_at -217.7 A
Saccharomyces cerevisiae chromosome VII, complete chromosome sequence. Found forward in NC_001139 between 105045 and 106044 with 100% identity.
2257_at 1587.2 A
Saccharomyces cerevisiae chromosome VII, complete chromosome sequence. Found forward in NC_001139 between 106045 and 107044 with 100% identity.
2258_at -82.5 A
Saccharomyces cerevisiae chromosome VII, complete chromosome sequence. Found forward in NC_001139 between 107045 and 108044 with 100% identity.
2259_at 671.9 P
Saccharomyces cerevisiae chromosome VII, complete chromosome sequence. Found forward in NC_001139 between 108045 and 109044 with 100% identity.
2260_g_at 217.5 A
Saccharomyces cerevisiae chromosome VII, complete chromosome sequence. Found forward in NC_001139 between 108045 and 109044 with 100% identity.
2261_s_at 517.8 P
Saccharomyces cerevisiae chromosome VII, complete chromosome sequence. Found forward in NC_001139 between 109045 and 109906 with 100% identity.
2262_at 1903.1 P
Saccharomyces cerevisiae chromosome VII, complete chromosome sequence. Found forward in NC_001139 between 131050 and 132049 with 100% identity.
2263_g_at 231.4 A
Saccharomyces cerevisiae chromosome VII, complete chromosome sequence. Found forward in NC_001139 between 131050 and 132049 with 100% identity.
2264_s_at -647.0 A
Saccharomyces cerevisiae chromosome VII, complete chromosome sequence. Found forward in NC_001139 between 132050 and 133049 with 100% identity.
2265_s_at -99.2 A
Saccharomyces cerevisiae chromosome VII, complete chromosome sequence. Found forward in NC_001139 between 133050 and 134049 with 100% identity.
2180_s_at 185.5 A
Saccharomyces cerevisiae chromosome VII, complete chromosome sequence. Found forward in NC_001139 between 134050 and 135049 with 100% identity.
2181_s_at 393.3 P
Saccharomyces cerevisiae chromosome VII, complete chromosome sequence. Found forward in NC_001139 between 135050 and 136049 with 100% identity.
2182_s_at 786.6 A
Saccharomyces cerevisiae chromosome VII, complete chromosome sequence. Found forward in NC_001139 between 136050 and 137049 with 100% identity.
2183_s_at 330.7 P
Saccharomyces cerevisiae chromosome VII, complete chromosome sequence. Found forward in NC_001139 between 137050 and 138049 with 100% identity.

2184_s_at 1415.6 P
Saccharomyces cerevisiae chromosome VII, complete chromosome sequence. Found forward in NC_001139 between 138050 and 139047 with 100% identity.
2185_at 488.5 A
Saccharomyces cerevisiae chromosome VII, complete chromosome sequence. Found forward in NC_001139 between 176031 and 177030 with 100% identity.
2186_at 647.3 P
Saccharomyces cerevisiae chromosome VII, complete chromosome sequence. Found forward in NC_001139 between 177031 and 178030 with 100% identity.
2187_at 380.7 P
Saccharomyces cerevisiae chromosome VII, complete chromosome sequence. Found forward in NC_001139 between 178031 and 179030 with 100% identity.
2188_at -131.4 A
Saccharomyces cerevisiae chromosome VII, complete chromosome sequence. Found forward in NC_001139 between 179031 and 180030 with 100% identity.
2189_at -53.0 A
Saccharomyces cerevisiae chromosome VII, complete chromosome sequence. Found forward in NC_001139 between 180031 and 181030 with 100% identity.
2190_g_at 2412.1 P
Saccharomyces cerevisiae chromosome VII, complete chromosome sequence. Found forward in NC_001139 between 180031 and 181030 with 100% identity.
2191_s_at 848.2 P
Saccharomyces cerevisiae chromosome VII, complete chromosome sequence. Found forward in NC_001139 between 181031 and 181622 with 100% identity.
2192_at 97.9 A
Saccharomyces cerevisiae chromosome VII, complete chromosome sequence. Found forward in NC_001139 between 241856 and 242855 with 100% identity.
2193_at 419.6 P
Saccharomyces cerevisiae chromosome VII, complete chromosome sequence. Found forward in NC_001139 between 242856 and 243855 with 100% identity.
2194_at 1373.3 A
Saccharomyces cerevisiae chromosome VII, complete chromosome sequence. Found forward in NC_001139 between 243856 and 244855 with 100% identity.
2195_at 61.1 A
Saccharomyces cerevisiae chromosome VII, complete chromosome sequence. Found forward in NC_001139 between 244856 and 245855 with 100% identity.
2196_s_at 350.4 A
Saccharomyces cerevisiae chromosome VII, complete chromosome sequence. Found forward in NC_001139 between 245856 and 246855 with 100% identity.
2197_s_at 656.0 P
Saccharomyces cerevisiae chromosome VII, complete chromosome sequence. Found forward in NC_001139 between 246856 and 247627 with 100% identity.
2198_at 470.6 P
Saccharomyces cerevisiae chromosome VII, complete chromosome sequence. Found forward in NC_001139 between 331616 and 332615 with 100% identity.
2199_at 522.6 A
Saccharomyces cerevisiae chromosome VII, complete chromosome sequence. Found forward in NC_001139 between 332616 and 333615 with 100% identity.
2200_at -33.5 A
Saccharomyces cerevisiae chromosome VII, complete chromosome sequence. Found forward in NC_001139 between 333616 and 334615 with 100% identity.
2201_at -2402.6 A
Saccharomyces cerevisiae chromosome VII, complete chromosome sequence. Found forward in NC_001139 between 334616 and 335615 with 100% identity.
2202_g_at -9.8 A
Saccharomyces cerevisiae chromosome VII, complete chromosome sequence. Found forward in

NC_001139 between 334616 and 335615 with 100% identity.

2203_s_at 191.3 A

Saccharomyces cerevisiae chromosome VII, complete chromosome sequence. Found forward in NC_001139 between 335616 and 336615 with 100% identity.

2204_s_at 599.8 P

Saccharomyces cerevisiae chromosome VII, complete chromosome sequence. Found forward in NC_001139 between 336616 and 337137 with 100% identity.

2205_at 425.8 A

Saccharomyces cerevisiae chromosome VII, complete chromosome sequence. Found forward in NC_001139 between 547463 and 548462 with 100% identity.

2206_g_at -58.9 A

Saccharomyces cerevisiae chromosome VII, complete chromosome sequence. Found forward in NC_001139 between 547463 and 548462 with 100% identity.

2207_s_at 289.7 A

Saccharomyces cerevisiae chromosome VII, complete chromosome sequence. Found forward in NC_001139 between 548463 and 549462 with 100% identity.

2208_s_at 456.4 P

Saccharomyces cerevisiae chromosome VII, complete chromosome sequence. Found forward in NC_001139 between 549463 and 550462 with 100% identity.

2209_s_at 227.7 A

Saccharomyces cerevisiae chromosome VII, complete chromosome sequence. Found forward in NC_001139 between 550463 and 551462 with 100% identity.

2210_s_at 509.1 A

Saccharomyces cerevisiae chromosome VII, complete chromosome sequence. Found forward in NC_001139 between 551463 and 552462 with 100% identity.

2211_s_at 945.5 P

Saccharomyces cerevisiae chromosome VII, complete chromosome sequence. Found forward in NC_001139 between 552463 and 553445 with 100% identity.

2212_at 355.1 P

Saccharomyces cerevisiae chromosome VII, complete chromosome sequence. Found forward in NC_001139 between 659764 and 660763 with 100% identity.

2213_at -1160.1 A

Saccharomyces cerevisiae chromosome VII, complete chromosome sequence. Found forward in NC_001139 between 660764 and 661763 with 100% identity.

2214_at -2100.0 A

Saccharomyces cerevisiae chromosome VII, complete chromosome sequence. Found forward in NC_001139 between 661764 and 662763 with 100% identity.

2215_g_at 1103.4 P

Saccharomyces cerevisiae chromosome VII, complete chromosome sequence. Found forward in NC_001139 between 661764 and 662763 with 100% identity.

2216_s_at 327.3 A

Saccharomyces cerevisiae chromosome VII, complete chromosome sequence. Found forward in NC_001139 between 662764 and 663763 with 100% identity.

2217_s_at 455.5 M

Saccharomyces cerevisiae chromosome VII, complete chromosome sequence. Found forward in NC_001139 between 663764 and 664763 with 100% identity.

2218_s_at 4402.2 P

Saccharomyces cerevisiae chromosome VII, complete chromosome sequence. Found forward in NC_001139 between 664764 and 665565 with 100% identity.

2219_at -477.1 A

Saccharomyces cerevisiae chromosome VII, complete chromosome sequence. Found forward in NC_001139 between 683060 and 684059 with 100% identity.

2220_at -212.7 A

Saccharomyces cerevisiae chromosome VII, complete chromosome sequence. Found forward in NC_001139 between 684060 and 685059 with 100% identity.

2221_at -253.7 A

Saccharomyces cerevisiae chromosome VII, complete chromosome sequence. Found forward in NC_001139 between 685060 and 686059 with 100% identity.
2222_at 23.7 A
Saccharomyces cerevisiae chromosome VII, complete chromosome sequence. Found forward in NC_001139 between 686060 and 687059 with 100% identity.
2138_at 13.1 A
Saccharomyces cerevisiae chromosome VII, complete chromosome sequence. Found forward in NC_001139 between 687060 and 688059 with 100% identity.
2139_g_at 190.6 A
Saccharomyces cerevisiae chromosome VII, complete chromosome sequence. Found forward in NC_001139 between 687060 and 688059 with 100% identity.
2140_s_at 378.2 A
Saccharomyces cerevisiae chromosome VII, complete chromosome sequence. Found forward in NC_001139 between 688060 and 689059 with 100% identity.
2141_s_at 285.6 A
Saccharomyces cerevisiae chromosome VII, complete chromosome sequence. Found forward in NC_001139 between 689060 and 689459 with 100% identity.
2142_at 690.1 P
Saccharomyces cerevisiae chromosome VII, complete chromosome sequence. Found forward in NC_001139 between 860395 and 861394 with 100% identity.
2143_at -405.5 A
Saccharomyces cerevisiae chromosome VII, complete chromosome sequence. Found forward in NC_001139 between 861395 and 862394 with 100% identity.
2144_at 104.0 A
Saccharomyces cerevisiae chromosome VII, complete chromosome sequence. Found forward in NC_001139 between 862395 and 863394 with 100% identity.
2145_at -12.1 A
Saccharomyces cerevisiae chromosome VII, complete chromosome sequence. Found forward in NC_001139 between 863395 and 864394 with 100% identity.
2146_at -824.9 A
Saccharomyces cerevisiae chromosome VII, complete chromosome sequence. Found forward in NC_001139 between 864395 and 865394 with 100% identity.
2147_at 453.5 A
Saccharomyces cerevisiae chromosome VII, complete chromosome sequence. Found forward in NC_001139 between 865395 and 866330 with 100% identity.
2148_at -146.8 A
Saccharomyces cerevisiae chromosome VII, complete chromosome sequence. Found forward in NC_001139 between 923127 and 924126 with 100% identity.
2149_at -149.7 A
Saccharomyces cerevisiae chromosome VII, complete chromosome sequence. Found forward in NC_001139 between 924127 and 925126 with 100% identity.
2150_g_at 99.4 A
Saccharomyces cerevisiae chromosome VII, complete chromosome sequence. Found forward in NC_001139 between 924127 and 925126 with 100% identity.
2151_s_at -15.7 A
Saccharomyces cerevisiae chromosome VII, complete chromosome sequence. Found forward in NC_001139 between 925127 and 926126 with 100% identity.
2152_s_at -331.1 A
Saccharomyces cerevisiae chromosome VII, complete chromosome sequence. Found forward in NC_001139 between 926127 and 927126 with 100% identity.
2153_s_at 236.3 A
Saccharomyces cerevisiae chromosome VII, complete chromosome sequence. Found forward in NC_001139 between 927127 and 928126 with 100% identity.
2154_s_at 32.8 A
Saccharomyces cerevisiae chromosome VII, complete chromosome sequence. Found forward in NC_001139 between 928127 and 929126 with 100% identity.

2155_s_at 412.6 A
Saccharomyces cerevisiae chromosome VII, complete chromosome sequence. Found forward in NC_001139 between 929127 and 930126 with 100% identity.
2156_s_at -263.9 A
Saccharomyces cerevisiae chromosome VII, complete chromosome sequence. Found forward in NC_001139 between 930127 and 930307 with 100% identity.
2157_at 186.8 A
Saccharomyces cerevisiae chromosome VII, complete chromosome sequence. Found forward in NC_001139 between 955166 and 956165 with 100% identity.
2158_at 480.5 A
Saccharomyces cerevisiae chromosome VII, complete chromosome sequence. Found forward in NC_001139 between 956166 and 957165 with 100% identity.
2159_at -504.2 A
Saccharomyces cerevisiae chromosome VII, complete chromosome sequence. Found forward in NC_001139 between 957166 and 958165 with 100% identity.
2160_at 513.4 P
Saccharomyces cerevisiae chromosome VII, complete chromosome sequence. Found forward in NC_001139 between 958166 and 959165 with 100% identity.
2161_at 186.6 A
Saccharomyces cerevisiae chromosome VII, complete chromosome sequence. Found forward in NC_001139 between 959166 and 960165 with 100% identity.
2162_g_at 7856.3 P
Saccharomyces cerevisiae chromosome VII, complete chromosome sequence. Found forward in NC_001139 between 959166 and 960165 with 100% identity.
2163_s_at 17283.4 P
Saccharomyces cerevisiae chromosome VII, complete chromosome sequence. Found forward in NC_001139 between 960166 and 960596 with 100% identity.
2164_at -8.0 A
Saccharomyces cerevisiae chromosome VII, complete chromosome sequence. Found forward in NC_001139 between 1031505 and 1032504 with 100% identity.
2165_g_at -38.1 A
Saccharomyces cerevisiae chromosome VII, complete chromosome sequence. Found forward in NC_001139 between 1031505 and 1032504 with 100% identity.
2166_s_at 92.7 A
Saccharomyces cerevisiae chromosome VII, complete chromosome sequence. Found forward in NC_001139 between 1032505 and 1033504 with 100% identity.
2167_s_at 233.2 P
Saccharomyces cerevisiae chromosome VII, complete chromosome sequence. Found forward in NC_001139 between 1033505 and 1034504 with 100% identity.
2168_s_at 536.7 A
Saccharomyces cerevisiae chromosome VII, complete chromosome sequence. Found forward in NC_001139 between 1034505 and 1035504 with 100% identity.
2169_s_at 277.4 A
Saccharomyces cerevisiae chromosome VII, complete chromosome sequence. Found forward in NC_001139 between 1035505 and 1036504 with 100% identity.
2170_s_at 302.1 P
Saccharomyces cerevisiae chromosome VII, complete chromosome sequence. Found forward in NC_001139 between 1036505 and 1037190 with 100% identity.
2171_at -28.6 A
Saccharomyces cerevisiae chromosome VII, complete chromosome sequence. Found forward in NC_001139 between 1051406 and 1052405 with 100% identity.
2172_at 431.5 A
Saccharomyces cerevisiae chromosome VII, complete chromosome sequence. Found forward in NC_001139 between 1052406 and 1053405 with 100% identity.
2173_g_at 407.3 A
Saccharomyces cerevisiae chromosome VII, complete chromosome sequence. Found forward in

NC_001139 between 1052406 and 1053405 with 100% identity.
2174_s_at	913.0	P
Saccharomyces cerevisiae chromosome VII, complete chromosome sequence. Found forward in NC_001139 between 1053406 and 1054405 with 100% identity.
2175_s_at	799.8	P
Saccharomyces cerevisiae chromosome VII, complete chromosome sequence. Found forward in NC_001139 between 1054406 and 1055405 with 100% identity.
2176_s_at	2442.7	P
Saccharomyces cerevisiae chromosome VII, complete chromosome sequence. Found forward in NC_001139 between 1055406 and 1056405 with 100% identity.
2177_s_at	13681.4	P
Saccharomyces cerevisiae chromosome VII, complete chromosome sequence. Found forward in NC_001139 between 1056406 and 1056753 with 100% identity.
2178_at	214.5	A
Saccharomyces cerevisiae chromosome VII, complete chromosome sequence. Found forward in NC_001139 between 1084878 and 1085877 with 100% identity.
2179_at	299.1	A
Saccharomyces cerevisiae chromosome VIII, complete chromosome sequence. Found forward in NC_001140 between 39533 and 40532 with 100% identity.
2100_g_at	524.2	A
Saccharomyces cerevisiae chromosome VIII, complete chromosome sequence. Found forward in NC_001140 between 39533 and 40532 with 100% identity.
2101_s_at	-508.1	A
Saccharomyces cerevisiae chromosome VIII, complete chromosome sequence. Found forward in NC_001140 between 40533 and 41532 with 100% identity.
2102_s_at	-43.3	A
Saccharomyces cerevisiae chromosome VIII, complete chromosome sequence. Found forward in NC_001140 between 41533 and 42532 with 100% identity.
2103_s_at	79.9	A
Saccharomyces cerevisiae chromosome VIII, complete chromosome sequence. Found forward in NC_001140 between 42533 and 43532 with 100% identity.
2104_s_at	2365.3	P
Saccharomyces cerevisiae chromosome VIII, complete chromosome sequence. Found forward in NC_001140 between 43533 and 44532 with 100% identity.
2105_s_at	679.0	A
Saccharomyces cerevisiae chromosome VIII, complete chromosome sequence. Found forward in NC_001140 between 44533 and 45188 with 100% identity.
2106_at	349.0	A
Saccharomyces cerevisiae chromosome VIII, complete chromosome sequence. Found forward in NC_001140 between 84563 and 85562 with 100% identity.
2107_at	-205.0	A
Saccharomyces cerevisiae chromosome VIII, complete chromosome sequence. Found forward in NC_001140 between 150066 and 151065 with 100% identity.
2108_at	40.3	A
Saccharomyces cerevisiae chromosome VIII, complete chromosome sequence. Found forward in NC_001140 between 151066 and 152065 with 100% identity.
2109_g_at	27.2	A
Saccharomyces cerevisiae chromosome VIII, complete chromosome sequence. Found forward in NC_001140 between 151066 and 152065 with 100% identity.
2110_s_at	-60.3	A
Saccharomyces cerevisiae chromosome VIII, complete chromosome sequence. Found forward in NC_001140 between 152066 and 153065 with 100% identity.
2111_s_at	72.4	A
Saccharomyces cerevisiae chromosome VIII, complete chromosome sequence. Found forward in NC_001140 between 153066 and 154065 with 100% identity.
2112_s_at	272.3	A

Saccharomyces cerevisiae chromosome VIII, complete chromosome sequence. Found forward in NC_001140 between 154066 and 155065 with 100% identity.
2113_s_at -192.6 A
Saccharomyces cerevisiae chromosome VIII, complete chromosome sequence. Found forward in NC_001140 between 155066 and 156065 with 100% identity.
2114_s_at 543.9 A
Saccharomyces cerevisiae chromosome VIII, complete chromosome sequence. Found forward in NC_001140 between 156066 and 156943 with 100% identity.
2115_at 16.0 A
Saccharomyces cerevisiae chromosome VIII, complete chromosome sequence. Found forward in NC_001140 between 299647 and 300646 with 100% identity.
2116_at 195.1 P
Saccharomyces cerevisiae chromosome VIII, complete chromosome sequence. Found forward in NC_001140 between 300647 and 301646 with 100% identity.
2117_at -1331.4 A
Saccharomyces cerevisiae chromosome VIII, complete chromosome sequence. Found forward in NC_001140 between 301647 and 302646 with 100% identity.
2118_at -287.6 A
Saccharomyces cerevisiae chromosome VIII, complete chromosome sequence. Found forward in NC_001140 between 302647 and 303646 with 100% identity.
2119_g_at -1809.8 A
Saccharomyces cerevisiae chromosome VIII, complete chromosome sequence. Found forward in NC_001140 between 302647 and 303646 with 100% identity.
2120_s_at 478.9 A
Saccharomyces cerevisiae chromosome VIII, complete chromosome sequence. Found forward in NC_001140 between 303647 and 304646 with 100% identity.
2121_s_at -669.5 A
Saccharomyces cerevisiae chromosome VIII, complete chromosome sequence. Found forward in NC_001140 between 304647 and 305646 with 100% identity.
2122_s_at 110.1 A
Saccharomyces cerevisiae chromosome VIII, complete chromosome sequence. Found forward in NC_001140 between 305647 and 306646 with 100% identity.
2123_s_at -289.8 A
Saccharomyces cerevisiae chromosome VIII, complete chromosome sequence. Found forward in NC_001140 between 306647 and 307646 with 100% identity.
2124_s_at 217.9 P
Saccharomyces cerevisiae chromosome VIII, complete chromosome sequence. Found forward in NC_001140 between 307647 and 308646 with 100% identity.
2125_s_at 190.9 A
Saccharomyces cerevisiae chromosome VIII, complete chromosome sequence. Found forward in NC_001140 between 308647 and 309646 with 100% identity.
2126_s_at 137.4 A
Saccharomyces cerevisiae chromosome VIII, complete chromosome sequence. Found forward in NC_001140 between 309647 and 310646 with 100% identity.
2127_s_at -32.1 A
Saccharomyces cerevisiae chromosome VIII, complete chromosome sequence. Found forward in NC_001140 between 310647 and 311646 with 100% identity.
2128_s_at 90.9 A
Saccharomyces cerevisiae chromosome VIII, complete chromosome sequence. Found forward in NC_001140 between 311647 and 312646 with 100% identity.
2129_s_at 661.4 P
Saccharomyces cerevisiae chromosome VIII, complete chromosome sequence. Found forward in NC_001140 between 312647 and 313497 with 100% identity.
2130_at -95.1 A
Saccharomyces cerevisiae chromosome VIII, complete chromosome sequence. Found forward in NC_001140 between 430206 and 431205 with 100% identity.

2131_at -184.1 A

Saccharomyces cerevisiae chromosome VIII, complete chromosome sequence. Found forward in NC_001140 between 431206 and 432205 with 100% identity.

2132_at -212.1 A

Saccharomyces cerevisiae chromosome VIII, complete chromosome sequence. Found forward in NC_001140 between 432206 and 433205 with 100% identity.

2133_at -160.4 A

Saccharomyces cerevisiae chromosome VIII, complete chromosome sequence. Found forward in NC_001140 between 433206 and 434205 with 100% identity.

2134_at -2.0 A

Saccharomyces cerevisiae chromosome VIII, complete chromosome sequence. Found forward in NC_001140 between 434206 and 435205 with 100% identity.

2135_at 541.9 A

Saccharomyces cerevisiae chromosome VIII, complete chromosome sequence. Found forward in NC_001140 between 435206 and 436205 with 100% identity.

2136_at 624.3 A

Saccharomyces cerevisiae chromosome VIII, complete chromosome sequence. Found forward in NC_001140 between 436206 and 437169 with 100% identity.

2137_at -189.9 A

Saccharomyces cerevisiae chromosome VIII, complete chromosome sequence. Found forward in NC_001140 between 522872 and 523871 with 100% identity.

11394_at 469.6 A

Saccharomyces cerevisiae chromosome VIII, complete chromosome sequence. Found forward in NC_001140 between 523872 and 524871 with 100% identity.

11395_at 175.5 A

Saccharomyces cerevisiae chromosome VIII, complete chromosome sequence. Found forward in NC_001140 between 524872 and 525871 with 100% identity.

11396_g_at 25.9 A

Saccharomyces cerevisiae chromosome VIII, complete chromosome sequence. Found forward in NC_001140 between 524872 and 525871 with 100% identity.

11397_f_at 51.7 A

Saccharomyces cerevisiae chromosome VIII, complete chromosome sequence. Found forward in NC_001140 between 525872 and 526871 with 100% identity.

11398_s_at -345.4 A

Saccharomyces cerevisiae chromosome VIII, complete chromosome sequence. Found forward in NC_001140 between 526872 and 527871 with 100% identity.

11399_s_at 797.6 A

Saccharomyces cerevisiae chromosome VIII, complete chromosome sequence. Found forward in NC_001140 between 527872 and 528114 with 100% identity.

11400_s_at -27.8 A

Saccharomyces cerevisiae chromosome VIII, complete chromosome sequence. Found forward in NC_001140 between 532177 and 533176 with 100% identity.

11401_at -439.6 A

Saccharomyces cerevisiae chromosome VIII, complete chromosome sequence. Found forward in NC_001140 between 533177 and 534176 with 100% identity.

11402_at 138.3 A

Saccharomyces cerevisiae chromosome VIII, complete chromosome sequence. Found forward in NC_001140 between 534177 and 535176 with 100% identity.

11403_at 457.4 A

Saccharomyces cerevisiae chromosome VIII, complete chromosome sequence. Found forward in NC_001140 between 535177 and 536176 with 100% identity.

11404_at 140.3 A

Saccharomyces cerevisiae chromosome VIII, complete chromosome sequence. Found forward in NC_001140 between 537177 and 537754 with 100% identity.

11405_at 5938.8 P

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

NC_001140 between 543488 and 544487 with 100% identity.
11406_f_at 1033.7 M
Saccharomyces cerevisiae chromosome VIII, complete chromosome sequence. Found forward in NC_001140 between 544488 and 545487 with 100% identity.
11407_f_at 1320.9 P
Saccharomyces cerevisiae chromosome VIII, complete chromosome sequence. Found forward in NC_001140 between 546488 and 547487 with 100% identity.
11408_f_at 21988.0 P
Saccharomyces cerevisiae chromosome VIII, complete chromosome sequence. Found forward in NC_001140 between 547488 and 548487 with 100% identity.
11409_f_at 435.8 P
Saccharomyces cerevisiae chromosome VIII, complete chromosome sequence. Found forward in NC_001140 between 548488 and 549487 with 100% identity.
11410_at -5.5 A
Saccharomyces cerevisiae chromosome VIII, complete chromosome sequence. Found forward in NC_001140 between 549488 and 549898 with 100% identity.
11411_at 4.3 A
Saccharomyces cerevisiae chromosome IX, complete chromosome sequence. Found forward in NC_001141 between 9696 and 10695 with 100% identity.
11412_at -52.2 A
Saccharomyces cerevisiae chromosome IX, complete chromosome sequence. Found forward in NC_001141 between 10696 and 11695 with 100% identity.
11413_s_at 1.6 A
Saccharomyces cerevisiae chromosome IX, complete chromosome sequence. Found forward in NC_001141 between 11696 and 12695 with 100% identity.
11414_s_at -104.3 A
Saccharomyces cerevisiae chromosome IX, complete chromosome sequence. Found forward in NC_001141 between 12696 and 13695 with 100% identity.
11415_f_at -84.3 A
Saccharomyces cerevisiae chromosome IX, complete chromosome sequence. Found forward in NC_001141 between 13696 and 14695 with 100% identity.
11416_at 231.1 A
Saccharomyces cerevisiae chromosome IX, complete chromosome sequence. Found forward in NC_001141 between 106607 and 107606 with 100% identity.
11417_at 236.1 P
Saccharomyces cerevisiae chromosome IX, complete chromosome sequence. Found forward in NC_001141 between 107607 and 108606 with 100% identity.
11418_at -744.3 A
Saccharomyces cerevisiae chromosome IX, complete chromosome sequence. Found forward in NC_001141 between 108607 and 109606 with 100% identity.
11419_at 191.1 A
Saccharomyces cerevisiae chromosome IX, complete chromosome sequence. Found forward in NC_001141 between 109607 and 110606 with 100% identity.
11420_at -545.9 A
Saccharomyces cerevisiae chromosome IX, complete chromosome sequence. Found forward in NC_001141 between 110607 and 111606 with 100% identity.
11421_at 134.6 A
Saccharomyces cerevisiae chromosome IX, complete chromosome sequence. Found forward in NC_001141 between 111607 and 112606 with 100% identity.
11422_at 242.0 A
Saccharomyces cerevisiae chromosome IX, complete chromosome sequence. Found forward in NC_001141 between 112607 and 113606 with 100% identity.
11423_at -45.3 A
Saccharomyces cerevisiae chromosome IX, complete chromosome sequence. Found forward in NC_001141 between 113607 and 114606 with 100% identity.
11424_g_at 621.5 A

Saccharomyces cerevisiae chromosome IX, complete chromosome sequence. Found forward in NC_001141 between 113607 and 114606 with 100% identity.

11425_s_at 2789.2 A

Saccharomyces cerevisiae chromosome IX, complete chromosome sequence. Found forward in NC_001141 between 114607 and 115606 with 100% identity.

11426_s_at 298.3 A

Saccharomyces cerevisiae chromosome IX, complete chromosome sequence. Found forward in NC_001141 between 115607 and 116404 with 100% identity.

11427_at -768.3 A

Saccharomyces cerevisiae chromosome IX, complete chromosome sequence. Found forward in NC_001141 between 204053 and 205052 with 100% identity.

11428_at 78.1 A

Saccharomyces cerevisiae chromosome IX, complete chromosome sequence. Found forward in NC_001141 between 205053 and 206052 with 100% identity.

11429_at 494.3 A

Saccharomyces cerevisiae chromosome IX, complete chromosome sequence. Found forward in NC_001141 between 365963 and 366962 with 100% identity.

11430_at -304.0 A

Saccharomyces cerevisiae chromosome IX, complete chromosome sequence. Found forward in NC_001141 between 366963 and 367962 with 100% identity.

11431_at -427.8 A

Saccharomyces cerevisiae chromosome IX, complete chromosome sequence. Found forward in NC_001141 between 367963 and 368962 with 100% identity.

11432_at 3176.2 A

Saccharomyces cerevisiae chromosome IX, complete chromosome sequence. Found forward in NC_001141 between 368963 and 369962 with 100% identity.

11433_at -838.8 A

Saccharomyces cerevisiae chromosome IX, complete chromosome sequence. Found forward in NC_001141 between 369963 and 370962 with 100% identity.

11434_g_at -51.7 A

Saccharomyces cerevisiae chromosome IX, complete chromosome sequence. Found forward in NC_001141 between 369963 and 370962 with 100% identity.

11435_s_at 218.6 A

Saccharomyces cerevisiae chromosome IX, complete chromosome sequence. Found forward in NC_001141 between 370963 and 371962 with 100% identity.

11436_s_at -79.4 A

Saccharomyces cerevisiae chromosome IX, complete chromosome sequence. Found forward in NC_001141 between 371963 and 372495 with 100% identity.